



MolthMark

AI-Enhanced Biomarker Discovery



Your Partner in Gene Marker Discovery

Academic customers

Push the boundaries of science in genomics and epigenomics, discovering new gene markers to understand the fundamental mechanisms underlying biological process and disease.

Industrial customers

Translate gene marker discoveries into practical applications, developing new diagnostics, treatments, and therapies to improve patient outcomes and advance public health.

Challenges in the Discovery of Gene Markers

Wet-Lab Sample Preparation

One of the biggest challenges in gene marker discovery is the meticulous preparation of high-quality samples, as any error in this critical initial phase can lead to unreliable results.

Multi-Omics Data Analysis

Analyzing multi-omics data is challenging due to its volume and complexity, but AI-enhanced techniques offer more accurate and comprehensive insights than traditional bioinformatics methods.

How can we identify gene markers at the genome-wide level?

MolthMark is a customized multi-omics platform designed for genome-wide gene marker identification. It serves both academic and industrial customers, supporting them from multi-omics sample preparation to comprehensive omics data analysis in their quest to discover gene markers.



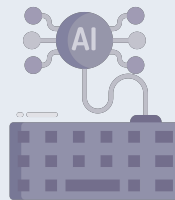
What we provide:

One-stop Wet Lab Service



- Tissue or cell sample preparation: Ensuring high-quality samples for reliable results.
- Multi-omics library generation: Creating libraries for various omics analyses.
- Next-generation sequencing: Comprehensive sequencing services including RNA-seq, ATAC-seq, ChIP-seq, CUT&Tag, and more.

AI-enhanced Omics Data Analysis



- Integrated multi-omics data analysis: From raw data to comprehensive reports.
- More accurate than traditional bioinformatics analysis: Leveraging AI for precision.
- Transform your data into valuable gene marker discoveries: Making sense of complex data to drive meaningful insights.

Contact us

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Visit our website at www.molth.com for more information.

