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*Rhodobacter sphaeroides* is a metabolically diverse photosynthetic alphaproteobacterium found ubiquitously in soil and freshwater habitats. Here we present the annotated genome sequence of *R. sphaeroides* WS8N.

*Rhodobacter sphaeroides* can grow using either aerobic or anaerobic respiration and can photosynthesize. *R. sphaeroides* can use a diverse array of different carbon and nitrogen sources and is capable of N₂ fixation when other nitrogen sources are scarce. Organic acids are the preferred carbon sources during anaerobic respiration and can photosynthesize.

A total of 4,205 predicted coding sequences were identified. The average length of each coding sequence was 299 amino acids, with a total coding percentage of 88.7%. There are 52 tRNA genes and 9 rRNA genes. The 5S, 16S, and 23S rRNA molecules are encoded once on the large chromosome and twice on the small chromosome. Thirty-three genes encode chemotaxis signaling proteins, i.e., 13 chemoreceptors (9 transmembrane and 4 soluble), 4 CheA proteins, 6 CheY proteins, 4 CheW proteins, 3 CheR proteins, 2 CheB proteins, and 1 CheD protein. All of these are located on the large chromosome, with the exception of six of the chemoreceptor genes and one of the cheY genes, which are on the small chromosome.

Comparative genome analysis shows that while the chromosome gene organization of WS8N is similar to that of previously sequenced strains of *R. sphaeroides*, the plasmid composition differs considerably, with ATCC_17029 having one, WS8N and KD131 each having two (6), and 2.4.1 and ATCC_17025 each having five (2).

Nucleotide sequence accession number. This Whole Genome Shotgun project has been deposited at DDBJ/EMBL/Genbank under accession no. AFER00000000. The version described in this paper is the first version, AFER01000000.

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REFERENCES


