

Resource Summary Report

Generated by [RRID](#) on Aug 13, 2026

H2AFZ-human

RRID:AB_304345

Type: Antibody

Proper Citation

Abcam Cat# ab4174, RRID:AB_304345

Antibody Information

URL: http://antibodyregistry.org/AB_304345

Proper Citation: Abcam Cat# ab4174, RRID:AB_304345

Target Antigen: H2AFZ

Host Organism: rabbit

Clonality: polyclonal

Comments: ENCODE PROJECT External validation DATA SET is released testing lot 460460 for any cell type or tissues; status is awaiting lab characterization

Antibody Name: H2AFZ-human

Description: This polyclonal targets H2AFZ

Target Organism: homo sapiens

Antibody ID: AB_304345

Vendor: Abcam

Catalog Number: ab4174

Record Creation Time: 20250820T045634+0000

Record Last Update: 20250820T202107+0000

Ratings and Alerts

- ENCODE PROJECT External validation for lot: 460460 is available under ENCODE ID: ENCAB000AOU - ENCODE

No alerts have been found for H2AFZ-human.

Data and Source Information

Source: [Antibody Registry](#)

Usage and Citation Metrics

We found 19 mentions in open access literature.

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

Tollenaere A, et al. (2026) Mechanisms of gene regulation by SRCAP and H2A.Z. Nature communications, 17(1).

Chen H, et al. (2026) Genome-wide rotational and translational phasing of nucleosomes with human transcription factors. Molecular cell, 86(14), 2722.

Louzon S, et al. (2025) Age- and cell-type-specific effects of histone variant H2BE in the brain. Cell reports, 44(12), 116655.

Sethi SC, et al. (2025) Chromatin remodeling activity of EP400 safeguards chromosomal stability by preventing CENP-A mislocalization. Cell reports, 44(11), 116423.

Patty BJ, et al. (2024) Widespread impact of nucleosome remodelers on transcription at cis-regulatory elements. bioRxiv : the preprint server for biology.

Lee JH, et al. (2024) TGF-?? and RAS jointly unmask primed enhancers to drive metastasis. Cell, 187(22), 6182.

Bomber ML, et al. (2023) Human SMARCA5 is continuously required to maintain nucleosome spacing. Molecular cell, 83(4), 507.

Miao L, et al. (2022) The landscape of pioneer factor activity reveals the mechanisms of chromatin reprogramming and genome activation. Molecular cell, 82(5), 986.

Janas JA, et al. (2022) Tip60-mediated H2A.Z acetylation promotes neuronal fate specification and bivalent gene activation. Molecular cell, 82(24), 4627.

Sun S, et al. (2022) Znhit1 controls meiotic initiation in male germ cells by coordinating with Stra8 to activate meiotic gene expression. Developmental cell, 57(7), 901.

Ohhata T, et al. (2021) Dynamics of transcription-mediated conversion from euchromatin to facultative heterochromatin at the Xist promoter by Tsix. Cell reports, 34(13), 108912.

Jung YH, et al. (2019) Maintenance of CTCF- and Transcription Factor-Mediated Interactions from the Gametes to the Early Mouse Embryo. Molecular cell, 75(1), 154.

Behera V, et al. (2019) Interrogating Histone Acetylation and BRD4 as Mitotic Bookmarks of Transcription. *Cell reports*, 27(2), 400.

Ketchum CC, et al. (2018) Early histone H4 acetylation during chromatin remodeling in equine spermatogenesis. *Biology of reproduction*, 98(1), 115.

Kim J, et al. (2018) Replication Stress Shapes a Protective Chromatin Environment across Fragile Genomic Regions. *Molecular cell*, 69(1), 36.

Clouaire T, et al. (2018) Comprehensive Mapping of Histone Modifications at DNA Double-Strand Breaks Deciphers Repair Pathway Chromatin Signatures. *Molecular cell*, 72(2), 250.

Kieffer-Kwon KR, et al. (2017) Myc Regulates Chromatin Decompaction and Nuclear Architecture during B Cell Activation. *Molecular cell*, 67(4), 566.

Rao SSP, et al. (2017) Cohesin Loss Eliminates All Loop Domains. *Cell*, 171(2), 305.

Cui Z, et al. (2017) SKIP controls flowering time via the alternative splicing of SEF pre-mRNA in Arabidopsis. *BMC biology*, 15(1), 80.