

# Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 16, 2026

## Montpellier GenomiX Core Facility

RRID:SCR\_023091

Type: Tool

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### Proper Citation

Montpellier GenomiX Core Facility (RRID:SCR\_023091)

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### Resource Information

**URL:** <http://www.mgx.cnrs.fr>

**Proper Citation:** Montpellier GenomiX Core Facility (RRID:SCR\_023091)

**Description:** Offers genomic technologies to academic laboratories and biotechnology companies. Application portfolio includes Whole genome (re)sequencing, including the identification of variants (SNVs, mutations, indels, CNVs); Targeted sequencing, for instance exomes; Transcriptome analyses (RNA-Seq, small RNA-Seq, microarrays), including in single cells (single-cell 3 RNA-seq); Determination of chromatin structure and dynamics (ChIP-Seq, FAIRE-Seq, Hi-C); Epigenetic analyses (ChIP-Seq, RRBS, Bisulphite-Seq); Genotyping (RAD-Seq, GBS, microarrays).

**Abbreviations:** MGX

**Synonyms:** Montpellier GenomiX

**Resource Type:** access service resource, core facility, service resource

**Keywords:** USEEdit, ABRF, genomic technologies

**Availability:** Open

**Resource Name:** Montpellier GenomiX Core Facility

**Resource ID:** SCR\_023091

**Alternate IDs:** ABRF\_1653

**Alternate URLs:** <https://coremarketplace.org/?FacilityID=1653&citation=1>

**Record Creation Time:** 20221230T050203+0000

**Record Last Update:** 20260912T200422+0000

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### Ratings and Alerts

No rating or validation information has been found for Montpellier GenomiX Core Facility.

No alerts have been found for Montpellier GenomiX Core Facility.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 11 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [SPARC SAWG](#) .

Debiais-Thibaud M, et al. (2026) Transcriptomic signature of differentiating catshark cartilage unravels the co-evolution of the Spp2 gene family with skeletal mineralisation in cartilaginous fish. BMC biology, 24(1).

Ara??jo NH, et al. (2025) The receptor-like cytoplasmic kinase AeRLCK2 mediates Nod-independent rhizobial symbiosis in Aeschynomene legumes. The Plant cell, 37(8).

Gaucher J, et al. (2024) Long-term intermittent hypoxia in mice induces inflammatory pathways implicated in sleep apnea and steatohepatitis in humans. iScience, 27(2), 108837.

de la Fuente C, et al. (2024) Glutaredoxin regulation of primary root growth is associated with early drought stress tolerance in pearl millet. eLife, 12.

Pieri A, et al. (2024) Transcriptomic response to nitrogen availability reveals signatures of adaptive plasticity during tetraploid wheat domestication. The Plant cell, 36(9), 3809.

van der Lans SPA, et al. (2023) Colistin resistance mutations in phoQ can sensitize Klebsiella pneumoniae to IgM-mediated complement killing. Scientific reports, 13(1), 12618.

Boulanger M, et al. (2023) DeSUMOylation of chromatin-bound proteins limits the rapid transcriptional reprogramming induced by daunorubicin in acute myeloid leukemias. Nucleic acids research, 51(16), 8413.

Chambard M, et al. (2023) Living yeast-based biostimulants: different genes for the same results? Frontiers in plant science, 14, 1171564.

King E, et al. (2023) Paraburkholderia phytofirmans PsJN colonization of rice endosphere triggers an atypical transcriptomic response compared to rice native Burkholderia s.l. endophytes. Scientific reports, 13(1), 10696.

Akkawi C, et al. (2023) Murine leukemia virus (MLV) P50 protein induces cell transformation via transcriptional regulatory function. Retrovirology, 20(1), 16.

Lebdy R, et al. (2023) The nucleolar protein GNL3 prevents resection of stalled replication forks. EMBO reports, 24(12), e57585.