

# Draft Genome Assembly of *Ralstonia pickettii* Type Strain K-288 (ATCC 27853)

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**We present the genome assembly of *Ralstonia pickettii* K-288 (ATCC 27511), consisting of 27 contigs placed into a single scaffold. This 4.76-Mbp genome has 64.0% G+C content and 4,425 coding sequences. Because this is the type strain, inclusion of its data set among other *Ralstonia* genomes should provide a historical genomic perspective.**

Received 25 August 2014 Accepted 26 August 2014 Published 25 September 2014

**Citation** Daligault HE, Davenport KW, Minogue TD, Broomall SM, Bruce DC, Chain PS, Coyne SR, Gibbons HS, Jaissle J, Lo C-C, Meincke L, Munk AC, Rosenzweig CN, Johnson SL. 2014. Draft genome assembly of *Ralstonia pickettii* type strain K-288 (ATCC 27853). *Genome Announc.* 2(5):e00973-14. doi:10.1128/genomeA.00973-14.

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*Ralstonia pickettii* is a Gram-negative rod-shaped member of the  $\beta$ -proteobacteria commonly found in moist environments and is an increasing cause of nosocomial human infection (1, 2). *R. pickettii* K-288 (ATCC 27511) is the type strain of the genus, originally isolated from a tracheotomy patient. As of this writing, only six genome assemblies of *R. pickettii* (3 complete and 3 draft) are available in the public database and none for this type strain, which was originally described in 1973 (3).

High-quality genomic DNA was extracted from a 100-mL bacterial culture of a purified isolate using the QIAGEN Genomic Tip-500 at the USAMRIID Diagnostic Systems Division (DSD). Draft sequence data included a 100-bp Illumina library (279-fold genome coverage) and a separate long-insert paired-end library (9,590-  $\pm$  2,397-bp insert, 42-fold genome coverage) (Roche 454 Titanium platform). The two data sets were assembled together in Newbler (Roche, version 2.6) and the consensus sequences were computationally shredded into 2-kbp overlapping fake reads (shreds). The raw reads were also assembled in Velvet (version 1.1.05), and those consensus sequences were computationally shredded into 1.5-kbp overlapping shreds (4). All draft data were then assembled together in Allpaths (version 39750), and the consensus sequences were computationally shredded into 10-kbp overlapping shreds (5). We then integrated the Newbler consensus shreds, Velvet consensus shreds, Allpaths consensus shreds, and a subset of the long-insert read pairs using parallel Phrap version SPS-4.24 (High Performance Software, LLC). Possible misassemblies were corrected, and some gap closure was accomplished with manual editing in Consed (6–8).

Automatic annotation of the *R. pickettii* K-288 genome utilized an Ergatis-based workflow at LANL with minor manual curation.

The final annotated assembly includes 4,425 coding sequences, 5 rRNAs, and 49 tRNAs in the 4,762,999-bp genome.

**Nucleotide sequence accession number.** This genome is available in NCBI under the accession number [JV010000000](https://www.ncbi.nlm.nih.gov/nuccore/JV010000000).

## ACKNOWLEDGMENTS

Funding for this effort was provided by the Defense Threat Reduction Agency's Joint Science and Technology Office (DTRA J9-CB/JSTO).

This article is approved by LANL for unlimited release (LA-UR-14-25650).

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