

Resource Summary Report

Generated by [RRID](#) on Apr 19, 2025

SOPRA

RRID:SCR_005035

Type: Tool

Proper Citation

SOPRA (RRID:SCR_005035)

Resource Information

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

Proper Citation: SOPRA (RRID:SCR_005035)

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 [RRID](#).

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).

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

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

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.