Histone H3 (K9me3) polyclonal antibody

Catalog # PAB31325 Size 50 ug

Applications



ChIP

ChIP assays were performed using human HeLa cells. A titration consisting of 0.2, 0.5, 1, 2 and 5 ug of antibody per ChIP experiment was analyzed. IgG (1 ug/IP) was used as a negative IP control.



ChIP

ChIP-Sea

ChIP assays were performed using human K562 cells. A titration consisting of 0.2, 0.5, 1 and 2 ug of antibody per ChIP experiment was analyzed. IgG (1 ug/IP) was used as a negative IP control. Quantitative PCR was performed with primers specific for the promoter of the active genes GAPDH, c-fos and EIF4A2, used as negative controls, and for ZNF510 and the Sat2 satellite repeat, used as positive controls. The figure shows the recovery, expressed as a % of input (the relative amount of immunoprecipitated DNA compared to input DNA after qPCR analysis).

- Standard Sala

ChIP was performed on sheared chromatin from 100,000 K562 cells using antibody. The figure shows the H3K9me3 signal distribution along the long arm of human chromosome 19 and a zoomin to an enriched region containing several ZNF repeat genes and the signal distribution in a 200 kb region from chromosome 12 surrounding the ZNF12 gene.

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Product Information





Western Blot

Western Blot analysis of (1) 25 ug whole cell extracts of Hela cells, (2) 15 ug histone extracts of Hela cells, (3) 1 ug of recombinant histone H2A, (4) 1 ug of recombinant histone H2B, (5) 1 ug of recombinant histone H3, (6) 1 ug of recombinant histone H4.

Immunofluorescence

Immunofluorescent staining of Hela cell line with antibody followed by an antirabbit antibody conjugated to Alexa488 (top). The middle panel shows staining of the nuclei with DAPI. A merge of the two stainings (bottom).



Enzyme-linked Immunoabsorbent Assay

ELISA is a quantitative method used to determine the titer of the antibody using a serial dilution of antibody against Histone H3 (K9me3). The antigen used was a peptide containing the histone modification of interest. By plotting the absorbance against the antibody dilution, the titer of the antibody was estimated to be 1:11500.



Dot Blot

Cross reactivity test using the Histone H3 (K9me3) antibody. Dot Blot analysis was performed with peptides containing other histone modifications and the unmodified H3K9. One hundred to 0.2 pmol of the respective peptides were spotted on a membrane. The antibody was used at a dilution of 1:20000. The figure shows a high specificity of the antibody for the modification of interest.

Specification	
Product Description	Rabbit polyclonal antibody raised against synthetic peptide of Histone H3 (K9me3).
Immunogen	A synthetic peptide (conjugated with KLH) corresponding to Histone H3, trimethylated at lysine 9.
Host	Rabbit
Reactivity	Human, Mouse
Form	Liquid
Purification	Affinity purification
Recommend Usage	ELISA (1:5000) Western Blot (1:1000) ChIP (1 ug/IP) Dot Blot (1:20000) Immunofluorescence (1:500) The optimal working dilution should be determined by the end user.
Storage Buffer	In PBS (0.05% sodium azide, 0.05% proclin 300).
Storage Instruction	Store at -20°C. For long term storage store at -80°C. Aliquot to avoid repeated freezing and thawing.
Note	This product contains sodium azide: a POISONOUS AND HAZARDOUS SUBSTANCE which shoul d be handled by trained staff only.

Applications

ChIP

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ChIP

ChIP assays were performed using human K562 cells. A titration consisting of 0.2, 0.5, 1 and 2 ug of antibody per ChIP experiment was analyzed. IgG (1 ug/IP) was used as a negative IP control. Quantitative PCR was performed with primers specific for the promoter of the active genes GAPDH, c-fos and EIF4A2, used as negative controls, and for ZNF510 and the Sat2 satellite repeat, used as positive controls. The figure shows the recovery, expressed as a % of input (the relative amount of immunoprecipitated DNA compared to input DNA after qPCR analysis).

ChIP-Seq

ChIP was performed on sheared chromatin from 100,000 K562 cells using antibody. The figure shows the H3K9me3 signal distribution along the long arm of human chromosome 19 and a zoomin to an enriched region containing several ZNF repeat genes and the signal distribution in a 200 kb region from chromosome 12 surrounding the ZNF12 gene.

Western Blot

Western Blot analysis of (1) 25 ug whole cell extracts of Hela cells, (2) 15 ug histone extracts of Hela cells, (3) 1 ug of recombinant histone H2A, (4) 1 ug of recombinant histone H2B, (5) 1 ug of recombinant histone H3, (6) 1 ug of recombinant histone H4.

Immunofluorescence

Immunofluorescent staining of Hela cell line with antibody followed by an anti-rabbit antibody conjugated to Alexa488 (top). The middle panel shows staining of the nuclei with DAPI. A merge of the two stainings (bottom).

Enzyme-linked Immunoabsorbent Assay

ELISA is a quantitative method used to determine the titer of the antibody using a serial dilution of antibody against Histone H3 (K9me3). The antigen used was a peptide containing the histone modification of interest. By plotting the absorbance against the antibody dilution, the titer of the antibody was estimated to be 1:11500.

Dot Blot

Cross reactivity test using the Histone H3 (K9me3) antibody.

Dot Blot analysis was performed with peptides containing other histone modifications and the unmodified H3K9. One hundred to 0.2 pmol of the respective peptides were spotted on a membrane. The antibody was used at a dilution of 1:20000. The figure shows a high specificity of the antibody for the modification of interest.

Gene Info — HIST1H3A

Entrez GenelD	8350
Protein Accession#	<u>P68431</u>
Gene Name	HIST1H3A
Gene Alias	H3/A, H3FA
Gene Description	histone cluster 1, H3a
Omim ID	<u>602810</u>

🍟 Abnova	Product Information
Gene Ontology	Hyperlink
Gene Summary	Histones are basic nuclear proteins that are responsible for the nucleosome structure of the chro mosomal fiber in eukaryotes. This structure consists of approximately 146 bp of DNA wrapped ar ound a nucleosome, an octamer composed of pairs of each of the four core histones (H2A, H2B, H3, and H4). The chromatin fiber is further compacted through the interaction of a linker histone, H 1, with the DNA between the nucleosomes to form higher order chromatin structures. This gene is intronless and encodes a member of the histone H3 family. Transcripts from this gene lack polyA t ails; instead, they contain a palindromic termination element. This gene is found in the large histon e gene cluster on chromosome 6p22-p21.3. [provided by RefSeq
Other Designations	H3 histone family, member A histone 1, H3a

Publication Reference

• Epigenetic dynamics of monocyte-to-macrophage differentiation.

Wallner S, Schroder C, Leitao E, Berulava T, Haak C, Beiber D, Rahmann S, Richter AS, Manke T, Bonisch U, Arrigoni L, Frohler S, Klironomos F, Chen W, Rajewsky N, Müller F, Ebert P, Lengauer T, Barann M, Rosenstiel P, Gasparoni G, Nordstrom K, Walter J, Brors B, Zipprich G, Felder B, Klein-Hitpass L, Attenberger C, Schmitz G, Horsthemke B.

Epigenetics & Chromatin 2016 Jul; 9:33.

Application: ChIP-Seq, Human, Human macrophages, Human monocytes

DNA methylation heterogeneity defines a disease spectrum in Ewing sarcoma.

Sheffield NC, Pierron G, Klughammer J, Datlinger P, Schönegger A, Schuster M, Hadler J, Surdez D, Guillemot D, Lapouble E, Freneaux P, Champigneulle J, Bouvier R, Walder D, Ambros IM, Hutter C, Sorz E, Amaral AT, de Álava E, Schallmoser K, Strunk D, Rinner B, Liegl-Atzwanger B, Huppertz B, Leithner A, de Pinieux G, Terrier P, Laurence V, Michon J, Ladenstein R, Holter W, Windhager R, Dirksen U, Ambros PF, Delattre O, Kovar H, Bock C, Tomazou EM.

Nature Medicine 2017 Mar; 23(3):386.

Application: ChIP, Human, Ewing sarcoma tumors

Immunometabolic Pathways in BCG-Induced Trained Immunity.

Arts RJ, Carvalho A, La Rocca C, Palma C, Rodrigues F, Silvestre R, Kleinnijenhuis J, Lachmandas E, Gonçalves LG, Belinha A, Cunha C, Oosting M, Joosten LA, Matarese G, van Crevel R, Netea MG.

Cell Reports 2016 Dec; 17(10):2562.

Application: ChIP, Human, Human monocytes

<u>TET-dependent regulation of retrotransposable elements in mouse embryonic stem cells.</u>

de la Rica L, Deniz O, Cheng KC, Todd CD, Cruz C, Houseley J, Branco MR.

Genome Biology 2016 Nov; 17(1):234.

Application: ChIP-Seq, Mouse, Mouse embryonic stem cells



<u>β-Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance.</u>

Novakovic B, Habibi E, Wang SY, Arts RJ, Davar R, Megchelenbrink W, Kim B, Kuznetsova T, Kox M, Zwaag J, Matarese F, van Heeringen SJ, Janssen-Megens EM, Sharifi N, Wang C, Keramati F, Schoonenberg V, Flicek P, Clarke L, Pickkers P, Heath S, Gut I, Netea MG, Martens JH, Logie C, Stunnenberg HG.

Cell 2016 Nov; 167(5):1354.

Application: ChIP, Human, Monocytes

The Hematopoietic Transcription Factors RUNX1 and ERG Prevent AML1-ETO Oncogene Overexpression and Onset of the Apoptosis Program in t(8;21) AMLs.

Mandoli A, Singh AA, Prange KH, Tijchon E, Oerlemans M, Dirks R, Ter Huurne M, Wierenga AT, Janssen-Megens EM, Berentsen K, Sharifi N, Kim B, Matarese F, Nguyen LN, Hubner NC, Rao NA, van den Akker E, Altucci L, Vellenga E, Stunnenberg HG, Martens JH.

Cell Reports 2016 Nov; 17(8):2087.

Application: ChIP-Seq, Human, Kasumi-1 cells

Neonatal monocytes exhibit a unique histone modification landscape.

Bermick JR, Lambrecht NJ, denDekker AD, Kunkel SL, Lukacs NW, Hogaboam CM, Schaller MA. Clinical Epigenetics 2016 Sep; 8:99.

Application: ChIP-Seq, Human, Human mononuclear cells

<u>Comprehensive genome and epigenome characterization of CHO cells in response to evolutionary pressures</u> and over time.

Feichtinger J, Hernández I, Fischer C, Hanscho M, Auer N, Hackl M, Jadhav V, Baumann M, Krempl PM, Schmidl C, Farlik M, Schuster M, Merkel A, Sommer A, Heath S, Rico D, Bock C, Thallinger GG, Borth N.

Biotechnology and Bioengineering 2016 Oct; 113(10):2241.

Application: ChIP, Mouse, PF-MCB cells

Deciphering the principles that govern mutually exclusive expression of Plasmodium falciparum clag3 genes.

Rovira-Graells N, Crowley VM, Bancells C, Mira-Martinez S, Ribas de Pouplana L, Cortes A.

Nucleic Acids Research 2015 Sep; 43(17):8243.

Application: ChIP, Parasite, Parasite

Epigenome mapping reveals distinct modes of gene regulation and widespread enhancer reprogramming by the oncogenic fusion protein EWS-FLI1.

Eleni M Tomazou, Nathan C Sheffield, Christian Schmidl, Michael Schuster, Andreas Schonegger, Paul Datlinger, Stefan Kubicek, Christoph Bock, Heinrich Kovar.

Cell Reports 2015 Feb; 10(7):1082.

Application: ChIP-Seq, WB-Ce, Human, A673, SK-N-MC, STA-ET-7.2 cells



Pathway

• Systemic lupus erythematosus