# Resource Summary Report

Generated by dkNET on Aug 31, 2026

# Motif Mutation Analysis for Regulatory Genomic Elements

RRID:SCR_021902
Type: Tool

## Proper Citation

Motif Mutation Analysis for Regulatory Genomic Elements (RRID:SCR_021902)

## Resource Information

**URL:** https://github.com/vlink/marge

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**Description:** Software package that integrates genome wide genetic variation with epigenetic data to identify collaborative transcription factor pairs. Optimized to work with chromatin accessibility assays such as ATAC-seq or DNase I hypersensitivity, as well as transcription factor binding data collected by ChIP-seq. Used to identify combinations of cell type specific transcription factors while simultaneously interpreting functional effects of non-coding genetic variation.

**Abbreviations:** MMARGE

**Resource Type:** data analysis software, data processing software, software application, software resource, software toolkit

**Defining Citation:** PMID:29893919

**Keywords:** genome wide genetic variation, epigenetic data, identify collaborative transcription factor pairs, interpreting functional effects, non-coding genetic variation

**Funding:** NCI CA173903;
NHLBI R00 123485;
NIDDK DK091183;
NIGMS GM085764

**Availability:** Free, Available for download, Freely available

**Resource Name:** Motif Mutation Analysis for Regulatory Genomic Elements

**Resource ID:** SCR_021902

**Record Creation Time:** 20220421T050137+0000

**Record Last Update:** 20260829T182720+0000

## Ratings and Alerts

No rating or validation information has been found for Motif Mutation Analysis for Regulatory Genomic Elements.

No alerts have been found for Motif Mutation Analysis for Regulatory Genomic Elements.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 608 mentions in open access literature.

**Listed below are recent publications.** The full list is available at dkNET .


Liedtke V, et al. (2025) Linking LEDGF/p75 Overexpression With Microsatellite Instability and KRAS Mutations: A Small-Scale Study in Colorectal Cancer. Cancer control : journal of the Moffitt Cancer Center, 32, 10732748251313499.

Zhu W, et al. (2025) Comprehensive analysis of CLEC family genes in gastric cancer prognosis immune response and treatment. Scientific reports, 15(1), 5956.

da Rocha ACA, et al. (2025) Ganciclovir Resistance-Linked Mutations in the HCMV UL97 Gene: Sanger Sequencing Analysis in Samples from Transplant Recipients at a Tertiary Hospital in Southern Brazil. Diagnostics (Basel, Switzerland), 15(2).

Huang F, et al. (2024) M2 Macrophage Classification of Colorectal Cancer Reveals Intrinsic Connections with Metabolism Reprogramming and Clinical Characteristics. Pharmacogenomics and personalized medicine, 17, 383.

Ariyaratne D, et al. (2024) Simultaneous co-circulation of two genotypes of dengue virus serotype 3 causing a large outbreak in Sri Lanka in year 2023. medRxiv : the preprint server for health sciences.

Aba Ü, et al. (2024) A Novel Homozygous Germline Mutation in Transferrin Receptor 1 (TfR1) Leads to Combined Immunodeficiency and Provides New Insights into Iron-Immunity Axis. Journal of clinical immunology, 44(2), 55.

Xiang Z, et al. (2024) Engineering of a DNA/?PNA Hybrid Nanoreporter for ctDNA Mutation Detection via ?PNA Urinalysis. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(33), e2310225.

Lu H, et al. (2024) Prognostic Value of IGFBP6 in Breast Cancer: Focus on Glucometabolism. Technology in cancer research & treatment, 23, 15330338241271998.

Bhuiyan MSI, et al. (2024) Trichophyton mentagrophytes ITS Genotype VIII/Trichophyton indotineae Infection and Antifungal Resistance in Bangladesh. Journal of fungi (Basel, Switzerland), 10(11).

Li X, et al. (2024) Machine Learning-Based Pathomics Model to Predict the Prognosis in Clear Cell Renal Cell Carcinoma. Technology in cancer research & treatment, 23, 15330338241307686.

Kim HS, et al. (2024) Prognostic Model for High-Grade Neuroendocrine Carcinoma of the Lung Incorporating Genomic Profiling and Poly (ADP-ribose) Polymerase-1 Expression. JCO precision oncology, 8, e2300495.

Wu H, et al. (2024) Characterization of novel PHEX variants in X-linked hypophosphatemic rickets and genotype-PHEX activity correlation. The Journal of clinical endocrinology and metabolism.

Sun H, et al. (2024) Prediction of Clinical Precision Chemotherapy by Patient-Derived 3D Bioprinting Models of Colorectal Cancer and Its Liver Metastases. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(2), e2304460.

Mo X, et al. (2024) Impact of Mitophagy-Related Genes on the Diagnosis and Development of Esophageal Squamous Cell Carcinoma via Single-Cell RNA-seq Analysis and Machine Learning Algorithms. Journal of microbiology and biotechnology, 34(11), 2362.

Liu X, et al. (2024) Abnormal Cellular Populations Shape Thymic Epithelial Tumor Heterogeneity and Anti-Tumor by Blocking Metabolic Interactions in Organoids. Advanced science (Weinheim, Baden-Wurttemberg, Germany), 11(42), e2406653.

Shi Z, et al. (2024) CRISPR/Cas9-Based Functional Characterization of SfUGT50A15 Reveals Its Roles in the Resistance of Spodoptera frugiperda to Chlorantraniliprole, Emamectin Benzoate, and Benzoxazinoids. Insects, 15(5).

Andersson E, et al. (2024) Loss of Fshr Prevents Testicular Maturation in Atlantic Salmon (Salmo salar L.). Endocrinology, 165(4).

Zuo W, et al. (2024) A Novel Urine DNA Predictor for Noninvasive Early Diagnosis and Monitoring Minimal Residual Disease of Upper Tract Urothelial Carcinoma. Cancer medicine, 13(20), e70346.

Sukhan ZP, et al. (2024) Molecular Characterization, Expression Analysis, and CRISPR/Cas9 Mediated Gene Disruption of Myogenic Regulatory Factor 4 (MRF4) in Nile Tilapia. Current issues in molecular biology, 46(12), 13725.

Ge H, et al. (2024) A Novel Mutation of the ADAR1 Gene in a Chinese Family with Dyschromatosis Symmetrica Hereditaria and Literature Review. Clinical, cosmetic and investigational dermatology, 17, 2687.