The 16S rDNA gene and genomic sequences of the strain *Cellulosimicrobium cellulans* MP1 in the present study were deposited onto GenBank (NCBI) and released to public under accession numbers MW534740 and JAFGYF000000000, respectively.

Links:

<https://www.ncbi.nlm.nih.gov/nuccore/MW534740.1>

<https://www.ncbi.nlm.nih.gov/nuccore/JAFGYF000000000>

Information for the 16S rDNA gene sequence

# Cellulosimicrobium cellulans strain MP1 16S ribosomal RNA gene, partial sequence

GenBank: MW534740.1

[FASTA](https://www.ncbi.nlm.nih.gov/nuccore/MW534740.1?report=fasta) [Graphics](https://www.ncbi.nlm.nih.gov/nuccore/MW534740.1?report=graph)

[Go to:](https://www.ncbi.nlm.nih.gov/nuccore/MW534740.1%22%20%5Cl%20%22goto1966687909_0)

LOCUS MW534740 1510 bp DNA linear BCT 02-FEB-2021

DEFINITION Cellulosimicrobium cellulans strain MP1 16S ribosomal RNA gene,

 partial sequence.

ACCESSION MW534740

VERSION MW534740.1

KEYWORDS .

SOURCE Cellulosimicrobium cellulans

 ORGANISM [Cellulosimicrobium cellulans](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1710)

 Bacteria; Actinobacteria; Micrococcales; Promicromonosporaceae;

 Cellulosimicrobium.

REFERENCE 1 (bases 1 to 1510)

 AUTHORS Nguyen,V.T., Xuan,D.T., Ha,L.T., Tung,Q.N. and Tien,P.Q.

 TITLE Genome mining of the cellulolytic Cellulosimicrobium cellulans MP1

 isolated from wood-feeding termite

 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 1510)

 AUTHORS Nguyen,V.T., Xuan,D.T., Ha,L.T., Tung,Q.N. and Tien,P.Q.

 TITLE Direct Submission

 JOURNAL Submitted (28-JAN-2021) Fermentation technology, Institute of

 biotechnology, 18 Hoang Quoc Viet, Cau Giay, Ha Noi, Ha Noi, Ha Noi

 100000, Viet Nam

COMMENT ##Assembly-Data-START##

 Sequencing Technology :: ABI PRISM3100-Avant Genetic Analyzer

 ##Assembly-Data-END##

FEATURES Location/Qualifiers

 source 1..1510

 /organism="Cellulosimicrobium cellulans"

 /mol\_type="genomic DNA"

 /strain="MP1"

 /isolation\_source="wood-feeding termite"

 /host="wood-feeding termite"

 /db\_xref="taxon:[1710](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1710)"

 /country="Viet Nam"

 [rRNA](https://www.ncbi.nlm.nih.gov/nuccore/MW534740.1?from=1&to=1510) <1..>1510

 /product="16S ribosomal RNA"

ORIGIN

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 61 gatgaagccc agcttgctgg gtggattagt ggcgaacggg tgagtaacac gtgagtaacc

 121 tgcccttgac ttcgggataa ctccgggaaa ccggggctaa taccggatat gagccgtcct

 181 cgcatggggg tggttggaaa gtttttcggt cagggatggg ctcgcggcct atcagcttgt

 241 tggtggggtg atggcctacc aaggcgacga cgggtagccg gcctgagagg gcgaccggcc

 301 acactgggac tgagacacgg cccagactcc tacgggaggc agcagtgggg aatattgcac

 361 aatgggcgca agcctgatgc agcgacgccg cgtgagggat gaaggccttc gggttgtaaa

 421 cctctttcag cagggaagaa gcgcaagtga cggtacctgc agaagaagcg ccggctaact

 481 acgtgccagc agccgcggta atacgtaggg cgcaagcgtt gtccggaatt attgggcgta

 541 aagagctcgt aggcggtttg tcgcgtctgg tgtgaaaact cgaggctcaa cctcgagctt

 601 gcatcgggta cgggcagact agagtgcggt aggggagact ggaattcctg gtgtagcggt

 661 ggaatgcgca gatatcagga ggaacaccga tggcgaaggc aggtctctgg gccgcaactg

 721 acgctgagga gcgaaagcat ggggagcgaa caggattaga taccctggta gtccatgccg

 781 taaacgttgg gcactaggtg tggggctcat tccacgagtt ccgtgccgca gcaaacgcat

 841 taagtgcccc gcctggggag tacggccgca aggctaaaac tcaaaggaat tgacgggggc

 901 ccgcacaagc ggcggagcat gcggattaat tcgatgcaac gcgaagaacc ttaccaaggc

 961 ttgacatgca cgggaagccg ccagagatgg tggtctcttt ggacactcgt gcacaggtgg

 1021 tgcatggttg tcgtcagctc gtgtcgtgag atgttgggtt aagtcccgca acgagcgcaa

 1081 ccctcgtccc atgttgccag cgggttatgc cggggactca tgggagactg ccggggtcaa

 1141 ctcggaggaa ggtggggatg acgtcaaatc atcatgcccc ttatgtcttg ggcttcacgc

 1201 atgctacaat ggccggtaca aagggctgcg ataccgtaag gtggagcgaa tcccaaaaag

 1261 ccggtctcag ttcggattgg ggtctgcaac tcgaccccat gaagtcggag tcgctagtaa

 1321 tcgcagatca gcaacgctgc ggtgaatacg ttcccgggcc ttgtacacac cgcccgtcaa

 1381 gtcacgaaag tcggtaacac ccgaagccca tggcccaacc gttcgcgggg ggagtggtcg

 1441 aaggtgggac tggcgattgg gactaagtcg taacaaggta gccgtaccgg aaggtgcggc

 1501 tggatcacct

//

Genomic information of the strain MP1

# Cellulosimicrobium cellulans strain MP1, whole genome shotgun sequencing project

GenBank: JAFGYF000000000.1

* This entry is the master record for a whole genome shotgun sequencing project and contains no sequence data.

[Go to:](https://www.ncbi.nlm.nih.gov/nuccore/JAFGYF000000000%22%20%5Cl%20%22goto1993247178_0)

LOCUS JAFGYF010000000 23 rc DNA linear BCT 23-FEB-2021

DEFINITION Cellulosimicrobium cellulans strain MP1, whole genome shotgun

 sequencing project.

ACCESSION JAFGYF000000000

VERSION JAFGYF000000000.1

DBLINK BioProject: [PRJNA695363](https://www.ncbi.nlm.nih.gov/bioproject/PRJNA695363)

 BioSample: [SAMN17612315](https://www.ncbi.nlm.nih.gov/biosample/SAMN17612315)

KEYWORDS WGS.

SOURCE Cellulosimicrobium cellulans

 ORGANISM [Cellulosimicrobium cellulans](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1710)

 Bacteria; Actinobacteria; Micrococcales; Promicromonosporaceae;

 Cellulosimicrobium.

REFERENCE 1 (bases 1 to 23)

 AUTHORS Dao,T.-T.-X., Vu,T.-H.-N., Le,T.-H., Quach,N.-T., Le,P.-C. and

 Phi,Q.-T.

 TITLE A genomic perspective on the potential of symbiotic

 Cellulosimicrobium cellulans MP1 as producer of plant

 biomass-acting enzyme and exopolysaccharide

 JOURNAL Unpublished

REFERENCE 2 (bases 1 to 23)

 AUTHORS Dao,T.-T.-X., Vu,T.-H.-N., Le,T.-H., Quach,N.-T., Le,P.-C. and

 Phi,Q.-T.

 TITLE Direct Submission

 JOURNAL Submitted (03-FEB-2021) Vietnam Academy of Science and Technology

 (VAST) Culture Collection of Microorganisms, Institute of

 Biotechnology, 18 Hoang Quoc Viet, Hanoi, Vietnam, Hanoi 100000,

 Viet Nam

COMMENT The Cellulosimicrobium cellulans whole genome shotgun (WGS) project

 has the project accession JAFGYF000000000. This version of the

 project (01) has the accession number JAFGYF010000000, and consists

 of sequences JAFGYF010000001-JAFGYF010000023.

 The annotation was added by the NCBI Prokaryotic Genome Annotation

 Pipeline (PGAP). Information about PGAP can be found here:

 <https://www.ncbi.nlm.nih.gov/genome/annotation_prok/>

 Bacteria and source DNA available from Quyet-Tien Phi.

 ##Genome-Assembly-Data-START##

 Assembly Method :: SPAdes v. 3.13

 Genome Representation :: Full

 Expected Final Version :: Yes

 Genome Coverage :: 75.96x

 Sequencing Technology :: Illumina MiSeq

 ##Genome-Assembly-Data-END##

 ##Genome-Annotation-Data-START##

 Annotation Provider :: NCBI

 Annotation Date :: 02/18/2021 18:13:57

 Annotation Pipeline :: NCBI Prokaryotic Genome

 Annotation Pipeline (PGAP)

 Annotation Method :: Best-placed reference protein

 set; GeneMarkS-2+

 Annotation Software revision :: 5.1

 Features Annotated :: Gene; CDS; rRNA; tRNA; ncRNA;

 repeat\_region

 Genes (total) :: 4,088

 CDSs (total) :: 4,027

 Genes (coding) :: 3,964

 CDSs (with protein) :: 3,964

 Genes (RNA) :: 61

 rRNAs :: 1, 1, 1 (5S, 16S, 23S)

 complete rRNAs :: 1, 1, 1 (5S, 16S, 23S)

 tRNAs :: 55

 ncRNAs :: 3

 Pseudo Genes (total) :: 63

 CDSs (without protein) :: 63

 Pseudo Genes (ambiguous residues) :: 0 of 63

 Pseudo Genes (frameshifted) :: 19 of 63

 Pseudo Genes (incomplete) :: 44 of 63

 Pseudo Genes (internal stop) :: 5 of 63

 Pseudo Genes (multiple problems) :: 5 of 63

 ##Genome-Annotation-Data-END##

FEATURES Location/Qualifiers

 source 1..23

 /organism="Cellulosimicrobium cellulans"

 /mol\_type="genomic DNA"

 /strain="MP1"

 /isolation\_source="gut"

 /host="termite"

 /db\_xref="taxon:[1710](https://www.ncbi.nlm.nih.gov/Taxonomy/Browser/wwwtax.cgi?id=1710)"

 /country="Viet Nam: Nghe An province"

 /collection\_date="2017"

WGS [JAFGYF010000001-JAFGYF010000023](https://www.ncbi.nlm.nih.gov/Traces/wgs/JAFGYF01?display=contigs)

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