

# Genome Sequence of *Bartonella rattaaustraliani*, a Bacterium Isolated from an Australian Rat

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***Bartonella rattaaustraliani* is a facultative intracellular bacterium isolated from the blood of a *Rattus* sp. in Australia. The present study reports the draft genome of *B. rattaaustraliani* strain AUST/NH4 (CSUR B609<sup>T</sup>).**

Bacteria of the genus *Bartonella* are facultative intracellular bacteria that belong to the *Alphaproteobacteria* group (10). *Bartonella* species are arthropod-borne bacteria that cause intraerythrocytic infections (5) and long-term bacteremia in mammalian hosts. Many *Bartonella* species have been isolated from mammals, including humans, ruminants, rodents, and pets (2, 9). *B. rattaaustraliani* has been isolated for the first time from the blood of a wild rat (*Rattus tunneyi*) in Australia (3). The genome of this bacterium in comparison with those of other sequenced *Bartonella* species may help to elucidate the mechanism underlying long-term bacteremia and erythrocyte invasion (11) in order to understand the pathogenicity of *Bartonella* in humans.

The genome sequence of *B. rattaaustraliani* was fully sequenced by using a combination of the 454 GS FLX Titanium pyrosequencing system (Roche Diagnostics, Branford, CT) (8) with shotgun and 3-kb paired-end libraries. The 454 sequencing generated 485,548 reads (146,943,126 bp) that were assembled into contigs and scaffolds using Newbler version 2.6 (Roche). The assembly was checked using CLC Genomics Workbench v4.7.2 (CLC bio, Aarhus, Denmark). The functional annotation of predicted genes was achieved using Prodigal to predict open reading frames (ORFs) (4) and BLASTP (1). tRNAs and rRNAs were predicted using ARAGORN (7) and RNAmmer (6), respectively.

The draft genome of *B. rattaaustraliani* (2.1 Mb) is composed of 108 contigs (including 97 large contigs of more than 1,500 bp) in 28 scaffolds. The G+C content is 38.26%. The genome contains 48 RNA genes, including 43 tRNA and five rRNA genes (probably grouped in two operons). A total of 1,920 protein-coding sequences with an average size of 840 bp were identified, corresponding to 73.7% of the genome. Among these, 1,410 (73% of the total gene content) were assigned a putative function: 31% of the genes encode proteins involved in metabolism, 29% in information storage and processing, and 21% in cellular processes and signaling, and 19% encode proteins of poorly characterized functions. *Bartonella grahamii* as4aup is the closest species to *B. rattaaustraliani* based on the 16S rRNA sequence similarities. We identified 909 orthologous genes shared between *B. rattaaustraliani* and *B. grahamii*. Some functional features that distinguish these bacteria include genes encoding transcriptional regulators, site-specific recombinase, membrane proteins, and prophage proteins. The genome of *B. rattaaustraliani* contains three type IV se-

cretion system operons and two genes encoding flagellar motor components which suggest the capacity for motility.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited in GenBank/EMBL under accession numbers [CALW02000001](https://www.ncbi.nlm.nih.gov/nuccore/CALW02000001) to [CALW02000108](https://www.ncbi.nlm.nih.gov/nuccore/CALW02000108).

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