

Resource Summary Report

Generated by [NIF](#) on Sep 15, 2026

Sage Science

RRID:SCR_014808

Type: Tool

Proper Citation

Sage Science (RRID:SCR_014808)

Resource Information

URL: <http://www.sagescience.com/>

Proper Citation: Sage Science (RRID:SCR_014808)

Description: Biotechnology company that develops products for genomics research and molecular diagnostics, such as systems for DNA and protein analysis, DNA and protein fractionation technologies, and other sequencing equipment.

Synonyms: Sage Science Inc

Resource Type: instrument manufacture, material service resource, production service resource, service resource

Keywords: electrophoresis instrument, genomics, molecular diagnostics, dna, rna, sequencing, biotechnology, instrument, instrument supplier

Funding: Privately funded

Resource Name: Sage Science

Resource ID: SCR_014808

Alternate IDs: grid.470425.0

Alternate URLs: <https://ror.org/018z5vy82>

Record Creation Time: 20220129T080322+0000

Record Last Update: 20260912T195822+0000

Ratings and Alerts

No rating or validation information has been found for Sage Science.

No alerts have been found for Sage Science.

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 [NIF](#) .

Haile AT, et al. (2024) Limited genetic diversity found among genotypes of the Entada landrace (*Ensete ventricosum*, (Welw.) Chessman) from Ethiopia. *Frontiers in plant science*, 15, 1336461.

Buswell VG, et al. (2023) When One's Not Enough: Colony Pool-Seq Outperforms Individual-Based Methods for Assessing Introgression in *Apis mellifera mellifera*. *Insects*, 14(5).

Chen L, et al. (2022) Integrating Metabolomics and Transcriptomics to Unveil Atisine Biosynthesis in *Aconitum gymnantrum* Maxim. *International journal of molecular sciences*, 23(21).

Machado AM, et al. (2022) A genome assembly of the Atlantic chub mackerel (*Scomber colias*): a valuable teleost fishing resource. *GigaByte (Hong Kong, China)*, 2022, gigabyte40.

Liu J, et al. (2022) Full-Length Transcriptome Sequencing Reveals Alternative Splicing and lncRNA Regulation during Nodule Development in *Glycine max*. *International journal of molecular sciences*, 23(13).

Yi X, et al. (2022) Genome assembly of the JD17 soybean provides a new reference genome for comparative genomics. *G3 (Bethesda, Md.)*, 12(4).

Tang Q, et al. (2021) Single-Molecule Real-Time and Illumina Sequencing to Analyze Transcriptional Regulation of Flavonoid Synthesis in Blueberry. *Frontiers in plant science*, 12, 754325.

Li H, et al. (2021) Investigation Into Different Wood Formation Mechanisms Between Angiosperm and Gymnosperm Tree Species at the Transcriptional and Post-transcriptional Level. *Frontiers in plant science*, 12, 698602.

Espinosa E, et al. (2020) Protocol for High-Throughput Analysis of Sister-Chromatids Contacts. *STAR protocols*, 1(3), 100202.

Zhang D, et al. (2020) SMRT- and Illumina-based RNA-seq analyses unveil the ginsenoside biosynthesis and transcriptomic complexity in *Panax notoginseng*. *Scientific reports*, 10(1), 15310.

Hu H, et al. (2020) Analysis of Alternative Splicing and Alternative Polyadenylation in *Populus alba* var. *pyramidalis* by Single-Molecular Long-Read Sequencing. *Frontiers in genetics*, 11, 48.

Castandet B, et al. (2019) Systematic sequencing of chloroplast transcript termini from *Arabidopsis thaliana* reveals >200 transcription initiation sites and the extensive imprints of RNA-binding proteins and secondary structures. *Nucleic acids research*, 47(22), 11889.

Monat C, et al. (2019) TRITEX: chromosome-scale sequence assembly of Triticeae genomes with open-source tools. *Genome biology*, 20(1), 284.

Forde BM, et al. (2019) SMRT sequencing reveals differential patterns of methylation in two O111:H- STEC isolates from a hemolytic uremic syndrome outbreak in Australia. *Scientific reports*, 9(1), 9436.

Feng S, et al. (2019) Reconstruction of the full-length transcriptome atlas using PacBio Iso-Seq provides insight into the alternative splicing in *Gossypium australe*. *BMC plant biology*, 19(1), 365.

Mattingsdal M, et al. (2018) A continuous genome assembly of the corkwing wrasse (*Symphodus melops*). *Genomics*, 110(6), 399.

Pecrix Y, et al. (2018) Whole-genome landscape of *Medicago truncatula* symbiotic genes. *Nature plants*, 4(12), 1017.

Erill I, et al. (2017) Comparative Analysis of *Ralstonia solanacearum* Methyloomes. *Frontiers in plant science*, 8, 504.

Tomi? TT, et al. (2017) A new GTF2I-BRAF fusion mediating MAPK pathway activation in pilocytic astrocytoma. *PloS one*, 12(4), e0175638.