Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Apr 9, 2025

RNA Polymerase II 8WG16 Monoclonal Antibody, anti-RNA Polymerase II

RRID:AB_10013665
Type: Antibody

Proper Citation

(Covance Cat# MMS-126R, RRID:AB_10013665)

Antibody Information

URL: http://antibodyregistry.org/AB_10013665

Proper Citation: (Covance Cat# MMS-126R, RRID:AB_10013665)

Target Antigen: C-terminal heptapeptide repeat present on the largest subunit of pol II

Host Organism: mouse

Clonality: monoclonal

Comments: Applications: immunofluorescence, immunoblotting, immunoprecipitation, pol II purification and functional studies
ENCODE PROJECT External validation for lot# 14941801 is available under ENCODE ID: ENCAB281FBQ
Consolidated with AB_10063549 and AB_10119809

Antibody Name: RNA Polymerase II 8WG16 Monoclonal Antibody, anti-RNA Polymerase II

Description: This monoclonal targets C-terminal heptapeptide repeat present on the largest subunit of pol II

Clone ID: 8WG16

Defining Citation: PMID:19742326, PMID:20336069, PMID:18498094, PMID:18978947

Antibody ID: AB_10013665

Vendor: Covance

Catalog Number: MMS-126R

Alternative Catalog Numbers: MMS-126R-500, MMS-126R-200

Record Creation Time: 20231110T081731+0000

Record Last Update: 20241115T074148+0000

Ratings and Alerts

- ENCODE PROJECT External validation for lot: unknown is available under ENCODE ID: ENCAB675EUV - ENCODE https://www.encodeproject.org/antibodies/ENCAB675EUV

No alerts have been found for RNA Polymerase II 8WG16 Monoclonal Antibody, anti-RNA Polymerase II.

Data and Source Information

Source: Antibody Registry

Usage and Citation Metrics

We found 26 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Abril-Garrido J, et al. (2023) Structural basis of transcription reduction by a promoter-proximal +1 nucleosome. Molecular cell, 83(11), 1798.

Lerner J, et al. (2023) Different chromatin-scanning modes lead to targeting of compacted chromatin by pioneer factors FOXA1 and SOX2. Cell reports, 42(7), 112748.

Closser M, et al. (2022) An expansion of the non-coding genome and its regulatory potential underlies vertebrate neuronal diversity. Neuron, 110(1), 70.

Kaminski N, et al. (2022) RAD51AP1 regulates ALT-HDR through chromatin-directed homeostasis of TERRA. Molecular cell, 82(21), 4001.

Papadopoulos D, et al. (2022) MYCN recruits the nuclear exosome complex to RNA polymerase II to prevent transcription-replication conflicts. Molecular cell, 82(1), 159.

Shan W, et al. (2020) Systematic Characterization of Recurrent Genomic Alterations in Cyclin-Dependent Kinases Reveals Potential Therapeutic Strategies for Cancer Treatment.

Cell reports, 32(2), 107884.

Villa T, et al. (2020) Degradation of Non-coding RNAs Promotes Recycling of Termination Factors at Sites of Transcription. Cell reports, 32(3), 107942.

Lawlor N, et al. (2019) Multiomic Profiling Identifies cis-Regulatory Networks Underlying Human Pancreatic ? Cell Identity and Function. Cell reports, 26(3), 788.

Bertolini JA, et al. (2019) Mapping the Global Chromatin Connectivity Network for Sox2 Function in Neural Stem Cell Maintenance. Cell stem cell, 24(3), 462.

Yang P, et al. (2019) Multi-omic Profiling Reveals Dynamics of the Phased Progression of Pluripotency. Cell systems, 8(5), 427.

Duempelmann L, et al. (2019) Inheritance of a Phenotypically Neutral Epimutation Evokes Gene Silencing in Later Generations. Molecular cell, 74(3), 534.

Lung DK, et al. (2019) Bone Marrow Stromal Cells Transcriptionally Repress ESR1 but Cannot Overcome Constitutive ESR1 Mutant Activity. Endocrinology, 160(10), 2427.

Paraiso KD, et al. (2019) Endodermal Maternal Transcription Factors Establish Super-Enhancers during Zygotic Genome Activation. Cell reports, 27(10), 2962.

Hernandez C, et al. (2018) Dppa2/4 Facilitate Epigenetic Remodeling during Reprogramming to Pluripotency. Cell stem cell, 23(3), 396.

Liu X, et al. (2017) In Situ Capture of Chromatin Interactions by Biotinylated dCas9. Cell, 170(5), 1028.

Alfonso-Dunn R, et al. (2017) Transcriptional Elongation of HSV Immediate Early Genes by the Super Elongation Complex Drives Lytic Infection and Reactivation from Latency. Cell host & microbe, 21(4), 507.

García-Pichardo D, et al. (2017) Histone Mutants Separate R Loop Formation from Genome Instability Induction. Molecular cell, 66(5), 597.

Charney RM, et al. (2017) Foxh1 Occupies cis-Regulatory Modules Prior to Dynamic Transcription Factor Interactions Controlling the Mesendoderm Gene Program. Developmental cell, 40(6), 595.

Sdano MA, et al. (2017) A novel SH2 recognition mechanism recruits Spt6 to the doubly phosphorylated RNA polymerase II linker at sites of transcription. eLife, 6.

Kang K, et al. (2017) Interferon-? Represses M2 Gene Expression in Human Macrophages by Disassembling Enhancers Bound by the Transcription Factor MAF. Immunity, 47(2), 235.