

Table S5. Unique genes of *Listeria* pathogens (UGLP) referenced to Livanovii 1638

ORF_id	Sequence_id	Group_id	start	end	strand	COG_id	COG_annotation	VFDB_annotation	Uniprot_annotation
orf_5	CPO34771.1	group_223	2999	7495	-	COG1674	D/DNA segregation ATPase FtsK/SpoIIIE or related protein;FtsK;	-	Type VII secretion system protein EscC OS=Staphylococcus aureus (strain N315)  OX-158879 GNescC PE-3 SV=1
orf_6	CPO34771.1	group_264	7509	7937	-	COG4649	U/E5X protein secretion system component YnfC;YnfC;	-	Uncharacterized protein EscK OS=Staphylococcus aureus (strain N315)  OX-158879 GNescC PE-3 SV=1
orf_7	CPO34771.1	group_264	8045	8587	-	COG4649	U/E5X protein secretion system component YnfC;YnfC;	-	Uncharacterized protein EscK OS=Staphylococcus aureus (strain N315)  OX-158879 GNescC PE-3 SV=1
orf_31	CPO34771.1	group_2236	33169	34254	-	COG4949	M/Glucosamine 6-phosphate synthetase, contains amidotransferase and phos-	-	PTS system beta-glucose-6-phosphate isomerase (isomerizing) OS=Pyrococcus furiosus (strain ATCC 43587 / DSM 3638 / VCB)  OX-186497 GN-glmS PE-3 SV=3
orf_33	CPO34771.1	group_2212	35627	38029	-	-	-	-	-
orf_34	CPO34771.1	group_2260	38026	38991	-	COG1940	Kc/Sugar kinase of the NBD/HSF70 family, may contain an R-terminal HTH dor-	-	Glucokinase OS=Alkalibacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125)  OX-272558 GN-glcK PE-3 SV=1
orf_35	CPO34771.1	group_2241	39194	40252	-	COG1609	K/DNA-binding transcriptional regulator, Lac/PurK family;PurK;	-	HTH-type transcriptional repressor PurK OS=Haemophilus influenzae (strain PT33)  OX-74930 GNpurK PE-3 SV=1
orf_45	CPO34771.1	group_1367	48706	49513	-	COG2100	G/Glucophosphatase system (IA component);GlcP;	-	PTS system beta-glucose-6-phosphate isomerase (isomerizing) OS=Alkalibacillus halodurans (strain ATCC BAA-125 / DSM 18197 / FERM 7344 / JCM 9153 / C-125)  OX-272558 GN-glcP PE-3 SV=1
orf_48	CPO34771.1	group_1520	51509	51841	-	COG1325	C/Heme/copper-type cytochrome/quinol oxidase, subunit 4;Cyod	-	Quinol oxidase subunit 4 OS=Listeria sp. (strain ATCC 23059 / NRRL B-14472 / W23)  OX-655816 GN-cyod PE-1 SV=1
orf_49	CPO34771.1	group_1819	51843	52454	-	COG1845	C/Heme/copper-type cytochrome/quinol oxidase, subunit 3;Cyoc	-	Quinol oxidase subunit 3 OS=Listeria sp. (strain ATCC 23059 / NRRL B-14472 / W23)  OX-655816 GN-cyoc PE-1 SV=1
orf_51	CPO34771.1	group_1537	54493	55545	-	COG1622	C/Heme/copper-type cytochrome/quinol oxidase, subunit 2;Cyoc	-	Probable quinol oxidase subunit 2 OS=Staphylococcus epidermidis (strain ATCC 12228 / FDA PI 1200 / VKM 8-1787)  OX-272626 GN-cyoc PE-1 SV=1
orf_53	CPO34771.1	group_1364	56949	57920	-	COG3007	I/Mevalonate pyrophosphate decarboxylase;MVD;isoprenoid biosynthesis	-	Diphosphomevalonate decarboxylase OS=Dictyostelium discoideum  OX-44689 GN-mvd PE-3 SV=1
orf_55	CPO34771.1	group_1722	58989	59507	-	COG1670	JQ/Protein N-acetyltransferase, RimM/RimI, family;RimI;	-	Spermidine N(1)-acetyltransferase OS=Wigglesworthia glossinidia brevipalpis  OX-36870 GN-speG PE-3 SV=1
orf_56	CPO34771.1	group_331	59523	61037	-	COG1502	I/Phosphatidylserine/phosphatidylglycerophosphate/cardiolipin synthase;CisF-	-	Cardiolipin synthase 1 OS=Listeria anthracis  OX-1392 GN-cds1 PE-3 SV=1
orf_59	CPO34771.1	group_1688	65780	66892	-	COG1195	I/Recombinational DNA repair ATPase RecF;RecF;	-	DNA replication and repair protein RecF OS=Listeria welshimeri serovar 6b (strain ATCC BAA-680 / CLIP 11262)  OX-272626 GN-recF PE-3 SV=1
orf_64	CPO34771.1	group_1960	71944	72414	-	-	-	-	-
orf_65	CPO34771.1	group_2024	72582	72716	-	COG0230	J/Ribosomal protein L34;RplM;Ribosome 50S subunit	-	50S ribosomal protein L34 OS=Listeria welshimeri serovar 6b (strain ATCC 35887 / DSM 20650 / CP 8149 / NCTC 11857 / SLCC 5334 / V8)  OX-386043 GN-rplM PE-3 SV=1
orf_69	CPO34771.1	group_1319	74741	75202	-	COG4405	R/Predicted RNA binding protein YnfH, contains PUA-like ASCH domain;YnfH	-	-
orf_71	CPO34771.1	group_215	7795	83789	-	COG1305	G/Transglutaminase-like enzyme, putative cysteine proteinase;YnfA;	-	-
orf_72	CPO34771.1	group_2160	83938	84963	-	COG1609	K/DNA-binding transcriptional regulator, Lac/PurK family;PurK;	-	Uncharacterized HTH-type transcriptional regulator YnfW OS=Escherichia coli (strain K12)  OX-83333 GN-ynfW PE-4 SV=1
orf_73	CPO34771.1	group_136	85189	86889	-	COG3366	G/Glycosylase/amyase (phosphorylase);AmyA;	-	Glucosylglycerate phosphorylase OS=Escherichia coli (strain K12)  OX-83333 GN-ygm PE-1 SV=2
orf_74	CPO34771.1	group_2202	86886	88184	-	COG1653	G/ABC-type glycerol 3-phosphate transport system, periplasmic component;U	-	Putative ABC transporter periplasmic-binding protein YnfN OS=Escherichia coli (strain K12)  OX-83333 GN-ynfN PE-3 SV=1
orf_75	CPO34771.1	group_2204	88251	89140	-	COG1612	G/ABC-type sugar transport system, periplasmic component;U	-	Inner membrane ABC transporter periplasmic-binding protein YnfM OS=Escherichia coli (strain K12)  OX-83333 GN-ynfM PE-3 SV=1
orf_76	CPO34771.1	group_2177	89127	89978	-	COG3995	G/ABC-type glycerol 3-phosphate transport system, periplasmic component;U	-	Inner membrane ABC transporter periplasmic-binding protein YnfN OS=Escherichia coli (strain K12)  OX-83333 GN-ynfN PE-3 SV=1
orf_77	CPO34771.1	group_1769	89996	91048	-	COG1063	ER/Threonine dehydrogenase or related D-dependent dehydrogenase;ThNc-	-	D-2-glycidyl-D-glutamate OS=Escherichia coli (strain K12)  OX-83333 GN-ygd PE-1 SV=1
orf_78	CPO34771.1	group_2216	91058	91855	-	COG1082	G/Sugar phosphatase isomerase/epimerase;YgR;	-	3-dehydroxy-D-glucose-4-epimerase OS=Escherichia coli (strain K12)  OX-83333 GN-ygd PE-1 SV=2
orf_79	CPO34771.1	group_1824	91911	92943	-	COG0673	R/Predicted dehydrogenase;AldH;	-	D-glucose 3-dehydrogenase OS=Escherichia coli (strain K12)  OX-83333 GN-ygd PE-1 SV=1
orf_83	CPO34771.1	group_1451	97021	97341	-	COG3118	O/Chaperonin GroEL, contains thiodoxin-like and TPR-like domains, YnfN/-	-	Thiodoxin 1 OS=Chlorobaculum tepidum (strain ATCC 49562 / DSM 12025 / NRRL 10386 / T15)  OX-194439 GN-trx1 PE-3 SV=1
orf_84	CPO34771.1	group_1889	97400	97999	-	COG3560	R/Fatty acid repression mutant protein (predicted oxidoreductase);FMR2;	-	Putative nitroreductase HBN1 OS=Saccharomyces cerevisiae (strain ATCC 204508 / S288c)  OX-559292 GN-HBN1 PE-1 SV=1
orf_90	CPO34771.1	group_538	111588	114777	-	COG0445	I/tRNA U34 5'-carboxymethylaminomethyl modifying enzyme MnmG/Gda/Mn-	-	tRNA uridine 5'-carboxymethylaminomethyl modification enzyme MnmG OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)  OX-169963 GN-mnmG PE-3 SV=1
orf_103	CPO34771.1	group_1625	118843	118842	-	-	-	-	-
orf_113	CPO34771.1	group_1374	126840	127598	-	-	-	-	-
orf_119	CPO34771.1	group_1287	133273	133170	-	-	-	-	-
orf_120	CPO34771.1	group_1335	133220	135550	-	COG2018	N/Gamma-glutamylcysteine synthetase;GdaA;	-	-
orf_123	CPO34771.1	group_1780	137826	138500	-	COG4858	S/Uncharacterized membrane-anchored protein	-	Glutathione biosynthesis bifunctional protein GshAB OS=Listeria welshimeri serovar 6b (strain ATCC 35887 / DSM 20650 / CP 8149 / NCTC 11857 / SLCC 5334 / V8)  OX-386043 GN-gshAB PE-3 SV=1
orf_136	CPO34771.1	group_1841	148651	149181	-	COG2110	J/O-acetyl-ADP-ribose deacetylase (regulator of RNase III), contains Macro dor-	-	Macro domain-containing protein Hmo2759 OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)  OX-169963 GN-hmo2759 PE-4 SV=1
orf_137	CPO34771.1	group_1550	149464	150930	-	COG0517	T/GS domain;CBS;	-	Inosine 5'-monophosphate dehydrogenase OS=Listeria sp. (strain 168)  OX-224308 GN-gshAB PE-1 SV=2
orf_140	CPO34771.1	group_1741	151337	157004	-	COG1286	R/Predicted acyl esterase;	-	Coxiase esterase OS=Rhodococcus sp. (strain MB1 Brunei)  OX-104109 GN-cox PE-3 SV=1
orf_143	CPO34771.1	group_87	160441	162162	-	COG1132	V/ABC-type multidrug transport system, ATPase and permease component;M	-	Uncharacterized ABC transporter ATP-binding protein YnfB OS=Listeria sp. (strain 168)  OX-224308 GN-ynfB PE-3 SV=1
orf_146	CPO34771.1	group_2159	164728	165147	-	COG3871	S/General stress protein 26 (function unknown);YnfA;	-	General stress protein 26 OS=Listeria sp. (strain 168)  OX-224308 GN-ynfA PE-1 SV=2
orf_147	CPO34771.1	group_551	165483	166769	-	COG0072	J/Seryl-tRNA synthetase;SerS;aminoacyl-tRNA synthetases	-	Serine-tRNA ligase OS=Listeria monocytogenes serovar 4a (strain HCC23)  OX-525236 GN-serS PE-3 SV=1
orf_150	CPO34771.1	group_1679	169448	169837	-	COG0664	T/CAMP-binding domain of CRP or a regulatory subunit of cAMP-dependent p	-	-
orf_152	CPO34771.1	group_1629	170642	170899	-	-	-	-	-
orf_154	CPO34771.1	group_1829	172303	172584	-	-	-	-	-
orf_155	CPO34771.1	group_1600	172387	173276	-	COG0846	O/ADP-dependent protein deacetylase, SIR2 family;Sir2;	-	Mitomycin resistance protein McrB OS=Streptomyces lavendulae  OX-1914 GN-mcrB PE-4 SV=1
orf_159	CPO34771.1	group_1474	176221	178823	-	COG0546	C/Phosphoglycerate phosphatase, HAD superfamily;Gdh;	-	Putative phosphoglycerate phosphatase OS=Caldivarobacter subterraneus subsp. tengcongensis (strain DSM 15242 / JCM 11107 / NBRC 100824 / MB4)  OX-273068 GN-gppAK PE-3 SV=2
orf_162	CPO34771.1	group_2157	178429	178878	-	COG1846	K/DNA-binding transcriptional regulator, MarR family;MarR;	-	Uncharacterized HTH-type transcriptional regulator YnfB OS=Listeria sp. (strain 168)  OX-224308 GN-ynfB PE-4 SV=1
orf_163	CPO34771.1	group_1990	178875	180227	-	COG0334	V/Na+-driven multidrug efflux pump, Dnf/NorM/NATE family;NorM;	-	Multidrug export protein MepA OS=Staphylococcus haemolyticus (strain JCS4135)  OX-278908 GN-mepA PE-3 SV=1
orf_164	CPO34771.1	group_2138	180290	180733	-	COG2764	C/ADP-dependent glyoxalase, PfmB family;PfmB;	-	Protein YnfH OS=Escherichia coli (strain K12)  OX-83333 GN-ynfH PE-4 SV=1
orf_171	CPO34771.1	group_1861	183094	183142	-	COG0673	R/Predicted N-acetyltransferase, GlnAT family;GlnA;	-	Protein YnfH OS=Escherichia coli (strain K12)  OX-83333 GN-ynfH PE-4 SV=1
orf_172	CPO34771.1	group_2120	183595	184329	-	COG0789	K/DNA-binding transcriptional regulator, MarR family;MarR;	-	Multidrug export protein YnfH OS=Escherichia coli (strain K12)  OX-224308 GN-ynfH PE-3 SV=1
orf_173	CPO34771.1	group_784	184410	185129	-	COG0363	G/6-phosphogluconolactonase/Gluconamine 6-phosphate isomerase/deamina	-	Uncharacterized protein YnfK OS=Escherichia coli (strain K12)  OX-83333 GN-ynfK PE-3 SV=1
orf_175	CPO34771.1	group_701	186941	187411	-	COG1082	I/tRNA ArgL AD deaminase domain;YnfH;YnfH;	-	tRNA-specific deaminase YnfH OS=Listeria sp. (strain 168)  OX-224308 GN-ynfH PE-3 SV=1
orf_176	CPO34771.1	group_97	187789	189195	-	COG1271	C/Cytochrome bd-type quinol oxidase, subunit 1;YnfC;	-	Cytochrome bd ubiquinol oxidase subunit 1 OS=Listeria sp. (strain 168)  OX-224308 GN-ynfC PE-3 SV=1
orf_177	CPO34771.1	group_97	189182	190195	-	COG1294	C/Cytochrome bd-type quinol oxidase, subunit 2;YnfC;	-	Cytochrome bd ubiquinol oxidase subunit 2 OS=Listeria sp. (strain 168)  OX-224308 GN-ynfC PE-3 SV=1
orf_178	CPO34771.1	group_1310	190195	191919	-	COG4988	CO/ABC-type transport system involved in cytochrome bd biosynthesis, ATPa	-	ATP-binding/permease protein CyoC OS=Listeria sp. (strain 168)  OX-224308 GN-ynfC PE-3 SV=1
orf_180	CPO34771.1	group_1496	199965	201329	-	COG1455	G/Phosphotransferase system cellobiose-specific component IIC/CelB;	-	Cell wall permease YnfA OS=Listeria sp. (strain 168)  OX-224308 GN-ynfA PE-3 SV=1
orf_186	CPO34771.1	group_1521	201463	201684	-	-	-	-	-
orf_189	CPO34771.1	group_1475	201887	202351	-	-	-	-	-
orf_191	CPO34771.1	group_1711	204418	204735	-	COG0718	K/DNA-binding nucleoid-associated protein YnfB/FtsH;YnfB;	-	Nucleoid-associated protein YnfB OS=Listeria welshimeri serovar 6b (strain ATCC 35887 / DSM 20650 / CP 8149 / NCTC 11857 / SLCC 5334 / V8)  OX-386043 GN-ynfB OS-2654 PE-3 SV=1
orf_192	CPO34771.1	group_1721	204448	205440	-	COG0553	L/Recombinational DNA repair protein RecK;RecK;	-	Recombination protein RecK OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)  OX-169963 GN-recK PE-3 SV=1
orf_193	CPO34771.1	group_1476	205455	205697	-	-	-	-	-
orf_221	CPO34771.1	group_2032	216078	217326	-	COG0561	HK/hydroxymethylpyrimidine pyrophosphatase and other HAD family phospho-	-	Sugar phosphatase YnfA OS=Shigella flexneri  OX-623 GN-ynfA PE-3 SV=1
orf_227	CPO34771.1	group_1646	240754	241130	-	COG0412	T/Phosphatase/kinase subunit DhaM of the dihydroxyacid dehydratase DhaLM	-	PEP-epimerase YnfA OS=Shigella flexneri  OX-623 GN-ynfA PE-3 SV=1
orf_238	CPO34771.1	group_1670	250790	251536	-	COG1309	K/DNA-binding protein, AcrR family, contains nucleoid occlusion protein SmaA	-	Uncharacterized HTH-type transcriptional regulator YnfB OS=Listeria sp. (strain 168)  OX-224308 GN-ynfB PE-4 SV=1
orf_239	CPO34771.1	group_463	251908	254478	+	COG0474	P/Magnesium-transporting ATPase (P-type);MgtA;	(mgtB) MgtA transport protein (MgtB) (VF0106)	Magnesium-transporting ATPase, P-type 1 OS=Salmonella typhimurium (strain LT2 / SGGC412 / ATCC 700702)  OX-99287 GN-mgtB PE-1 SV=3
orf_242	CPO34771.1	group_85	256811	257113	-	COG1447	G/Phosphotransferase system cellobiose-specific component IIA/CelC;	-	Lichenan-specific phosphotransferase enzyme IIA component OS=Listeria sp. (strain 168)  OX-224308 GN-ynfA PE-3 SV=1
orf_243	CPO34771.1	group_1442	262997	263554	-	COG1286	P-K+ transport ATPase, ATPase subunit;KdpC;	-	Potassium-transporting ATPase P1 OS=Listeria sp. (strain 168)  OX-224308 GN-ynfA PE-3 SV=1
orf_248	CPO34771.1	group_1290	262997	263554	-	COG1286	P-K+ transport ATPase, ATPase subunit;KdpC;	-	Potassium-transporting ATPase P1 OS=Listeria sp. (strain 168)  OX-224308 GN-ynfA PE-3 SV=1
orf_249	CPO34771.1	group_769	263574	266270	-	COG2025	Tk-sensing histidine kinase KdpK/KdpB;	-	Sensor protein KdpB OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)  OX-169963 GN-kdpB PE-3 SV=1
orf_250	CPO34771.1	group_2100	266265	266955	-	COG0673	T/Glutamate aminohydrolase/FerII-dependent fatty formamide hydrolase (F-	-	Transcriptional regulator YnfH OS=Listeria sp. (strain 168)  OX-224308 GN-ynfH PE-3 SV=1
orf_254	CPO34771.1	group_7	269612	270067	-	COG0698	G/Ribose 5-phosphate isomerase RpiB/RpiB;Penicillin phosphatase;YnfC	-	Penicillin phosphatase YnfC OS=Listeria sp. (strain 168)  OX-224308 GN-ynfC PE-3 SV=1
orf_256	CPO34771.1	group_2132	270701	271513	-	COG4977	K/Transcriptional regulator GlnA, contains an internal domain and an AraC-ty	-	Uncharacterized protein YnfA OS=Listeria sp. (strain 168)  OX-224308 GN-ynfA PE-3 SV=1
orf_258	CPO34771.1	group_1900	271918	272286	-	COG2315	K/Predicted DNA-binding protein with double-winged structural motif, MincQ/Yj	-	-
orf_259	CPO34771.1	group_2075	272363	273175	-	-	-	-	-
orf_265	CPO34771.1	group_324	278874	279905	-	COG1063	ER/Threonine dehydrogenase or related D-dependent dehydrogenase;ThNc-	-	-
orf_266	CPO34771.1	group_7	280100	280540	-	COG0698	G/Ribose 5-phosphate isomerase RpiB/RpiB;Penicillin phosphatase;YnfC	-	-
orf_267	CPO34771.1	group_132	280549	281233	-	COG0366	G/Pentose-5-phosphate 3-epimerase;Rpe;Penicillin phosphatase pathway	-	-
orf_275	CPO34771.1	group_1581	291211	291624	-	COG1082	J/Ribosomal protein S12;RpsL;Ribosome 30S subunit	-	30S ribosomal protein S12 OS=Listeria sp. (strain 168)  OX-224308 GN-rplS PE-3 SV=1
orf_277	CPO34771.1	group_258	292191	294278	-	COG0490	E/Translation elongation factor EF-G, a GTPase;FusA;Translation factors	-	Elongation factor EF-G OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)  OX-169963 GN-fusA PE-3 SV=1
orf_278	CPO34771.1	group_1149	294388	295575	-	COG0050	I/Translation elongation factor EF-Tu, a GTPase;TufA;Translation factors	(tufA) elongation factor Tu OS=Listeria monocytogenes serovar 1/2a (strain ATCC BAA-679 / EGD-e)  OX-169963 GN-tufA PE-3 SV=1	
orf_289	CPO34771.1	group_165	304116	305105	-	COG1735	R/Predicted metal-dependent hydrolase, phosphotransferase family;Pnp-	-	Phosphotransferase YnfH OS=Listeria sp. (strain 168)  OX-224308 GN-ynfH PE-3 SV=1
orf_290	CPO34771.1	group_1842	305121	306212	-	COG1402	R/Creatine amidohydrolase/FerII-dependent fatty formamide hydrolase (F-	-	Transcriptional regulator YnfH OS=Listeria sp. (strain 168)  OX-224308 GN-ynfH PE-3 SV=1
orf_292	CPO34771.1	group_1926	306550	307293	-	COG4821	R/Uncharacterized conserved protein, contains S15 (Sugar Isomerase) phospho-	-	-
orf_295	CPO34771.1	group_1925	309257	310594	-	COG1409	T/3',5'-cyclic AMP phosphodiesterase CpdA/CpdA;	-	Probable cyclic nucleotide phosphodiesterase YnfC OS=Listeria sp. (strain 168)  OX-224308 GN-ynfC PE-3 SV=1
orf_297	CPO34771.1	group_1073	311676	312121	-	COG4769	S/Uncharacterized membrane protein	-	-
orf_298	CPO34771.1	group_1846	312254	312688</					