

Resource Summary Report

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SOAPindel

RRID:SCR_005272

Type: Tool

Proper Citation

SOAPindel (RRID:SCR_005272)

Resource Information

URL: <http://soap.genomics.org.cn/soapindel.html>

Proper Citation: SOAPindel (RRID:SCR_005272)

Description: Software focusing on calling indels from the next-generation paired-end sequencing data.

Abbreviations: SOAPindel

Resource Type: software resource

Defining Citation: [PMID:22972939](#)

Resource Name: SOAPindel

Resource ID: SCR_005272

Alternate IDs: OMICS_00099

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260725T190604+0000

Ratings and Alerts

No rating or validation information has been found for SOAPindel.

No alerts have been found for SOAPindel.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 44 mentions in open access literature.

Listed below are recent publications. The full list is available at [nidm-terms](#) .

Hu J, et al. (2024) Characterizing core microbiota and regulatory functions of the pig gut microbiome. *The ISME journal*, 18(1).

Sun X, et al. (2023) Metabolic interactions affect the biomass of synthetic bacterial biofilm communities. *mSystems*, 8(6), e0104523.

Liu JY, et al. (2023) Proposal to classify *Ralstonia solanacearum* phylotype I strains as *Ralstonia nicotianae* sp. nov., and a genomic comparison between members of the genus *Ralstonia*. *Frontiers in microbiology*, 14, 1135872.

Ma J, et al. (2023) Acquisition of Type I methyltransferase via horizontal gene transfer increases the drug resistance of *Aeromonas veronii*. *Microbial genomics*, 9(9).

Huang Y, et al. (2023) Epidemiological characteristics of multidrug-resistant *Acinetobacter baumannii* ST369 in Anhui, China. *mSystems*, 8(5), e0073123.

Luo H, et al. (2022) Genes and evolutionary fates of the amanitin biosynthesis pathway in poisonous mushrooms. *Proceedings of the National Academy of Sciences of the United States of America*, 119(20), e2201113119.

Xu G, et al. (2022) Combined assembly of long and short sequencing reads improve the efficiency of exploring the soil metagenome. *BMC genomics*, 23(1), 37.

Yang X, et al. (2022) Genetic characteristics of an amikacin-resistant *Brucella abortus* strain first isolated from *Marmota himalayana*. *Microbial pathogenesis*, 164, 105402.

Sun X, et al. (2022) *Bacillus velezensis* stimulates resident rhizosphere *Pseudomonas stutzeri* for plant health through metabolic interactions. *The ISME journal*, 16(3), 774.

Liu X, et al. (2022) Insights into Evolutionary, Genomic, and Biogeographic Characterizations of *Chryseobacterium nepalense* Represented by a Polyvinyl Alcohol-Degrading Bacterium, AC3. *Microbiology spectrum*, 10(5), e0217922.

Li J, et al. (2022) Cultured Bacteria Provide Insight into the Functional Potential of the Coral-Associated Microbiome. *mSystems*, 7(4), e0032722.

He Z, et al. (2022) Comparative genomic analyses of Polymyxin-resistant *Enterobacteriaceae* strains from China. *BMC genomics*, 23(1), 88.

Wang D, et al. (2021) Functional Genomics and Comparative Lineage-Specific Region Analyses Reveal Novel Insights into Race Divergence in *Verticillium dahliae*. *Microbiology spectrum*, 9(3), e0111821.

Wang B, et al. (2020) Genomic Analysis of *Bacillus megaterium* NCT-2 Reveals Its Genetic Basis for the Bioremediation of Secondary Salinization Soil. *International journal of genomics*, 2020, 4109186.

Cai Z, et al. (2020) Comparative genomics of *Klebsiella michiganensis* BD177 and related members of *Klebsiella* sp. reveal the symbiotic relationship with *Bactrocera dorsalis*. BMC genetics, 21(Suppl 2), 138.

Ye Y, et al. (2020) Discovery of Three 22-Membered Macrolides by Deciphering the Streamlined Genome of Mangrove-Derived *Streptomyces* sp. HM190. Frontiers in microbiology, 11, 1464.

Serrano C, et al. (2020) Clinical value of next generation sequencing of plasma cell-free DNA in gastrointestinal stromal tumors. BMC cancer, 20(1), 99.

Guang XM, et al. (2019) IDSSR: An Efficient Pipeline for Identifying Polymorphic Microsatellites from a Single Genome Sequence. International journal of molecular sciences, 20(14).

Wu Y, et al. (2019) Microevolution within ST11 group *Clostridioides difficile* isolates through mobile genetic elements based on complete genome sequencing. BMC genomics, 20(1), 796.

Tang J, et al. (2019) Complete Genome Sequence and Comparative Analysis of *Synechococcus* sp. CS-601 (SynAce01), a Cold-Adapted Cyanobacterium from an Oligotrophic Antarctic Habitat. International journal of molecular sciences, 20(1).