Resource Summary Report

Generated by FDI Lab - SciCrunch.org on May 8, 2025

HOMD

RRID:SCR_012770
Type: Tool

Proper Citation

HOMD (RRID:SCR_012770)

Resource Information

URL: http://www.homd.org/index.php

Proper Citation: HOMD (RRID:SCR_012770)

Description: THIS RESOURCE IS NO LONGER IN SERVICE.Documented on April 14,2022. Database of comprehensive information on the approximately 600 prokaryote species that are present in the human oral cavity. The majority of these species are uncultivated and unnamed, recognized primarily by their 16S rRNA sequences. The HOMD presents a provisional naming scheme for the currently unnamed species so that strain, clone, and probe data from any laboratory can be directly linked to a stably named reference entity. The HOMD links sequence data with phenotypic, phylogenetic, clinical, and bibliographic information. Full and partial oral bacterial genome sequences determined as part of this project and the Human Microbiome Project, are being added to the HOMD as they become available. HOMD offers easy to use tools for viewing all publicly available oral bacterial genomes. Data is also downloadable.

Abbreviations: HOMD

Synonyms: Human Oral Microbiome Database

Resource Type: data or information resource, database

Defining Citation: PMID:20624719, PMID:20656903

Keywords: taxon, genome, 16s rna, sequence, actinobacteria, bacteroidetes, chlamydiae, chloroflexi, euryarchaeota, firmicutes, fusobacteria, proteobacteria, spirochaetes, sr1, synergistetes, tenericutes, tm7, nomenclature, naming scheme, human, FASEB list

Funding: NIDCR ;
ARRA ;

DOE contract U01 DE016937;
DOE DE016937;
DOE DE015847;
DOE DE017106

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: HOMD

Resource ID: SCR_012770

Alternate IDs: nlx_22198

Record Creation Time: 20220129T080312+0000

Record Last Update: 20250507T060851+0000

Ratings and Alerts

No rating or validation information has been found for HOMD.

No alerts have been found for HOMD.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 137 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Schechter MS, et al. (2025) Ribosomal protein phylogeography offers quantitative insights into the efficacy of genome-resolved surveys of microbial communities. bioRxiv : the preprint server for biology.

Rocha ST, et al. (2025) The prevalence of motility-related genes within the human oral microbiota. Microbiology spectrum, 13(1), e0126424.

Fan X, et al. (2024) Altered salivary microbiota associated with high-sugar beverage consumption. Scientific reports, 14(1), 13386.

Mann AE, et al. (2024) Heterogeneous lineage-specific arginine deiminase expression within dental microbiome species. Microbiology spectrum, 12(4), e0144523.

Ovsepian A, et al. (2024) Microbial signatures in human periodontal disease: a

metatranscriptome meta-analysis. Frontiers in microbiology, 15, 1383404.

Yakar N, et al. (2024) Targeted elimination of Fusobacterium nucleatum alleviates periodontitis. Journal of oral microbiology, 16(1), 2388900.

Casarin RCV, et al. (2024) Metatranscriptomic analysis shows functional alterations in subgingival biofilm in young smokers with periodontitis: a pilot study. Journal of applied oral science : revista FOB, 32, e20240031.

Khan MW, et al. (2024) A cross-cohort analysis of dental plaque microbiome in early childhood caries. iScience, 27(8), 110447.

Min K, et al. (2024) Quantitative analysis of the effects of essential oil mouthrinses on clinical plaque microbiome: a parallel-group, randomized trial. BMC oral health, 24(1), 578.

Wang M, et al. (2024) ADAPT: Analysis of Microbiome Differential Abundance by Pooling Tobit Models. bioRxiv : the preprint server for biology.

Esberg A, et al. (2024) Saliva microbiome profiling by full-gene 16S rRNA Oxford Nanopore Technology versus Illumina MiSeq sequencing. NPJ biofilms and microbiomes, 10(1), 149.

Roca C, et al. (2024) Saliva sampling method influences oral microbiome composition and taxa distribution associated with oral diseases. PloS one, 19(3), e0301016.

Merali N, et al. (2024) The microbial composition of pancreatic ductal adenocarcinoma: a systematic review of 16S rRNA gene sequencing. International journal of surgery (London, England), 110(10), 6771.

van der Ploeg GR, et al. (2024) Multi-way modelling of oral microbial dynamics and host-microbiome interactions during induced gingivitis. NPJ biofilms and microbiomes, 10(1), 89.

Chopra A, et al. (2024) Exploring the presence of oral bacteria in non-oral sites of patients with cardiovascular diseases using whole metagenomic data. Scientific reports, 14(1), 1476.

Yama K, et al. (2024) Oral Microbiota Development in the First 60 Months: A Longitudinal Study. Journal of dental research, 103(12), 1249.

Zecha JAEM, et al. (2024) Oral microbial changes, oral mucositis and febrile neutropenia during myelosuppressive chemotherapy in patients diagnosed with a solid tumor or lymphoma. Frontiers in oral health, 5, 1461463.

Zhu B, et al. (2024) The association of maternal factors with the neonatal microbiota and health. Nature communications, 15(1), 5260.

Akase T, et al. (2024) Association of Fusobacterium nucleatum in human saliva with periodontal status and composition of the salivary microbiome including periodontopathogens. Microbiology spectrum, 12(12), e0085524.

Nagai T, et al. (2024) Optimal 16S rRNA gene amplicon sequencing analysis for oral microbiota to avoid the potential bias introduced by trimming length, primer, and database.

Microbiology spectrum, 12(12), e0351223.