

Draft Genome Sequence of *Rhodovulum* sp. Strain NI22, a Naphthalene-Degrading Marine Bacterium

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***Rhodovulum* sp. strain NI22 is a hydrocarbon-degrading member of the genus *Rhodovulum*. The draft genome of *Rhodovulum* sp. NI22 is 3.8 Mb in size, with 3,756 coding sequences and 64.4% G+C content. The catechol and gentisate pathways for naphthalene degradation are predicted to be present in *Rhodovulum* sp. NI22.**

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Rhodovulum sp. strain NI22 is an isolate of the genus *Rhodovulum*, capable of degrading hydrocarbons aerobically. This bacterium was isolated from coastal seawater from Key West, Florida, USA, after having been exposed to JP-5 aviation fuel.

Rhodovulum sp. NI22 is a Gram-negative, mesophilic, slightly halophilic, chemo-organotrophic, rod-shaped bacterium that can use naphthalene as its sole carbon and energy source. Based on the 16S rRNA gene sequence, *Rhodovulum* sp. NI22 is 95.0% similar to *Rhodovulum marinum*. Members of the genus *Rhodovulum* are often found in hydrocarbon-polluted marine environments, and some have been reported to degrade aromatic compounds such as phthalate (1–3).

Rhodovulum sp. NI22 was confirmed to efficiently degrade naphthalene in jet and diesel fuels. Therefore, we have sequenced its genome, to understand the underlying naphthalene degradation mechanisms of this bacterium.

Rhodovulum sp. NI22 was sequenced on a Roche 454-GS Junior platform using a whole-genome shotgun approach, resulting in 346,448 reads. The sequence reads were assembled with the Roche *de novo* Assembly software. The assembly reported 120 large (>500 bp) contigs, with an N_{50} of 57,970 bp. The longest contig was 288,171 bp. The draft genome sequence was 3,819,905 bases in length, with a G+C content of 64.4%. Rapid genome annotation using the RAST annotation server (4) described 3,756 coding sequences (CDSs) and 45 structural RNAs, which consisted of one 16S rRNA, one 23S rRNA, and 43 tRNAs. The coding sequences were classified into 442 subsystems, of which amino acids and derivatives ($n = 370$ CDSs); carbohydrates ($n = 357$); cofactors, vitamins, prosthetic groups, and pigments ($n = 281$); protein metabolisms ($n = 255$); membrane transport ($n = 174$); fatty acids, lipids, and isoprenoids ($n = 144$); stress response ($n = 135$); RNA metabolism ($n = 134$); nucleosides and nucleotides ($n = 109$); cell wall and capsule ($n = 97$); and metabolisms of aromatic compounds ($n = 70$) were the most abundant subsystems.

The NCBI Prokaryotic Genome Annotation Pipeline (http://www.ncbi.nlm.nih.gov/genome/annotation_prok) predicted

naphthalene 1,2-dioxygenase (*ndo*), catechol 1,2-dioxygenase (*catA*), and gentisate 1,2-dioxygenase (*gdo*) genes to be present in the genome of *Rhodovulum* sp. NI22. Naphthalene 1,2-dioxygenase undergoes the dihydroxylation of naphthalene during the first step of the upper catabolic pathway, while catechol 1,2-dioxygenase and gentisate 1,2-dioxygenase further metabolize salicylate via the catechol or gentisate lower pathways, respectively (5–7). Other important hydrocarbon-degrading genes observed were benzene 1,2-dioxygenase, biphenyl 2,3-dioxygenase, 2-nitropropane dioxygenase, protocatechuate 3,4-dioxygenase, and alkane 1-mono-oxygenase (*alkB*). The study of *Rhodovulum* sp. NI22 genome will provide valuable insight into the metabolism and adaptation of marine bacteria to aromatic hydrocarbon compounds.

Nucleotide sequence accession number. This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession number [JQFU00000000](https://www.ncbi.nlm.nih.gov/nuccore/JQFU00000000).

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