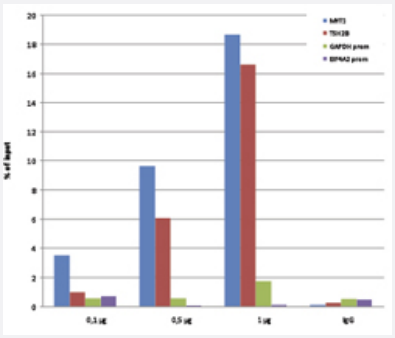
Histone H3 (K27me3) polyclonal antibody

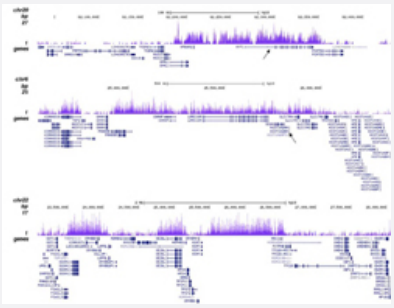
Catalog # PAB31318 Size 50 ug

Applications



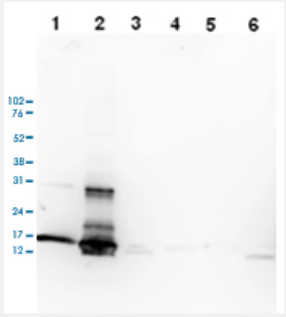
ChIP

ChIP assays were performed using human K562 cells. A titration consisting of 0.1, 0.5, and 1 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 and EIF4A2, used as negative controls, and TSH2B and MYT1, 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).



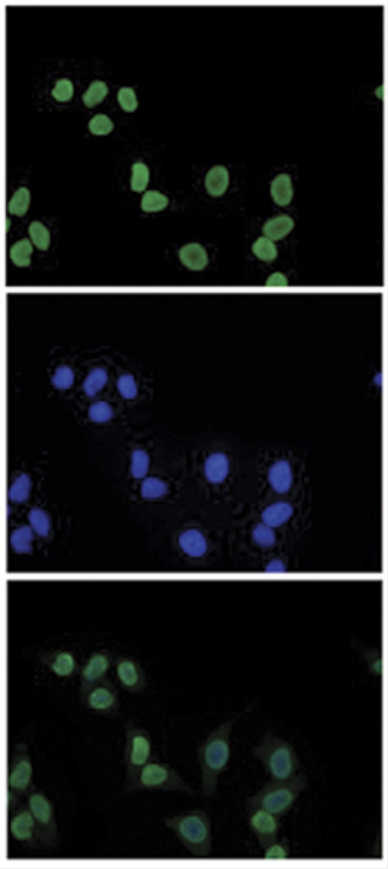
ChIP-Seq

ChIP was performed on sheared chromatin from 100,000 K562 cells using antibody. The figure show the signal distribution in two regions surrounding the MYT1 and TSH2B positive control genes, respectively. The position of the PCR amplicon, used for ChIP-qPCR is indicated with an arrow and the signal distribution in a 5 Mb region from chromosome 22.



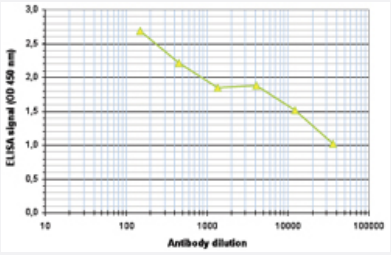
Western Blot

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.



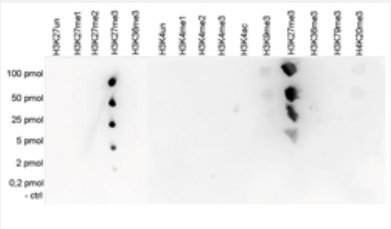
Immunofluorescence

Immunofluorescent staining of mouse NIH3T3 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 (K27me3). 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 1:22400.



Dot Blot

Cross reactivity test using the Histone H3 (K27me3) antibody.
Dot Blot analysis was performed with peptides containing other modifications or unmodified sequences of histone H3 and H4. 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 (K27me3).

Immunogen	A synthetic peptide (conjugated with KLH) corresponding to Histone H3, trimethylated at lysine 27.
Host	Rabbit
Reactivity	Fruit fly, Human, Mouse, Nematoda, Arabidopsis, Maize, Solanum lycopersicum, Populus
Form	Liquid
Purification	Affinity purification
Recommend Usage	ELISA (1:1000) Western Blot (1:1000) ChIP (1 ug/IP) Dot Blot/Peptide array (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

ChIP assays were performed using human K562 cells. A titration consisting of 0.1, 0.5, and 1 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 and EIF4A2, used as negative controls, and TSH2B and MYT1, 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 show the signal distribution in two regions surrounding the MYT1 and TSH2B positive control genes, respectively. The position of the PCR amplicon, used for ChIP-qPCR is indicated with an arrow and the signal distribution in a 5 Mb region from chromosome 22.

- 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 mouse NIH3T3 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 (K27me3). 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 1:22400.

- Dot Blot

Cross reactivity test using the Histone H3 (K27me3) antibody.
Dot Blot analysis was performed with peptides containing other modifications or unmodified sequences of histone H3 and H4. 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 GeneID	8350
Protein Accession#	P68431
Gene Name	HIST1H3A
Gene Alias	H3/A, H3FA
Gene Description	histone cluster 1, H3a
Omim ID	602810
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

- Global analysis of H3K27me3 as an epigenetic marker in prostate cancer progression.

  Ngollo M, Lebert A, Daures M, Judes G, Rifai K, Dubois L, Kemeny JL, Penault-Llorca F, Bignon YJ, Guy L, Bernard-Gallon D.

  BMC Cancer 2017 Apr; 17(1):261.

  Application: ChIP, Human, Normal and tumoral prostate biopsies

- Arabidopsis SWI/SNF chromatin remodeling complex binds both promoters and terminators to regulate gene expression.

  Archacki R, Yatusevich R, Buszewicz D, Krzyczmonik K, Patryn J, Iwanicka-Nowicka R, Biecek P, Wilczynski B, Koblowska M, Jerzmanowski A, Swiezewski S.

  Nucleic Acids Research 2017 Apr; 45(6):3116.

  Application: ChIP-Seq, Plant, Plant cells

- c-Myc Antagonises the Transcriptional Activity of the Androgen Receptor in Prostate Cancer Affecting Key Gene Networks.

  Barfeld SJ, Urbanucci A, Itkonen HM, Fazli L, Hicks JL, Thiede B, Rennie PS, Yegnasubramanian S, DeMarzo AM, Mills IG.

  EbioMedicine 2017 Apr; 18:83.

  Application: ChIP, Human, LNCaP cells

- Epigenetically-driven anatomical diversity of synovial fibroblasts guides joint-specific fibroblast functions.

  Frank-Bertoncelj M, Trenkmann M, Klein K, Karouzakis E, Rehrauer H, Bratus A, Kolling C, Armaka M, Filer A, Michel BA, Gay RE, Buckley CD, Kollias G, Gay S, Ospelt C.

  Nature Communications 2017 Mar; 8:14852.

  Application: ChIP-Seq, Human, Human synovial fibroblasts

- RNF40 regulates gene expression in an epigenetic context-dependent manner.

  Xie W, Nagarajan S, Baumgart SJ, Kosinsky RL, Najafova Z, Kari V, Hennion M, Indenbirken D, Bonn S, Grundhoff A, Wegwitz F, Mansouri A, Johnsen SA.

  Genome Biology 2017 Feb; 18(1):32.

  Application: ChIP-Seq, WB-Ce, Mouse, MEFs

- Menin regulates Inhbb expression through an Akt/Ezh2-mediated H3K27 histone modification.

  Gherardi S, Ripoche D, Mikaelian I, Chanal M, Teinturier R, Goehrig D, Cordier-Bussat M, Zhang CX, Hennino A, Bertolino P.

  Biochimica et Biophysica Acta. Gene Regulatory Mechanisms 2017 Apr; 1860(4):427.

- Co-occurrence of histone H3 K27M and BRAF V600E mutations in paediatric midline grade I ganglioglioma.

  Pages M, Beccaria K, Boddaert N, Saffroy R, Besnard A, Castel D, Fina F, Barets D, Barret E, Lacroix L, Bielle F, Andreiuolo F, Tauziede-Espariat A, Figarella-Branger D, Puget S, Grill J, Chretien F, Varlet P.

  Brain Pathology 2018 Jan; 28(1):103.

  Application: IHC-P, Human, Human ganglioglioma

- 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

- FOXA1 Directs H3K4 Monomethylation at Enhancers via Recruitment of the Methyltransferase MLL3.

  Jozwik KM, Chernukhin I, Serandour AA, Nagarajan S, Carroll JS.

  Cell Reports 2016 Dec; 17(10):2715.

  Application: ChIP-Seq, Human, MCF-7 cells

- β-Glucan Reverses the Epigenetic State of LPS-Induced Immunological Tolerance.

  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

- Coordinate redeployment of PRC1 proteins suppresses tumor formation during Drosophila development.

  Loubiere V, Delest A, Thomas A, Bonev B, Schuettengruber B, Sati S, Martinez AM, Cavalli G.

  Nature Genetics 2016 Nov; 48(11):1436.

  Application: ChIP-Seq, IF, Firefly, Human, ES cells, Firefly embryos, Firefly eye discs, Firefly larval imaginal discs, Hs68 cells, K-562 cells

- BRD4 localization to lineage-specific enhancers is associated with a distinct transcription factor repertoire.

  Zeynab Najafova, Roberto Tirado-Magallanes, Malayannan Subramaniam, Tareq Hossan, Geske Schmidt, Sankari Nagarajan, Simon J Baumgart, Vivek Kumar Mishra, Upasana Bedi, Eric Hesse, Stefan Knapp, John R Hawse, Steven A Johnsen.

  Nucleic Acids Research 2017 Jan; 45(1):127.

  Application: ChIP-Seq, Human, Human osteoblast cells

- Clinical, Imaging, Histopathological and Molecular Characterization of Anaplastic Ganglioglioma.

  Zanello M, Pages M, Tauziede-Espariat A, Saffroy R, Puget S, Lacroix L, Dezamis E, Devaux B, Chrétien F, Andreiuolo F, Sainte-Rose C, Zerah M, Dhermain F, Dumont S, Louvel G, Meder JF, Grill J, Dufour C, Pallud J, Varlet P.

  Journal of Neuropathology and Experimental Neurology 2016 Oct; 75(10):971.

  Application: IHC-P, Human, Human anaplastic Ganglioglioma

- reChIP-seq reveals widespread bivalency of H3K4me3 and H3K27me3 in CD4(+) memory T cells.

  Kinkley S, Helmuth J, Polansky JK, Dunkel I, Gasparoni G, Fröhler S, Chen W, Walter J, Hamann A, Chung HR.

  Nature Communications 2016 Aug; 7:12514.

  Application: ChIP, Re-ChIP, Human, CD4+ central memory Tcells

- The dynamic interactome and genomic targets of Polycomb complexes during stem-cell differentiation.

  Kloet SL, Makowski MM, Baymaz HI, van Voorthuijsen L, Karemaker ID, Santanach A, Jansen PWTC, Di Croce L, Vermeulen M.

  Nature Structural & Molecular Biology 2016 Jul; 23(7):682.

  Application: ChIP-Seq, WB-Ce, Mouse, Mouse embryonic stem cells, Mouse neural progenitor cells

- PHF13 is a molecular reader and transcriptional co-regulator of H3K4me2/3.

  Chung HR, Xu C, Fuchs A, Mund A, Lange M, Staege H, Schubert T, Bian C, Dunkel I, Eberharter A, Regnard C, Klinker H, Meierhofer D, Cozzuto L, Winterpacht A, Di Croce L, Min J, Will H, Kinkley S.

  eLife 2016 May; 5:e10607.

  Application: WB-Ce, WB-Tr, Mouse, Mouse embryonic stem cells

- Comprehensive genome and epigenome characterization of CHO cells in response to evolutionary pressures 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

- Epigenetic regulation of diacylglycerol kinase alpha promotes radiation-induced fibrosis.

  Weigel C, Veldwijk MR, Oakes CC, Seibold P, Slynko A, Liesenfeld DB, Rabionet M, Hanke SA, Wenz F, Sperk E, Benner A, Rösli C, Sandhoff R, Assenov Y, Plass C, Herskind C, Chang-Claude J, Schmezer P, Popanda O.

  Nature Communications 2016 Mar; 7:10893.

  Application: ChIP, Human, Human dermal fibroblasts

- Chromatin Preparation and Chromatin Immuno-precipitation from Drosophila Embryos.

  Löser E, Latreille D, Iovino N.

  Methods in Molecular Biology 2016 Jan; 1480:23.

  Application: ChIP, Human, Mammalian cells

- Standardizing chromatin research: a simple and universal method for ChIP-seq.

  Arrigoni L, Richter AS, Betancourt E, Bruder K, Diehl S, Manke T, Bonisch U.

  Nucleic Acids Research 2016 Apr; 44(7):e67.

  Application: ChIP-Seq, Human, HepG2 cells, Human hepatocytes, Human monocytes, IMR-90 cells

- The homeoprotein DLX3 and tumor suppressor p53 co-regulate cell cycle progression and squamous tumor growth.

  Palazzo E, Kellett M, Cataisson C, Gormley A, Bible PW, Pietroni V, Radoja N, Hwang J, Blumenberg M, Yuspa SH, Morasso MI.

  Oncogene 2016 Jun; 35(24):3114.

  Application: ChIP, Human, Human keratinocytes

- Reinforcement of STAT3 activity reprogrammes human embryonic stem cells to naive-like pluripotency.

  Chen H, Aksoy I, Gonnot F, Osteil P, Aubry M, Hamela C, Rognard C, Hochard A, Voisin S, Fontaine E, Mure M, Afanassieff M, Cleroux E, Guibert S, Chen J, Vallot C, Acloque H, Genthon C, Donnadieu C, De Vos J, Sanlaville D, Guérin JF, Weber M, Stanton LW, Rougeulle C, Pain B, Bourillot PY, Savatier P.

  Nature Communications 2015 May; 6:7095.

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

- A cohesin-OCT4 complex mediates Sox enhancers to prime an early embryonic lineage.

  Abboud N, Moore-Morris T, Hiriart E, Yang H, Bezerra H, Gualazzi MG, Stefanovic S, Guénantin AC, Evans SM, Pucéat M.

  Nature Communications 2015 Apr; 6:6749.

  Application: ChIP, Human, HUESCs

- A lncRNA regulates alternative splicing via establishment of a splicing-specific chromatin signature.

  Gonzalez I, Munita R, Agirre E, Dittmer TA, Gysling K, Misteli T, Luco RF.

  Nature Structural & Molecular Biology 2015 May; 22(5):370.

  Application: ChIP, Human, Human mesenchymal stem cells

- 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

- Global effects of the CSR-1 RNA interference pathway on the transcriptional landscape.

  Cecere G, Hoersch S, O'Keeffe S, Sachidanandam R, Grishok A.

  Nature Structural & Molecular Biology 2014 Apr; 21(4):358.

  Application: ChIP, Nematoda, Nematoda embryos

Pathway

- Systemic lupus erythematosus