

# Resource Summary Report

Generated by PRECISE-TBI on Sep 19, 2026

## Antibody Validation Database

RRID:SCR\_011996

Type: Tool

### Proper Citation

Antibody Validation Database (RRID:SCR\_011996)

### Resource Information

**URL:** <http://compbio.med.harvard.edu/antibodies/>

**Proper Citation:** Antibody Validation Database (RRID:SCR\_011996)

**Description:** The aim of this site is to collect and to share experimental results on antibodies that would otherwise remain in laboratories, thus aiding researchers in selection and validation of antibodies.

**Abbreviations:** Antibody Validation Database

**Resource Type:** data or information resource, data repository, database, service resource, storage service resource

**Funding:** NHGRI U01 HG004258;  
NHGRI U01 HG004270;  
OER U01 ES017166

**Availability:** The community can contribute to this resource

**Resource Name:** Antibody Validation Database

**Resource ID:** SCR\_011996

**Alternate IDs:** OMICS\_01769

**Record Creation Time:** 20220129T080307+0000

**Record Last Update:** 20260912T195743+0000

### Ratings and Alerts

No rating or validation information has been found for Antibody Validation Database.

No alerts have been found for Antibody Validation Database.

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## Data and Source Information

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

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## Usage and Citation Metrics

We found 15 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [PRECISE-TBI](#) .

Attianese B, et al. (2025) Functional dissection of H3K4 methyltransferases reveals distinct catalytic and non-catalytic roles in *C. elegans* development. *Development* (Cambridge, England), 152(21).

Zhao Y, et al. (2023) ChIP-seq profiling of H3K4me3 and H3K27me3 in an invasive insect, *Bactrocera dorsalis*. *Frontiers in genetics*, 14, 1108104.

Wang J, et al. (2020) Comprehensive Chromosome End Remodeling during Programmed DNA Elimination. *Current biology : CB*, 30(17), 3397.

Rakow S, et al. (2020) Assaying epigenome functions of PRMTs and their substrates. *Methods* (San Diego, Calif.), 175, 53.

Gilda JE, et al. (2015) Western Blotting Inaccuracies with Unverified Antibodies: Need for a Western Blotting Minimal Reporting Standard (WBMRS). *PloS one*, 10(8), e0135392.

Guo Y, et al. (2015) Enrichment of H3K9me2 on Unsynapsed Chromatin in *Caenorhabditis elegans* Does Not Target de Novo Sites. *G3* (Bethesda, Md.), 5(9), 1865.

Kungulovski G, et al. (2015) Quality of histone modification antibodies undermines chromatin biology research. *F1000Research*, 4, 1160.

Castillo-Gonzalez C, et al. (2015) Geminivirus-encoded TrAP suppressor inhibits the histone methyltransferase SUVH4/KYP to counter host defense. *eLife*, 4, e06671.

Kungulovski G, et al. (2014) Application of histone modification-specific interaction domains as an alternative to antibodies. *Genome research*, 24(11), 1842.

Gurard-Levin ZA, et al. (2014) Histone modifications and a choice of variant: a language that helps the genome express itself. *F1000prime reports*, 6, 76.

Shen L, et al. (2013) Human Transcriptome and Chromatin Modifications: An ENCODE Perspective. *Genomics & informatics*, 11(2), 60.

Wei G, et al. (2012) Genome-wide mapping of nucleosome occupancy, histone modifications, and gene expression using next-generation sequencing technology. *Methods in enzymology*, 513, 297.

Kellner WA, et al. (2012) Genome-wide phosphoacetylation of histone H3 at *Drosophila* enhancers and promoters. *Genome research*, 22(6), 1081.

Vielle A, et al. (2012) H4K20me1 contributes to downregulation of X-linked genes for *C. elegans* dosage compensation. *PLoS genetics*, 8(9), e1002933.

Quinn AM, et al. (2011) Methods for Activity Analysis of the Proteins that Regulate Histone Methylation. *Current chemical genomics*, 5(Suppl 1), 95.