

Resource Summary Report

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SOPRA

RRID:SCR_005035

Type: Tool

Proper Citation

SOPRA (RRID:SCR_005035)

Resource Information

URL: <http://www.physics.rutgers.edu/~anirvans/SOPRA/>

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Description: Software tool to exploit the mate pair/paired-end information for assembly of short reads from high throughput sequencing platforms, e.g. Illumina and SOLiD.

Abbreviations: SOPRA

Synonyms: SOPRA - Statistical Optimization of Paired Read Assembly, Statistical Optimization of Paired Read Assembly

Resource Type: software resource

Defining Citation: [PMID:20576136](#)

Keywords: bio.tools

Funding:

Availability: Acknowledgement requested

Resource Name: SOPRA

Resource ID: SCR_005035

Alternate IDs: biotools:sopra, OMICS_00049

Alternate URLs: <https://bio.tools/sopra>

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250410T065223+0000

Ratings and Alerts

No rating or validation information has been found for SOPRA.

No alerts have been found for SOPRA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Saif OM, et al. (2023) Design and Optimization of a Self-Protected Thin Film c-Si Solar Cell against Reverse Bias. Materials (Basel, Switzerland), 16(6).

Tonin R, et al. (2023) Ice holes microrefugia harbor genetically and functionally distinct populations of Vaccinium vitis-idaea (Ericaceae). Scientific reports, 13(1), 13055.

Salles P, et al. (2022) Bendable Polycrystalline and Magnetic CoFe₂O₄ Membranes by Chemical Methods. ACS applied materials & interfaces, 14(10), 12845.

Li M, et al. (2022) RegScaf: a regression approach to scaffolding. Bioinformatics (Oxford, England), 38(10), 2675.

Cannazza P, et al. (2021) Characterization of Komagataeibacter Isolate Reveals New Prospects in Waste Stream Valorization for Bacterial Cellulose Production. Microorganisms, 9(11).

Siciliani de Cumis M, et al. (2021) Direct Comb Vernier Spectroscopy for Fractional Isotopic Ratio Determinations. Sensors (Basel, Switzerland), 21(17).

Di Carlo G, et al. (2020) Electric-Field-Induced Second Harmonic Generation Nonlinear Optic Response of A4 ?-Pyrrolic-Substituted ZnII Porphyrins: When Cubic Contributions Cannot Be Neglected. Inorganic chemistry, 59(11), 7561.

Sudre G, et al. (2020) Responsive Adsorption of N-Isopropylacrylamide Based Copolymers on Polymer Brushes. Polymers, 12(1).

Morard M, et al. (2020) Genome structure reveals the diversity of mating mechanisms in *Saccharomyces cerevisiae* x *Saccharomyces kudriavzevii* hybrids, and the genomic instability that promotes phenotypic diversity. *Microbial genomics*, 6(3).

Ali N, et al. (2019) Ferromagnetism from non-magnetic ions: Ag-doped ZnO. *Scientific reports*, 9(1), 20039.

Macías LG, et al. (2019) Comparative Genomics Between *Saccharomyces kudriavzevii* and *S. cerevisiae* Applied to Identify Mechanisms Involved in Adaptation. *Frontiers in genetics*, 10, 187.

Iwasaka H, et al. (2018) A Possible Trifunctional β -Carotene Synthase Gene Identified in the Draft Genome of *Aurantiochytrium* sp. Strain KH105. *Genes*, 9(4).

Xu J, et al. (2017) Genomic Basis of Adaptive Evolution: The Survival of *Amur Ide* (*Leuciscus waleckii*) in an Extremely Alkaline Environment. *Molecular biology and evolution*, 34(1), 145.

Chen L, et al. (2016) Genome Sequence of the Edible Cultivated Mushroom *Lentinula edodes* (Shiitake) Reveals Insights into Lignocellulose Degradation. *PloS one*, 11(8), e0160336.

Gao S, et al. (2016) OPERA-LG: efficient and exact scaffolding of large, repeat-rich eukaryotic genomes with performance guarantees. *Genome biology*, 17, 102.

Farrant GK, et al. (2015) WiseScaffolder: an algorithm for the semi-automatic scaffolding of Next Generation Sequencing data. *BMC bioinformatics*, 16, 281.

Rastogi S, et al. (2015) Unravelling the genome of Holy basil: an "incomparable" "elixir of life" of traditional Indian medicine. *BMC genomics*, 16(1), 413.

El-Metwally S, et al. (2013) Next-generation sequence assembly: four stages of data processing and computational challenges. *PLoS computational biology*, 9(12), e1003345.

Kremer FS, et al. () Approaches for in silico finishing of microbial genome sequences. *Genetics and molecular biology*, 40(3), 553.