Supplementary Materials

Table S1. Identification of the selected LAB strains

Isolate	Identification result	BLAST result	Accession number	Similarity (%)	Length of obtained sequencing read
FB1	*Enterococcus faecium*	*E. faecium* strain K6	KY490549.1	99	1,424/1,425
FB2	*Ligilactobacillus animalis*	*L. animalis* strain: JCM 8692	AB911530.1	99	1,382/1,383
Pom1	*Lactobacillus* sp.	*Lactobacillus* sp. strain CC-MHH1034	MH379635.1	99	1,375/1,381
Pom2	*Lactobacillus* sp.	*Lactobacillus* sp. strain CC-MHH1034	MH379635.1	99	1,372/1,376
Pom4	*Enterococcus hirae*	*E. hirae* strain NCTC12368	LR134297.1	99	1,422/1,427
Pom5	*Limosilactobacillus fermentum*	*Lactobacillus salivarius* strain HBUAS54044	MH473275.1	99	1,380/1,381
Pom9	*Lactobacillus* sp.	*Lactobacillus* sp. strain CC-MHH1034	MH3796	99	1,370/1,376
Chi3	*E. hirae*	*E. hirae* strain NCTC12368	LR134297.1	99	1,383/1,385
Chi4	*E. faecium*	*E. faecium* strain K6	KY490549.1	100	1,437/1,437
Chi5	*E. faecium*	*E. faecium* strain HCD4-5	MH111453.1	100	1,438/1,438
Chi6	*Enterococcus avium*	*E. avium* strain HCD9-2	MH111483.1	99	1,420/1,421
Chi7	*Pediococcus pentosaceus*	*P. pentosaceus* strain HBUAS53395	MK402182.1	99	1,396/1,398
Chi8	*P. pentosaceus*	*P. pentosaceus* strain HBUAS53395	MK402182.1	99	1,414/1,416
MD1	*E. hirae*	*E. hirae* strain: ZZU A1	LC119115.1	99	1,413/1,418
MD2	*Streptococcus lutetiensis*	*S. lutetiensis* strain HCD23-2	MH111574.1	99	1,425/1,427
MD3	*Limosilactobacillus fermentum*	*Lactobacillus fermentum* strain YL-11	CP034193.1	99	1,078/1,081
MD12	*Limosilactobacillus fermentum*	*Lactobacillus fermentum* strain LMEM 5	MK418591.1	99	1,449/1,451
MD13	*Enterococcus faecalis*	*E. faecalis* strain LMEM 50	MK418586.1	99	1,029/1,030
Shi1	*Limosilactobacillus fermentum*	*Lactobacillus fermentum* strain YL-11	CP034193.1	99	1,426/1,427
PD3	*E. faecalis*	*E. faecalis* strain ACD47-2	MH127511.1	100	1,424/1,424

LAB, lactic acid bacteria; BLAST, basic local alignment search tool.

Table S2. **List of antimicrobial resistance genes and their locations in *Enterococcus hirae* Pom4 and *Ligilactobacillus animalis* FB2 genome**

Probiotic strain	RGI criterion	ARO term	Detection criterion	AMR gene family	Drug class	Resistance mechanism	Identity of matching region (%)	Length of reference sequence (%)
E. hirae Pom4	Perfect	AAC(6')-Ian	Protein homolog model	AAC(6')	Aminoglycoside antibiotic	Antibiotic inactivation	100	100
	Strict	tet(45)	Protein homolog model	Major facilitator superfamily (MFS) antibiotic efflux pump	Tetracycline antibiotic	Antibiotic efflux	76.71	93.45
	Strict	tetM	Protein homolog model	Tetracycline-resistant ribosomal protection protein	Tetracycline antibiotic	Antibiotic target protection	94.52	100
L. animalis FB2	Strict	tetM	Protein homolog model	Tetracycline-resistant ribosomal protection protein	Tetracycline antibiotic	Antibiotic target protection	98.28	100.3

RGI, resistance gene identifier; ARO, antibiotic resistance ontology; AMR, antimicrobial resistance.

Table S3. **Plasmid information of *Enterococcus hirae* Pom4 and *Pediococcus pentosaceus* Chi8**

Probiotic strain	Plasmid	Contig	Plasmid	
			Identity (%)	Plasmid replicon type
E. hirae Pom4	Plasmid 1	NODE_19_length_21758_cov_274.41128	100	repUS43 (Rep_trans)
	Plasmid 2	NODE_23_length_7056_cov_287.63347	100	Rep2 (Inc18)
	Plasmid 3	NODE_19_length_21758_cov_274.411282	98.27	repUS15 (RepA_N)
	Plasmid 4	NODE_19_length_21758_cov_274.411282	99.75	repUS12 (Rep1)
P. pentosaceus Chi8	Plasmid 1	NODE_6_length_10603_cov_2129.251663	99.78	Rep28 (Rep3)

Table S4. Prophage information of the selected LAB strains

Probiotic strain	Region	Region length (kb)	Completeness	Total CDS	Most common phage	GC content (%)
Enterococcus hirae Pom4	1	54	Intact	67	PHAGE_Bacill_phBC6A52_NC_004821(11)	34.82
Limosilactobacillus fermentum Pom5	1	8.4	Incomplete	10	PHAGE_Nodula_vB_NspS_kac65v151_NC_048756(2)	51.18
	2	10.5	Incomplete	11	PHAGE_Lactob_Sha1_NC_019489(2)	44.22
	3	9.6	Incomplete	10	PHAGE_Lactob_CL1_NC_028888(2)	51.75
Pediococcus pentosaceus Chi8	1	52.8	Intact	56	PHAGE_Lactob_Sha1_NC_019489(14)	36.56
	2	41.6	Incomplete	13	PHAGE_Bacill_G_NC_023719(2)	36.00
	3	15.1	Incomplete	22	PHAGE_Entero_phiFL3A_NC_013648(2)	33.43
	4	10.5	Incomplete	13	PHAGE_Lactob_BH1_NC_048737(1)	36.04
Ligilactobacillus animalis FB2	1	10.4	Incomplete	11	PHAGE_Klebsi_ST147_VIM1phi7.1_NC_049451(1)	42.77
	2	7.9	Incomplete	8	PHAGE_Klebsi_ST147_VIM1phi7.1_NC_049451(1)	41.03
	3	22.7	Questionable	28	PHAGE_Geobac_E2_NC_009552(4)	41.32
	4	9	Incomplete	8	PHAGE_Synech_S_SSM4_NC_020875(1)	43.27
	5	8.2	Incomplete	8	PHAGE_Bacill_G_NC_023719(2	41.54
	6	8	Incomplete	8	PHAGE_Bacill_G_NC_023719(2)	42.46
	7	8.7	Incomplete	7	PHAGE_Bacill_G_NC_023719(3)	41.79
	8	6.9	Incomplete	7	PHAGE_Entero_phiEF24C_NC_009904(4)	40.85

LAB, lactic acid bacteria; CDS, coding sequence; GC, guanine-cytosine.

Table S5. Genes associated with stress responses

Stress response protein			Function	Probiotic strain			
Protein class	Protein subsystem	Protein		*Enterococcus hirae* Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
Cell envelope, capsule and slime layer	Gram-positive (monoderm) cell wall components	D-alanylation of teichoic acid	D-alanyl carrier protein	Poly(glycerophosphate_chain)_D-alanine_transfer_protein_DltD	Acyl_carrier_protein		Undecaprenyl-diphosphatase_(EC_3.6.1.27)
				D-alanine--poly(phosphoribitol)_ligase_subunit_1_(EC_6.1.1.13)	D-alanine--poly(phosphoribitol)_ligase_ACP_subunit_(EC_6.1.1.13)		UDP-galactopyranose_mutase_(EC_5.4.99.9)
				D-alanine--poly(phosphoribitol)_ligase_ACP_subunit_(EC_6.1.1.13)	D-alanine--poly(phosphoribitol)_ligase_subunit_1_(EC_6.1.1.13)		
				Acyl_carrier_protein	D-alanyl_transfer_protein_DltB		
				Acyl_carrier_protein	Component_involved_in_D-alanylation_of_teichoic_acids		
				D-alanyl_transfer_protein_DltB	Poly(glycerophosphate_chain)_D-alanine_transfer_protein_DltD		
		dTDP-rhamnose synthesis	EPS-producing		dTDP-glucose_4,6-dehydratase_(EC_4.2.1.46)		
					Cell envelope-associated LytR-CpsA-Psr transcriptional attenuators		
		Cell envelope-associated LytR-CpsA-Psr transcriptional attenuators	Bacterial cell envelope maintenance			Cell_envelope-associated_transcriptional_attenuator_LytR-CpsA-Psr,_subfamily_F2	
						Cell_envelope-associated_transcriptional_attenuator_LytR-CpsA-Psr,_subfamily_F2	
		Wall polysaccharide pyruvylation	Peptidoglycan-associated polymer biosynthesis		Polysaccharide_pyruvyl_transferase_CsaB	Polysaccharide_pyruvyl_transferase_CsaB	
Cell cycle, cell division and death	Programmed cell death and toxin-antitoxin systems	YoeB-YefM toxin-antitoxin system	Regulating cell growth and death under various stress conditions		YoeB_toxin_protein		

Table S5. Genes associated with stress responses (continued)

Stress response protein			Function	Probiotic strain			
Protein class	Protein subsystem	Protein		*Enterococcus hirae* Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
		Cell cycle, Cell division and death	Regulation of cell growth and death			MazEF toxin-antitoxing (programmed cell death) system	
DNA processing	DNA repair	DNA repair			DNA_repair_protein_RecN	DNA_repair_protein_RecN	
					DNA_repair_protein_RadA	DNA_repair_protein_RadA	
						DNA_polymerase_IV_(EC_2.7.7.7)	
						DNA_repair_exonuclease_family_protein_YhaO	
					Exodeoxyribonuclease_VII_large_subunit_(EC_3.1.11.6)	Exodeoxyribonuclease_VII_large_subunit_(EC_3.1.11.6)	
					Exodeoxyribonuclease_III_(EC_3.1.11.2)		
					Exodeoxyribonuclease_VII_small_subunit_(EC_3.1.11.6)		
						Exodeoxyribonuclease_VII_small_subunit_(EC_3.1.11.6)	
						Endonuclease_IV_(EC_3.1.21.2)	
						Exodeoxyribonuclease_III_(EC_3.1.11.2)	
						DinG_family_ATP-dependent_helicase_YoaA	DinG_family_ATP-dependent_helicase_YoaA
					Methylated-DNA--protein-cysteine_methyltransferase_(EC_2.1.1.63)	Methylated-DNA--protein-cysteine_methyltransferase_(EC_2.1.1.63)	
					Single-stranded_DNA-binding_protein	Single-stranded_DNA-binding_protein	
					SOS-response_repressor_and_protease_LexA_(EC_3.4.21.88)	SOS-response_repressor_and_protease_LexA_(EC_3.4.21.88)	

Table S5. Genes associated with stress responses (continued)

Stress response protein			Function	Probiotic strain			
Protein class	Protein subsystem	Protein		*Enterococcus hirae* Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
		DNA repair, bacterial RecBCD pathway	Repair of double-stranded DNA breaks by homologous recombination	ATP-dependent_helicase/nuclease_AddAB,_subunit_A	ATP-dependent_helicase/nuclease_AddAB,_subunit_A	ATP-dependent_helicase/nuclease_AddAB,_subunit_A	ATP-dependent_helicase/nuclease_AddAB,_subunit_A
				ATP-dependent_helicase/nuclease_AddAB,_subunit_B	ATP-dependent_helicase/nuclease_AddAB,_subunit_B		ATP-dependent_helicase/nuclease_AddAB,_subunit_B
				RecD-like_DNA_helicase_YrrC	RecD-like_DNA_helicase_YrrC	RecD-like_DNA_helicase_YrrC	RecD-like_DNA_helicase_YrrC
		DNA repair, bacterial SbcCD exonuclease	Cleavage of DNA hairpin structures		Exonuclease_SbcC		Exonuclease_SbcC
					Exonuclease_SbcD		Exonuclease_SbcD
		DNA repair, bacterial RecFOR pathway	DNA double-strand-break repair through ESDSA			ATP-dependent_DNA_helicase_RecQ	
					DNA_recombination_and_repair_protein_RecF	DNA_recombination_and_repair_protein_RecF	
					DNA_recombination_and_repair_protein_RecO	DNA_recombination_and_repair_protein_RecO	
					Nucleoid-associated_protein_YaaK	Nucleoid-associated_protein_YaaK	
					RecA_protein	RecA_protein	RecA_protein
					Regulatory_protein_RecX	Regulatory_protein_RecX	Regulatory_protein_RecX
					Recombination_protein_RecR	Recombination_protein_RecR	
					Single-stranded-DNA-specific_exonuclease_RecJ	Single-stranded-DNA-specific_exonuclease_RecJ	
					Single-stranded_DNA-binding_protein	Single-stranded_DNA-binding_protein	
		DNA repair, bacterial UvrD and related helicases	DNA repair, replication, and recombination		ATP-dependent_DNA_helicase_UvrD/PcrA_(EC_3.6.4.12)	ATP-dependent_DNA_helicase_UvrD/PcrA_(EC_3.6.4.12)	ATP-dependent_DNA_helicase_UvrD/PcrA_(EC_3.6.4.12)
		DNA repair, UvrABC system	Nucleotide excision repair		Excinuclease_ABC_subunit_A	Excinuclease_ABC_subunit_A	Excinuclease_ABC_subunit_A
					Excinuclease_ABC_subunit_B	Excinuclease_ABC_subunit_B	Excinuclease_ABC_subunit_B
					Excinuclease_ABC_subunit_C	Excinuclease_ABC_subunit_C	Excinuclease_ABC_subunit_C

Table S5. **Genes associated with stress responses (continued)**

Stress response protein			Function	Probiotic strain			
Protein class	Protein subsystem	Protein		*Enterococcus hirae* Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
		DNA repair, bacterial MutHLS system	Recognition and repair of mispaired bases		DNA_mismatch_repair_protein_MutS Recombination_inhibitory_protein_MutS2 DNA_mismatch_repair_protein_MutL	DNA_mismatch_repair_protein_MutS Recombination_inhibitory_protein_MutS2 DNA_mismatch_repair_protein_MutL	DNA_mismatch_repair_protein_MutS Recombination_inhibitory_protein_MutS2
	DNA protection	ImpB/MucB/SamB family protein	Ultraviolet (UV) protection	ImpB/MucB/SamB family protein			
Fatty acids, lipids, and isoprenoids	Fatty acids	Putative oxidase COG2907	Synthesis of CFAs, salt-stress adaptation		Oxidoreductase, short-chain_dehydrogenase/reductase_family_(EC_1.1.1.-) Cyclopropane-fatty-acyl-phospholipid_synthase_(EC_2.1.1.79)		
Stress response	Stress response	Universal stress protein family	Cellular responses adaptation to stationary phase		Universal_stress_protein_family	Universal_stress_protein_family	Universal stress protein family
		Glutathione biosynthesis and gamma-glutamyl cycle		Glutaredoxin-like_protein_NrdH,_required_for_reduction_of_Ribonucleotide_reductase_class_Ib Glutathione_reductase_(EC_1.8.1.7)	Glutamate--cysteine_ligase_(EC_6.3.2.2)		Glutamate--cysteine_ligase_(EC_6.3.2.2)
		Hfl operon	GTPase, modulator of FtsH protease				Ribosome_LSU-associated_GTP-binding_protein_HflX
	Heat/cold shock	Heat shock dnaK gene cluster extended, cluster containing glutathione synthetase	Response to sudden increases of environmental temperature by assisting protein folding		16S_rRNA_(cytidine(1402)-2'-O)-methyltransferase_(EC_2.1.1.198) 16S_rRNA_(uracil(1498)-N(3))-methyltransferase_(EC_2.1.1.193)	16S_rRNA_(cytidine(1402)-2'-O)-methyltransferase_(EC_2.1.1.198) 16S_rRNA_(uracil(1498)-N(3))-methyltransferase_(EC_2.1.1.193) Chaperone_protein_DnaJ	16S_rRNA_(cytidine(1402)-2'-O)-methyltransferase_(EC_2.1.1.198) 16S_rRNA_(uracil(1498)-N(3))-methyltransferase_(EC_2.1.1.193) Chaperone_protein_DnaJ

Table S5. Genes associated with stress responses (continued)

Stress response protein			Function	Probiotic strain			
Protein class	Protein subsystem	Protein		*Enterococcus hirae* Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
						Chaperone_protein_DnaK	Chaperone_protein_DnaK
						DNA_replication_intiation_control_protein_YabA	DNA_replication_intiation_control_protein_YabA
						Heat_shock_protein_10_kDa_family_chaperone_GroES	
						Heat_shock_protein_60_kDa_family_chaperone_GroEL	
						Heat-inducible_transcription_repressor_HrcA	
						Heat_shock_protein_GrpE	Heat-inducible_transcription_repressor_HrcA
						Nucleoside_5-triphosphatase_RdgB_(dHAPTP,_dITP,_XTP-specific)_(EC_3.6.1.66)	Nucleoside_5-triphosphatase_RdgB_(dHAPTP,_dITP,_XTP-specific)_(EC_3.6.1.66)
						Ribosomal_protein_L11_methyltransferase	Ribosomal_protein_L11_methyltransferase
						tmRNA-binding_protein_SmpB	tmRNA-binding_protein_SmpB
						Translation_elongation_factor_LepA	Translation_elongation_factor_LepA
					Putative_pre-16S_rRNA_nuclease_YqgF		Putative_pre-16S_rRNA_nuclease_YqgF
		Cold_shock_protein_of_CSP_family	Response to rapid temperature downshift		Cold shock protein of CSP family	Cold_shock_protein_of_CSP_family	Cold shock proteins of CSP family
	Osmotic stress	Choline uptake and conversion to betaine clusters (osmoregulation)	Choline uptake		ABC_transporter,_permease_protein_(cluster_13,_osmolytes)		
				Betaine_ABC_transporter,_ATP-binding_protein_BusAA			
				Betaine_ABC_transporter,_permease_protein_BusAB.1			

Table S5. Genes associated with stress responses (continued)

Stress response protein			Function	Probiotic strain			
Protein class	Protein subsystem	Protein		*Enterococcus hirae* Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
				Betaine_ABC_transporter,_substrate-binding_protein_BusAB.2			
						Betaine/carnitine/choline_transporter_(BCCT)_family	
						Choline_ABC_transport_system,_permease_protein_OpuBB	
						Choline_ABC_transport_system,_choline-binding_protein_OpuBC	
						Choline_ABC_transport_system,_permease_protein_OpuBD	
						Choline_ABC_transport_system,_ATP-binding_protein_OpuBA	
				Glycine_betaine_ABC_transport_system,_ATP-binding_protein_OpuAA_(EC_3.6.3.32)		Glycine_betaine_ABC_transport_system,_ATP-binding_protein_OpuAA_(EC_3.6.3.32)	Glycine_betaine_ABC_transport_system,_ATP-binding_protein_OpuAA_(EC_3.6.3.32)
				Glycine_betaine_ABC_transport_system,_permease_protein_OpuAB		Glycine_betaine_ABC_transport_system,_permease_protein_OpuAB	Glycine_betaine_ABC_transport_system,_permease_protein_OpuAB
				Glycine_betaine_ABC_transport_system,_glycine_betaine-binding_protein_OpuAC		Glycine_betaine_ABC_transport_system,_glycine_betaine-binding_protein_OpuAC	Glycine_betaine_ABC_transport_system,_glycine_betaine-binding_protein_OpuAC
		Osmoregulation	Osmotic balance		Glycerol_uptake_facilitator_protein	Glycerol_uptake_facilitator_protein	Glycerol_uptake_facilitator_protein
						Aquaporin_Z	
	Acid/ bile resistance	Amino acid permease	Acquisition of exogenous amino acid	Amino acid permease family protein			
				Uncharacterized amino acid permease, GabP family	Uncharacterized amino acid permease, GabP family	Uncharacterized amino acid permease, GabP family	Uncharacterized amino acid permease, GabP family

Table S5. **Genes associated with stress responses (continued)**

Stress response protein			Function	Probiotic strain			
Protein class	Protein subsystem	Protein		*Enterococcus hirae* Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
				Uncharacterized amino acid permease YdaO	Uncharacterized amino acid permease YdaO	Uncharacterized amino acid permease YdaO	Uncharacterized amino acid permease YdaO
							Uncharacterized GabP-family amino acid permease LBA0729
							Uncharacterized GabP-family amino acid permease LBA0995
		Alcohol dehydrogenase	ETC	Alcohol dehydrogenase (EC 1.1.1.1)	Alcohol dehydrogenase (EC 1.1.1.1)	Alcohol dehydrogenase (EC 1.1.1.1)	Alcohol dehydrogenase (EC 1.1.1.1)
				Acetaldehyde dehydrogenase (EC 1.2.1.10) / Alcohol dehydrogenase (EC 1.1.1.1)	Acetaldehyde dehydrogenase (EC 1.2.1.10) / Alcohol dehydrogenase (EC 1.1.1.1)		Acetaldehyde dehydrogenase (EC 1.2.1.10) / Alcohol dehydrogenase (EC 1.1.1.1)
						Aryl-alcohol dehydrogenase related enzyme	
					Benzyl alcohol dehydrogenase		
				Zinc-type alcohol dehydrogenase-like protein		Zinc-type alcohol dehydrogenase-like protein	
				Bifunctional protein: zinc-containing alcohol dehydrogenase; quinone oxidoreductase (NADPH:quinone reductase) (EC 1.1.1.-); Similar to arginate lyase			
		Lactate dehydrogenase	Restores NAD+/NADH balance		D-lactate dehydrogenase (EC 1.1.1.28)	D-lactate dehydrogenase (EC 1.1.1.28)	D-lactate dehydrogenase (EC 1.1.1.28)
				L-lactate dehydrogenase (EC 1.1.1.27)	L-lactate dehydrogenase (EC 1.1.1.27)	L-lactate dehydrogenase (EC 1.1.1.27)	L-lactate dehydrogenase (EC 1.1.1.27)
					Predicted L-lactate dehydrogenase, Fe-S oxidoreductase subunit YkgE		Predicted L-lactate dehydrogenase, Fe-S oxidoreductase subunit YkgE

Table S5. Genes associated with stress responses (continued)

Stress response protein			Function	Probiotic strain			
Protein class	Protein subsystem	Protein		*Enterococcus hirae* Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
					Predicted L-lactate dehydrogenase, Iron-sulfur cluster-binding subunit YkgF		Predicted L-lactate dehydrogenase, Iron-sulfur cluster-binding subunit YkgF
					Predicted L-lactate dehydrogenase, hypothetical protein subunit YkgG		Predicted L-lactate dehydrogenase, hypothetical protein subunit YkgG
		Alanine dehydrogenase	Oxidative deamination reaction			Alanine dehydrogenase (EC 1.4.1.1)	
		F0F1-type ATP synthase	Proton translocation		ATP_synthase_F0_sector_subunit_a_(EC_3.6.3.14)	ATP_synthase_F0_sector_subunit_a_(EC_3.6.3.14)	ATP_synthase_F0_sector_subunit_a_(EC_3.6.3.14)
					ATP_synthase_F0_sector_subunit_b_(EC_3.6.3.14)	ATP_synthase_F0_sector_subunit_b_(EC_3.6.3.14)	ATP_synthase_F0_sector_subunit_b_(EC_3.6.3.14)
					ATP_synthase_F0_sector_subunit_c_(EC_3.6.3.14)	ATP_synthase_F0_sector_subunit_c_(EC_3.6.3.14)	ATP_synthase_F0_sector_subunit_c_(EC_3.6.3.14)
					ATP_synthase_alpha_chain_(EC_3.6.3.14)	ATP_synthase_alpha_chain_(EC_3.6.3.14)	ATP_synthase_alpha_chain_(EC_3.6.3.14)
					ATP_synthase_beta_chain_(EC_3.6.3.14)	ATP_synthase_beta_chain_(EC_3.6.3.14)	ATP_synthase_beta_chain_(EC_3.6.3.14)
					ATP_synthase_delta_chain_(EC_3.6.3.14)	ATP_synthase_delta_chain_(EC_3.6.3.14)	ATP_synthase_delta_chain_(EC_3.6.3.14)
					ATP_synthase_epsilon_chain_(EC_3.6.3.14)	ATP_synthase_epsilon_chain_(EC_3.6.3.14)	ATP_synthase_epsilon_chain_(EC_3.6.3.14)
					ATP_synthase_gamma_chain_(EC_3.6.3.14)	ATP_synthase_gamma_chain_(EC_3.6.3.14)	ATP_synthase_gamma_chain_(EC_3.6.3.14)
		DegP protein	Protease and chaperone activities	Serine protease, DegP/HtrA, do-like (EC 3.4.21.-)	Serine protease, DegP/HtrA, do-like (EC 3.4.21.-)	Serine protease, DegP/HtrA, do-like (EC 3.4.21.-)	
		Agrinine/ormithine antiporter	Import of arginine and export of ornithine	Arginine/ornithine antiporter ArcD	Arginine/ornithine antiporter ArcD	Arginine/ornithine antiporter ArcD	
		Glutaminase	Conversion of glutamine to glutamate	Glutaminase (EC 3.5.1.2)			
		Glutamate decarboxylase	Conversion of glutamate to gamma-amino butyric acid		Glutamate decarboxylase (EC 4.1.1.15)		

Table S5. Genes associated with stress responses (continued)

Stress response protein			Function	Probiotic strain			
Protein class	Protein subsystem	Protein		*Enterococcus hirae* Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
		Na+/H+ antiporter	Proton transporter	Na+/H+ antiporter	Na(+)/H(+) antiporter	Na+/H+ antiporter	Na(+)/H(+) antiporter
				Na+/H+ antiporter NapA	Na+/H+ antiporter NapA	Na+/H+ antiporter NapA	Na+/H+ antiporter NapA
		Bile hydrolysis	Catalysis the hydrolysis of the amide bond in conjugated bile acids		Bile hydrolysis	Choloylglycine_hydrolase_(EC_3.5.1.24)	Choloylglycine_hydrolase_(EC_3.5.1.24)

Table S6. Genes associated with adhesion and aggregation

Stress response protein			Function	Probiotic strain			
Protein class	Protein subsystem	Protein		*Enterococcus hirae* Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
Adhesion and aggregation	Adhesion	Sortase A, LPXTG specific	Binding to mucus	Sortase A, LPXTG specific	Sortase A, LPXTG specific	Sortase A, LPXTG specific	Sortase A, LPXTG specific
		Fibronectin/fibrinogen-binding protein	Facilitating binding to epithelial cells/ extracellular matrix	Fibronectin/fibrinogen-binding protein	Fibronectin/fibrinogen-binding protein	Fibronectin/fibrinogen-binding protein	Fibronectin/fibrinogen-binding protein
		Enolase (EC 4.2.1.11)	Binding to plasma components	Enolase (EC 4.2.1.11)	Enolase (EC 4.2.1.11)	Enolase (EC 4.2.1.11)	Enolase (EC 4.2.1.11)
		Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1)	Fibronectin binding protein	Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1)	Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1)	Pyruvate dehydrogenase E1 component subunit beta	Pyruvate dehydrogenase E1 component beta subunit (EC 1.2.4.1)
		Pyruvate dehydrogenase E1 component subunit alpha		Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)	Pyruvate dehydrogenase E1 component subunit alpha	Pyruvate dehydrogenase E1 component alpha subunit (EC 1.2.4.1)
		Predicted cell-wall-anchored protein SasA (LPXTG motif)	LPXTG-anchored cell wall proteins			Predicted cell-wall-anchored protein SasA (LPXTG motif)	
		Internalin, putative (LPXTG motif)	Adhesion to mucus			Internalin, putative (LPXTG motif)	
		Glyceraldehyde-3-phosphate dehydrogenase	Adhesion to plasma components		NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	Glyceraldehyde-3-phosphate dehydrogenase	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
	Aggregra-tion	Aggregation substance precursor	Increased bacterial adherence	Aggregation promoting factor	Aggregation promoting factor	Aggregation promoting factor	Aggregation promoting factor
		LysM peptidoglycan-binding domain-containing protein	Cell wall binding domain		Peptidoglycan-binding LysM	LysM domain	
		Translation elongation factor Tu GroEL chaperon	Adhesion to host extracellular matrix components	Translation elongation factor Tu	Translation elongation factor Tu	Translation elongation factor Tu	Translation elongation factor Tu
		Peptidyl-propyl cis-trans isomerase (EC 5.2.1.8)	Pathogen aggregation			Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)	
	Exopolysaccharide production	Exopolysaccharide biosynthesis	EPS production	Tyrosine-protein kinase EpsD (EC 2.7.10.2)	Tyrosine-protein kinase transmembrane modulator EpsC	Tyrosine-protein kinase transmembrane modulator EpsC	

Table S6. **Genes associated with adhesion and aggregation (continued)**

Stress response protein			Function	Probiotic strain			
Protein class	Protein subsystem	Protein		*Enterococcus hirae* Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
				Tyrosine-protein kinase transmembrane modulator EpsC	Tyrosine-protein kinase EpsD (EC 2.7.10.2)	Tyrosine-protein kinase EpsD (EC 2.7.10.2)	
				Undecaprenyl-phosphate galactosephosphotransferase (EC 2.7.8.6)			
				Lipopolysaccharide cholinephosphotransferase LicD3 (EC 2.7.8.-)			
		UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	Synthesis of UDP-glucose		UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)
		Glycosylphosphotransferase	Synthesis of complex carbohydrates	Glycosyltransferase	Glycosyltransferase	Glycosyltransferase	

Table S7. Genes associated with secondary metabolites (vitamins and essential amino acids)

Essential amino acid/ cofactor	Pathway	Probiotic strain			
		Enterococcus hirae Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
Arginine	Arginine biosynthesis		Argininosuccinate_synthase_(EC_6.3.4.5) N-acetyl-gamma-glutamyl-phosphate_reductase_(EC_1.2.1.38) N-acetylglutamate_synthase_(EC_2.3.1.1) Argininosuccinate_lyase_(EC_4.3.2.1) N-acetylglutamate_kinase_(EC_2.7.2.8) N-acetylornithine_aminotransferase_(EC_2.6.1.11) Ornithine_carbamoyltransferase_(EC_2.1.3.3) Glutamate_N-acetyltransferase_(EC_2.3.1.35)		
Histidine	Histidine biosynthesis		Histidinol-phosphate_aminotransferase_(EC_2.6.1.9) Imidazole_glycerol_phosphate_synthase_cyclase_subunit Phosphoribosylformimino-5-aminoimidazole_carboxamide_ribotide_isomerase_(EC_5.3.1.16) Imidazole_glycerol_phosphate_synthase_amidotransferase_subunit_HisH ATP_phosphoribosyltransferase_(EC_2.4.2.17)_=>_HisGs ATP_phosphoribosyltransferase_regulatory_subunit_(EC_2.4.2.17) Adenylosuccinate_synthetase_(EC_6.3.4.4) Histidinol_dehydrogenase_(EC_1.1.1.23) Histidinol-phosphatase_(EC_3.1.3.15) Imidazole_glycerol_phosphate_synthase_cyclase_subunit		

Table S7. Genes associated with secondary metabolites (vitamins and essential amino acids) (continued)

Essential amino acid/ cofactor	Pathway	Probiotic strain			
		Enterococcus hirae Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
			Imidazole_glycerol_phosphate_synthase_amidotransferase_subunit_HisH Phosphoribosyl-ATP_pyrophosphatase_(EC_3.6.1.31) Phosphoribosyl-AMP_cyclohydrolase_(EC_3.5.4.19) Imidazoleglycerol-phosphate_dehydratase_(EC_4.2.1.19) Imidazole_glycerol_phosphate_synthase_cyclase_subunit		
Lysine	Lysine DAP biosynthetic pathway		4-hydroxy-tetrahydrodipicolinate_synthase_(EC_4.3.3.7) N-acetyl-L,L-diaminopimelate_deacetylase_(EC_3.5.1.47) Diaminopimelate_decarboxylase_(EC_4.1.1.20) Aspartate-semialdehyde_dehydrogenase_(EC_1.2.1.11) FIG138056:_a_glutathione-dependent_thiol_reductase 4-hydroxy-tetrahydrodipicolinate_reductase_(EC_1.17.1.8) 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate_N-acetyltransferase_(EC_2.3.1.89) Aspartokinase_(EC_2.7.2.4) Diaminopimelate_epimerase_(EC_5.1.1.7)		4-hydroxy-tetrahydrodipicolinate_synthase_(EC_4.3.3.7) N-acetyl-L,L-diaminopimelate_deacetylase_(EC_3.5.1.47) Diaminopimelate_decarboxylase_(EC_4.1.1.20) Aspartate-semialdehyde_dehydrogenase_(EC_1.2.1.11) FIG138056:_a_glutathione-dependent_thiol_reductase 4-hydroxy-tetrahydrodipicolinate_reductase_(EC_1.17.1.8) 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate_N-acetyltransferase_(EC_2.3.1.89) Aspartokinase_(EC_2.7.2.4) Diaminopimelate_epimerase_(EC_5.1.1.7)
	Diaminopimelate synthesis				Diaminopimelate_decarboxylase_(EC_4.1.1.20) Aspartokinase_(EC_2.7.2.4) 4-hydroxy-tetrahydrodipicolinate_reductase_(EC_1.17.1.8)

Table S7. Genes associated with secondary metabolites (vitamins and essential amino acids) (continued)

Essential amino acid/ cofactor	Pathway	Probiotic strain			
		Enterococcus hirae Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
					N-acetyl-L,L-diaminopimelate_ deacetylase_(EC_3.5.1.47) Diaminopimelate_ epimerase_(EC_5.1.1.7) Aspartate-semialdehyde_ dehydrogenase_ (EC_1.2.1.11) 4-hydroxy-tetrahydrodipicolinate_ synthase_(EC_4.3.3.7) 2,3,4,5-tetrahydropyridine-2,6-dicarboxylate_N-acetyltransferase_ (EC_2.3.1.89)
Phenylalanine	Phenylalanine and tyrosine synthesis 1		Biosynthetic_Aromatic_ amino_acid_aminotransferase_alpha_(EC_2.6.1.57) Prephenate_dehydrogenase _(EC_1.3.1.12) Chorismate_mutase_I_ (EC_5.4.99.5)		
Theronine	Aspartate to threonine Module		Threonine_synthase_ (EC_4.2.3.1) Homoserine_kinase_ (EC_2.7.1.39) Homoserine_ dehydrogenase_ (EC_1.1.1.3) Aspartokinase_ (EC_2.7.2.4) Homoserine_ dehydrogenase_ (EC_1.1.1.3) Aspartate-semialdehyde_ dehydrogenase_ (EC_1.2.1.11)		
Tryptophane					
Valine					
Isoleucine					
Leucine					
Methionine					
Riboflavin	Riboflavin, FMN and FAD metabolism with fusion events		Riboflavin_kinase_ (EC_2.7.1.26) Substrate-specific_ component_RibU_of_ riboflavin_ECF_transporter	Riboflavin_kinase_ (EC_2.7.1.26) Substrate-specific_ component_RibU_of_ riboflavin_ECF_transporter	Riboflavin_kinase_ (EC_2.7.1.26) Substrate-specific_ component_RibU_of_ riboflavin_ECF_transporter

Table S7. Genes associated with secondary metabolites (vitamins and essential amino acids) (continued)

Essential amino acid/ cofactor	Pathway	Probiotic strain			
		Enterococcus hirae Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
			tRNA_pseudouridine(55)_synthase_(EC_5.4.99.25)	tRNA_pseudouridine(55)_synthase_(EC_5.4.99.25)	tRNA_pseudouridine(55)_synthase_(EC_5.4.99.25)
			Diaminohydroxyphosphoribosylaminopyrimidine_deaminase_(EC_3.5.4.26)	Diaminohydroxyphosphoribosylaminopyrimidine_deaminase_(EC_3.5.4.26)	
			3,4-dihydroxy-2-butanone_4-phosphate_synthase_(EC_4.1.99.12)	3,4-dihydroxy-2-butanone_4-phosphate_synthase_(EC_4.1.99.12)	
			ADP-ribose_pyrophosphatase_of_COG1058_family_(EC_3.6.1.13)	ADP-ribose_pyrophosphatase_of_COG1058_family_(EC_3.6.1.13)	
			FMN_adenylyltransferase_(EC_2.7.7.2)	FMN_adenylyltransferase_(EC_2.7.7.2)	FMN_adenylyltransferase_(EC_2.7.7.2)
			5-amino-6-(5-phosphoribosylamino)uracil_reductase_(EC_1.1.1.193)	5-amino-6-(5-phosphoribosylamino)uracil_reductase_(EC_1.1.1.193)	
			Riboflavin_synthase_eubacterial/eukaryotic_(EC_2.5.1.9)	Riboflavin_synthase_eubacterial/eukaryotic_(EC_2.5.1.9)	
			GTP_cyclohydrolase_II_(EC_3.5.4.25)	GTP_cyclohydrolase_II_(EC_3.5.4.25)	
			6,7-dimethyl-8-ribityllumazine_synthase_(EC_2.5.1.78)	6,7-dimethyl-8-ribityllumazine_synthase_(EC_2.5.1.78)	
Biotin	Biotin synthesis and utilization		Biotin_carboxylase_of_acetyl-CoA_carboxylase_(EC_6.3.4.14)	Biotin_carboxylase_of_acetyl-CoA_carboxylase_(EC_6.3.4.14)	
			Substrate-specific_component_BioY_of_biotin_ECF_transporter	Substrate-specific_component_BioY_of_biotin_ECF_transporter	
			Biotin--protein_ligase_(EC_6.3.4.9)(EC_6.3.4.10)(EC_6.3.4.11)(EC_6.3.4.15)	Biotin--protein_ligase_(EC_6.3.4.9)(EC_6.3.4.10)(EC_6.3.4.11)(EC_6.3.4.15)	
			Biotin_operon_repressor	Biotin_operon_repressor	
			3-ketoacyl-CoA_thiolase_(EC_2.3.1.16)		
Pyridoxin	Pyridoxin (Vitamin B6) biosynthesis		NAD-dependent_glyceraldehyde-3-phosphate_dehydrogenase_(EC_1.2.1.12)		NAD-dependent_glyceraldehyde-3-phosphate_dehydrogenase_(EC_1.2.1.12)
			D-3-phosphoglycerate_dehydrogenase_(EC_1.1.1.95)		
			Pyridoxal_kinase_(EC_2.7.1.35)		Pyridoxal_kinase_(EC_2.7.1.35)

Table S7. Genes associated with secondary metabolites (vitamins and essential amino acids) (continued)

Essential amino acid/ cofactor	Pathway	Probiotic strain			
		Enterococcus hirae Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
			Phosphoserine_aminotransferase_(EC_2.6.1.52)		
			1-deoxy-D-xylulose_5-phosphate_synthase_(EC_2.2.1.7)		
Folate	Folate biosynthesis		2-amino-4-hydroxy-6-hydroxymethyldihydropteridine_pyrophosphokinase_(EC_2.7.6.3)		
			5-formyltetrahydrofolate_cyclo-ligase_(EC_6.3.3.2)	5-formyltetrahydrofolate_cyclo-ligase_(EC_6.3.3.2)	
			ATPase_component_of_general_energizing_module_of_ECF_transporters	ATPase_component_of_general_energizing_module_of_ECF_transporters	
			ATPase_component_of_general_energizing_module_of_ECF_transporters	ATPase_component_of_general_energizing_module_of_ECF_transporters	
			Cell_division-associated,_ATP-dependent_zinc_metalloprotease_FtsH	Cell_division-associated,_ATP-dependent_zinc_metalloprotease_FtsH	Cell_division-associated,_ATP-dependent_zinc_metalloprotease_FtsH
			Dihydroneopterin_aldolase_(EC_4.1.2.25)		
			Dihydropteroate_synthase_(EC_2.5.1.15)		
			Dihydrofolate_synthase_(EC_6.3.2.12)	Dihydrofolate_synthase_(EC_6.3.2.12)	
			Dihydrofolate_reductase_(EC_1.5.1.3)	Dihydrofolate_reductase_(EC_1.5.1.3)	
			Dihydrofolate_synthase_(EC_6.3.2.12)		
			Folylpolyglutamate_synthase_(EC_6.3.2.17)	Folylpolyglutamate_synthase_(EC_6.3.2.17)	
			Folylpolyglutamate_synthase_(EC_6.3.2.17)		
			Formate--tetrahydrofolate_ligase_(EC_6.3.4.3)	Formate--tetrahydrofolate_ligase_(EC_6.3.4.3)	
			GTP_cyclohydrolase_I_(EC_3.5.4.16)_type_1	GTP_cyclohydrolase_II_(EC_3.5.4.25)	
			GTP_cyclohydrolase_II_(EC_3.5.4.25)		
			Hypoxanthine-guanine_phosphoribosyltransferase_(EC_2.4.2.8)	Hypoxanthine-guanine_phosphoribosyltransferase_(EC_2.4.2.8)	Hypoxanthine-guanine_phosphoribosyltransferase_(EC_2.4.2.8)
			Methionyl-tRNA_formyltransferase_(EC_2.1.2.9)	Methionyl-tRNA_formyltransferase_(EC_2.1.2.9)	

Table S7. Genes associated with secondary metabolites (vitamins and essential amino acids) (continued)

Essential amino acid/cofactor	Pathway	Probiotic strain			
		Enterococcus hirae Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
			Methylenetetrahydrofolate_dehydrogenase_(NADP+)_(EC_1.5.1.5)	Methylenetetrahydrofolate_dehydrogenase_(NADP+)_(EC_1.5.1.5)	
			S-adenosylmethionine_synthetase_(EC_2.5.1.6)	S-adenosylmethionine_synthetase_(EC_2.5.1.6)	
			Serine_hydroxymethyltransferase_(EC_2.1.2.1)	Serine_hydroxymethyltransferase_(EC_2.1.2.1)	
				Substrate-specific_component_FolT_of_folate_ECF_transporter	
			Thymidylate_synthase_(EC_2.1.1.45)	Thymidine_kinase_(EC_2.7.1.21)	
			Thymidine_kinase_(EC_2.7.1.21)	Thymidylate_synthase_(EC_2.1.1.45)	
			Transmembrane_component_of_general_energizing_module_of_ECF_transporters	Transmembrane_component_of_general_energizing_module_of_ECF_transporters	
			tRNA(Ile)-lysidine_synthetase_(EC_6.3.4.19)	tRNA(Ile)-lysidine_synthetase_(EC_6.3.4.19)	tRNA(Ile)-lysidine_synthetase_(EC_6.3.4.19)
Thiamin	Thiamin, thiazole, hydroxymethyl-pyrimidine salvage and uptake		Cysteine_desulfurase_(EC_2.8.1.7),_associated_with_tRNA_4-thiouridine_synthase	Cysteine_desulfurase_(EC_2.8.1.7),_associated_with_tRNA_4-thiouridine_synthase	Cysteine_desulfurase_(EC_2.8.1.7),_associated_with_tRNA_4-thiouridine_synthase
			Duplicated_ATPase_component_YkoD_of_energizing_module_of_thiamin-regulated_ECF_transporter_for_HydroxyMethylPyrimidine		
			Hydroxymethylpyrimidine_kinase_(EC_2.7.1.49)		
			Hydroxyethylthiazole_kinase_(EC_2.7.1.50)		
			Substrate-specific_component_YkoE_of_thiamin-regulated_ECF_transporter_for_HydroxyMethylPyrimidine		
			tRNA_4-thiouridine_synthase_(EC_2.8.1.4)	tRNA_4-thiouridine_synthase_(EC_2.8.1.4)	tRNA_4-thiouridine_synthase_(EC_2.8.1.4)
			Thiamin_pyrophosphokinase_(EC_2.7.6.2)	Thiamin_pyrophosphokinase_(EC_2.7.6.2)	Thiamin_pyrophosphokinase_(EC_2.7.6.2)
			Thiaminase_II_(EC_3.5.99.2)_involved_in_salvage_of_thiamin_pyrimidine_moiety		

Table S7. Genes associated with secondary metabolites (vitamins and essential amino acids) (continued)

Essential amino acid/ cofactor	Pathway	Probiotic strain			
		Enterococcus hirae Pom4	*Limosilactobacillus fermentum* Pom5	*Pediococcus pentosaceus* Chi8	*Ligilactobacillus animalis* FB2
			Transmembrane_component_YkoC_of_energizing_module_of_thiamin-regulated_ECF_transporter_for_HydroxyMethylPyrimidine		
				Thiamin_ABC_transporter_ThiY,_substrate-binding_component	
Lipoic acid	Lipoic acid metabolism	Lipoate-protein_ligase_A	Dihydrolipoamide_acetyltransferase_component_of_pyruvate_dehydrogenase_complex_(EC_2.3.1.12)	Dihydrolipoamide_acetyltransferase_component_of_pyruvate_dehydrogenase_complex_(EC_2.3.1.12)	Dihydrolipoamide_acetyltransferase_component_of_pyruvate_dehydrogenase_complex_(EC_2.3.1.12)
		Dihydrolipoamide_acetyltransferase_component_of_pyruvate_dehydrogenase_complex_(EC_2.3.1.12)	Lipoate-protein_ligase_A	Lipoate-protein_ligase_A	Lipoate-protein_ligase_A
		Lipoate-protein_ligase_A	Lipoamidase		
Lipoylated proteins			Dihydrolipoamide_acetyltransferase_component_of_pyruvate_dehydrogenase_complex_(EC_2.3.1.12)	Dihydrolipoamide_acetyltransferase_component_of_pyruvate_dehydrogenase_complex_(EC_2.3.1.12)	Dihydrolipoamide_dehydrogenase_of_pyruvate_dehydrogenase_complex_(EC_1.8.1.4)
			Dihydrolipoamide_dehydrogenase_of_pyruvate_dehydrogenase_complex_(EC_1.8.1.4)	Dihydrolipoamide_dehydrogenase_of_pyruvate_dehydrogenase_complex_(EC_1.8.1.4)	Dihydrolipoamide_acetyltransferase_component_of_pyruvate_dehydrogenase_complex_(EC_2.3.1.12)
			Pyruvate_dehydrogenase_E1_component_alpha_subunit_(EC_1.2.4.1)	Pyruvate_dehydrogenase_E1_component_alpha_subunit_(EC_1.2.4.1)	Pyruvate_dehydrogenase_E1_component_beta_subunit_(EC_1.2.4.1)
			Pyruvate_dehydrogenase_E1_component_beta_subunit_(EC_1.2.4.1)	Pyruvate_dehydrogenase_E1_component_beta_subunit_(EC_1.2.4.1)	Pyruvate_dehydrogenase_E1_component_alpha_subunit_(EC_1.2.4.1)