

# Whole-Genome Sequences of 12 Clinical Strains of *Listeria monocytogenes*

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***Listeria monocytogenes* is a foodborne pathogen of global concern due to the high mortality rate among immunocompromised patients. Whole-genome sequences of 12 strains of *L. monocytogenes* from humans were reported. The availability of these genomes should provide useful information on the evolutionary history and genetic diversity of *L. monocytogenes*.**

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*Listeria monocytogenes* is a Gram-positive intracellular pathogen that causes severe disease among immunocompromised individuals (1). *L. monocytogenes* is ubiquitous and able to survive in a wide range of environmental conditions (2). Most human listeriosis has been attributed to serotypes 1/2a, 1/2 b, and 4 b (3). In China, serotypes 1/2a, 1/2 b, and 1/2c account for over 90% of the *L. monocytogenes* strains found in food (4). Whole-genome sequencing has become an essential tool for investigating the evolution, diversity, and pathogenicity of foodborne bacterial pathogens (5–9). The draft genomes of 12 *L. monocytogenes* strains from hospitalized patients in Shanghai, China, between 2007 and 2012 were reported.

Genomic DNA was isolated from overnight cultures and sequenced using MiSeq (Illumina, San Diego, CA) to obtain draft genomes. Genomic data were assembled using Newbler 2.6 (Roche, Branford, CT), including SHL001 (33 contigs, 2.95 Mb, 476,844 bp  $N_{50}$  contig size, and 2,964 identified genes), SHL002 (22 contigs, 3.12 Mb, 301,779 bp  $N_{50}$  contig size, and 3,113 identified genes), SHL004 (18 contigs, 3.01 Mb, 579,300 bp  $N_{50}$  contig size, and 3,018 identified genes), SHL005 (17 contigs, 2.88 Mb, 437,049 bp  $N_{50}$  contig size, and 2,859 identified genes), SHL006 (30 contigs, 2.93 Mb, 476,139 bp  $N_{50}$  contig size, and 2,959 identified genes), SHL007 (43 contigs, 2.98 Mb, 355,359 bp  $N_{50}$  contig size, and 2,995 identified genes), SHL008 (26 contigs, 3.01 Mb, 293,078 bp  $N_{50}$  contig size, and 2,990 identified genes), SHL009 (32 contigs, 2.87 Mb, 541,739 bp  $N_{50}$  contig size, and 2,866 identified genes), SHL010 (84 contigs, 3.08 Mb, 259,950 bp  $N_{50}$  contig size, and 3,112 identified genes), SHL011 (17 contigs, 2.87 Mb, 543,519 bp  $N_{50}$  contig size, and 2,847 identified genes), SHL012 (23 contigs, 2.93 Mb, 355,398 bp  $N_{50}$  contig size, and 2,906 identified genes), and SHL013 (20 contigs, 2.86 Mb, 358,858 bp  $N_{50}$  contig size, and 2,806 identified genes). These sequences were annotated using the NCBI Prokaryotic Genomes Automatic Annotation Pipeline (10).

**Nucleotide sequence accession numbers.** The draft genome sequences of these 12 *L. monocytogenes* strains are available in GenBank under the accession numbers [APIB00000000](https://ncbi.nlm.nih.gov/nucl/APIB00000000), [APID00000000](https://ncbi.nlm.nih.gov/nucl/APID00000000), [APIE00000000](https://ncbi.nlm.nih.gov/nucl/APIE00000000), [APIF00000000](https://ncbi.nlm.nih.gov/nucl/APIF00000000), [APIG00000000](https://ncbi.nlm.nih.gov/nucl/APIG00000000), [APIH00000000](https://ncbi.nlm.nih.gov/nucl/APIH00000000), [APII00000000](https://ncbi.nlm.nih.gov/nucl/APII00000000), [APIJ00000000](https://ncbi.nlm.nih.gov/nucl/APIJ00000000), [APIK00000000](https://ncbi.nlm.nih.gov/nucl/APIK00000000), [APIL00000000](https://ncbi.nlm.nih.gov/nucl/APIL00000000), and [APIM00000000](https://ncbi.nlm.nih.gov/nucl/APIM00000000).

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