

p120
Rabbit Monoclonal antibody(Mab)
Catalog # AD80241**Specification**

p120 - Product info

Application	IHC-P
Primary Accession	Q00839
Reactivity	Human
Host	Rabbit
Clonality	Monoclonal
Calculated MW	90584

p120 - Additional info

Gene ID	3192
Gene Name	HNRNPU (HGNC:5048)

Other Names

Heterogeneous nuclear ribonucleoprotein U, hnRNP U, GRIP120, Nuclear p120 ribonucleoprotein, Scaffold-attachment factor A {ECO:0000303|PubMed:1324173, ECO:0000303|Ref.3}, SAF-A {ECO:0000303|PubMed:1324173, ECO:0000303|Ref.3}, p120, pp120, HNRNPU (http://www.genenames.org/cgi-bin/gene_symbol_report?hgnc_id=5048)

Dilution

IHC-P~~Ready-to-use

Storage

Maintain refrigerated at 2-8°C

Precautions

p120 Antibody is for research use only and not for use in diagnostic or therapeutic procedures.

p120 - Protein Information

Name HNRNPU ([HGNC:5048](#))

Function

DNA- and RNA-binding protein involved in several cellular processes such as nuclear chromatin organization, telomere-length regulation, transcription, mRNA alternative splicing and stability, Xist-mediated transcriptional silencing and mitotic cell progression (PubMed:[10490622](#), PubMed:[18082603](#), PubMed:[19029303](#), PubMed:[22325991](#), PubMed:[25986610](#), PubMed:[28622508](#)). Plays a role in the regulation of interphase large-scale

gene-rich chromatin organization through chromatin-associated RNAs (caRNAs) in a transcription-dependent manner, and thereby maintains genomic stability (PubMed:[1324173](#), PubMed:[8174554](#), PubMed:[28622508](#)). Required for the localization of the long non-coding Xist RNA on the inactive chromosome X (Xi) and the subsequent initiation and maintenance of X-linked transcriptional gene silencing during X-inactivation (By similarity). Plays a role as a RNA polymerase II (Pol II) holoenzyme transcription regulator (PubMed:[8174554](#), PubMed:[9353307](#), PubMed:[10490622](#), PubMed:[15711563](#), PubMed:[19617346](#), PubMed:[23811339](#)). Promotes transcription initiation by direct association with the core-TFIID basal transcription factor complex for the assembly of a functional pre-initiation complex with Pol II in an actin-dependent manner (PubMed:[10490622](#), PubMed:[15711563](#)). Blocks Pol II transcription elongation activity by inhibiting the C-terminal domain (CTD) phosphorylation of Pol II and dissociates from Pol II pre-initiation complex prior to productive transcription elongation (PubMed:[10490622](#)). Positively regulates CBX5-induced transcriptional gene silencing and retention of CBX5 in the nucleus (PubMed:[19617346](#)). Negatively regulates glucocorticoid-mediated transcriptional activation (PubMed:[9353307](#)). Key regulator of transcription initiation and elongation in embryonic stem cells upon leukemia inhibitory factor (LIF) signaling (By similarity). Involved in the long non-coding RNA H19-mediated Pol II transcriptional repression (PubMed:[23811339](#)). Participates in the circadian regulation of the core clock component ARNTL/BMAL1 transcription (By similarity). Plays a role in the regulation of telomere length (PubMed:[18082603](#)). Plays a role as a global pre-mRNA alternative splicing modulator by regulating U2 small nuclear ribonucleoprotein (snRNP) biogenesis (PubMed:[22325991](#)). Plays a role in mRNA stability (PubMed:[17174306](#), PubMed:[17289661](#), PubMed:[19029303](#)). Component of the CRD-mediated complex that promotes MYC mRNA stabilization (PubMed:[19029303](#)). Enhances the expression of specific genes, such as tumor necrosis factor TNFA, by regulating

mRNA stability, possibly through binding to the 3'- untranslated region (UTR) (PubMed:[17174306](#)). Plays a role in mitotic cell cycle regulation (PubMed:[21242313](#), PubMed:[25986610](#)). Involved in the formation of stable mitotic spindle microtubules (MTs) attachment to kinetochore, spindle organization and chromosome congression (PubMed:[21242313](#)). Phosphorylation at Ser- 59 by PLK1 is required for chromosome alignment and segregation and progression through mitosis (PubMed:[25986610](#)). Contributes also to the targeting of AURKA to mitotic spindle MTs (PubMed:[21242313](#)). Binds to double- and single-stranded DNA and RNA, poly(A), poly(C) and poly(G) oligoribonucleotides (PubMed:[1628625](#), PubMed:[8068679](#), PubMed:[8174554](#), PubMed:[9204873](#), PubMed:[9405365](#)). Binds to chromatin-associated RNAs (caRNAs) (PubMed:[28622508](#)). Associates with chromatin to scaffold/matrix attachment region (S/MAR) elements in a chromatin-associated RNAs (caRNAs)-dependent manner (PubMed:[7509195](#), PubMed:[1324173](#), PubMed:[9204873](#), PubMed:[9405365](#), PubMed:[10671544](#), PubMed:[11003645](#), PubMed:[11909954](#), PubMed:[28622508](#)). Binds to the Xist RNA (PubMed:[26244333](#)). Binds the long non-coding H19 RNA (PubMed:[23811339](#)). Binds to SMN1/2 pre-mRNAs at G/U-rich regions (PubMed:[22325991](#)). Binds to small nuclear RNAs (snRNAs) (PubMed:[22325991](#)). Binds to the 3'-UTR of TNFA mRNA (PubMed:[17174306](#)). Binds (via RNA-binding RGG-box region) to the long non-coding Xist RNA; this binding is direct and bridges the Xist RNA and the inactive chromosome X (Xi) (By similarity). Also negatively regulates embryonic stem cell differentiation upon LIF signaling (By similarity). Required for embryonic development (By similarity). Binds to brown fat long non-coding RNA 1 (Blnc1); facilitates the recruitment of Blnc1 by ZBTB7B required to drive brown and beige fat development and thermogenesis (By similarity).

Nucleus. Nucleus matrix. Chromosome. Nucleus speckle. Cytoplasm, cytoskeleton, microtubule organizing center, centrosome. Chromosome, centromere, kinetochore. Cytoplasm, cytoskeleton,

Cellular Location

spindle Cytoplasm, cytoskeleton, spindle pole. Midbody. Cytoplasm. Cell surface. Cytoplasmic granule. Note=Localizes at inactive X chromosome (Xi) regions (PubMed:11003645, PubMed:14608463, PubMed:15563465). Localizes in the nucleus during interphase (PubMed:21242313). At metaphase, localizes with mitotic spindle microtubules (MTs) (PubMed:21242313). At anaphase, localizes in the mitotic spindle midzone (PubMed:21242313). Localizes in spindle MTs proximal to spindle poles in a TPX2- and AURKA- dependent manner (PubMed:21242313). The Ser-59 phosphorylated form localizes to centrosomes during prophase and metaphase, to mitotic spindles in anaphase and to the midbody during cytokinesis (PubMed:25986610). Colocalizes with SMARCA4 in the nucleus (By similarity). Colocalizes with CBX5 in the nucleus (PubMed:19617346). Colocalizes with NR3C1 in nuclear speckles (PubMed:9353307). Localized in cytoplasmic ribonucleoprotein (RNP) granules containing untranslated mRNAs (PubMed:17289661) {ECO:0000250|UniProtKB:Q8VEK3, ECO:0000269|PubMed:11003645, ECO:0000269|PubMed:14608463, ECO:0000269|PubMed:15563465, ECO:0000269|PubMed:17289661, ECO:0000269|PubMed:19617346, ECO:0000269|PubMed:21242313, ECO:0000269|PubMed:25986610, ECO:0000269|PubMed:9353307} Widely expressed.

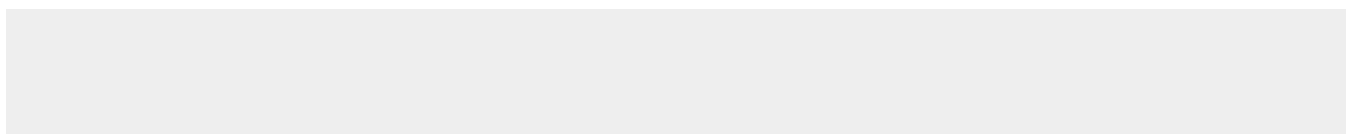
Tissue Location

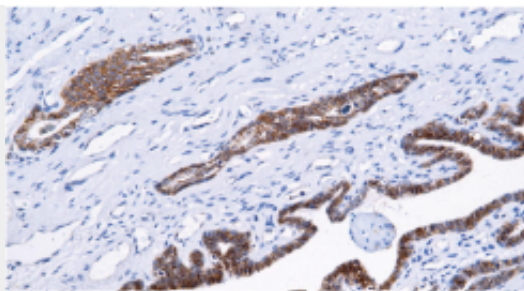
p120 - Protocols

Provided below are standard protocols that you may find useful for product applications.

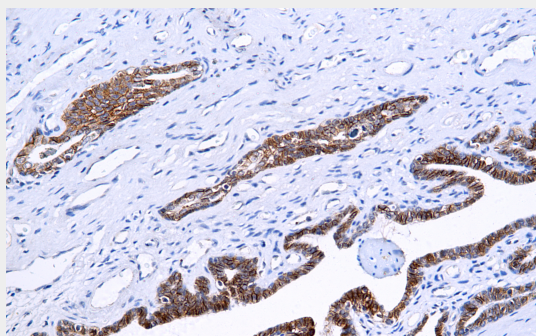
- [Western Blot](#)
- [Blocking Peptides](#)
- [Dot Blot](#)
- [Immunohistochemistry](#)
- [Immunofluorescence](#)
- [Immunoprecipitation](#)
- [Flow Cytometry](#)
- [Cell Culture](#)

p120 - Images





Normal breast tissues



Immunohistochemical analysis of paraffin-embedded human normal breast tissue using AD80241 performed on the Abcarta® FAIP-30 Fully automated IHC platform. Tissue was fixed with formaldehyde at room temperature, antigen retrieval was by heat mediation with a Citrate buffer (pH 6.0). Samples were incubated with primary antibody (Ready-to-use) for 15 min at room temperature. AmpSee™ Detection Systems [Abcepta:AR005] was used as the secondary antibody.