

Resource Summary Report

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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: 20260829T175530+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 22 mentions in open access literature.

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

Zhan Y, et al. (2026) The +1 nucleosome functions in RNA Pol II transcription initiation and the transition to elongation. Molecular cell.

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.

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.

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

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

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.

- 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.
- Lawlor N, et al. (2019) Multiomic Profiling Identifies cis-Regulatory Networks Underlying Human Pancreatic ? Cell Identity and Function. *Cell reports*, 26(3), 788.
- Paraiso KD, et al. (2019) Endodermal Maternal Transcription Factors Establish Super-Enhancers during Zygotic Genome Activation. *Cell reports*, 27(10), 2962.
- Lung DK, et al. (2019) Bone Marrow Stromal Cells Transcriptionally Repress ESR1 but Cannot Overcome Constitutive ESR1 Mutant Activity. *Endocrinology*, 160(10), 2427.
- Duempelmann L, et al. (2019) Inheritance of a Phenotypically Neutral Epimutation Evokes Gene Silencing in Later Generations. *Molecular cell*, 74(3), 534.
- Yang P, et al. (2019) Multi-omic Profiling Reveals Dynamics of the Phased Progression of Pluripotency. *Cell systems*, 8(5), 427.
- Hernandez C, et al. (2018) Dppa2/4 Facilitate Epigenetic Remodeling during Reprogramming to Pluripotency. *Cell stem cell*, 23(3), 396.
- García-Pichardo D, et al. (2017) Histone Mutants Separate R Loop Formation from Genome Instability Induction. *Molecular cell*, 66(5), 597.
- 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.
- Liu X, et al. (2017) In Situ Capture of Chromatin Interactions by Biotinylated dCas9. *Cell*, 170(5), 1028.
- 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.
- 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.