Resource Summary Report

Generated by RRID on Aug 10, 2026

Allelic Dosage corrected Allele Specific human Transcription factor binding sites

RRID:SCR_021863
Type: Tool

Proper Citation

Allelic Dosage corrected Allele Specific human Transcription factor binding sites (RRID:SCR_021863)

Resource Information

URL: https://adastra.autosome.ru/zanthar

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Description: Landscape of allele specific transcription factor binding in human genome. Creators conducted meta analysis of ChIP-Seq experiments and assembled database of allele specific binding events listing more than half million entries at nearly 270 thousand single nucleotide polymorphisms for several hundred human transcription factors and cell types.

Abbreviations: ADASTRA

Resource Type: database, data or information resource

Defining Citation: DOI:10.1038/s41467-021-23007-0

Keywords: Allele specific transcription factor binding, human genome, nucleotide polymorphisms, human transcription factors

Availability: Free, Freely available

Resource Name: Allelic Dosage corrected Allele Specific human Transcription factor binding sites

Resource ID: SCR_021863

Record Creation Time: 20220129T080357+0000

Record Last Update: 20260808T190435+0000

Ratings and Alerts

No rating or validation information has been found for Allelic Dosage corrected Allele Specific human Transcription factor binding sites.

No alerts have been found for Allelic Dosage corrected Allele Specific human Transcription factor binding sites.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

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

Han D, et al. (2024) Comparative analysis of models in predicting the effects of SNPs on TF-DNA binding using large-scale in vitro and in vivo data. Briefings in bioinformatics, 25(2).

Shi W, et al. (2023) Integration of risk variants from GWAS with SARS-CoV-2 RNA interactome prioritizes FUBP1 and RAB2A as risk genes for COVID-19. Scientific reports, 13(1), 19194.

Tahara S, et al. (2023) Transcription factor-binding k-mer analysis clarifies the cell type dependency of binding specificities and cis-regulatory SNPs in humans. BMC genomics, 24(1), 597.

Nakamura K, et al. (2022) Functional analysis of the 1p34.3 risk locus implicates GNL2 in high-grade serous ovarian cancer. American journal of human genetics, 109(1), 116.

Abramov S, et al. (2021) Landscape of allele-specific transcription factor binding in the human genome. Nature communications, 12(1), 2751.