HPA

RRID:SCR_006710
Type: Tool

Proper Citation

HPA (RRID:SCR_006710)

Resource Information

**URL:** http://www.proteinatlas.org/

**Proper Citation:** HPA (RRID:SCR_006710)

**Description:** Public database with millions of high-resolution images showing the spatial distribution of proteins in different normal human tissues and cancer types, as well as different human cell lines. The data is released together with application-specific validation performed for each antibody, including immunohistochemistry, Western blot analysis and, for a large fraction, a protein array assay and immunofluorescent based confocal microscopy. The database has been developed in a gene-centric manner with the inclusion of all human genes predicted from genome efforts. Search functionalities allow for complex queries regarding protein expression profiles, protein classes and chromosome location. Antibodies included have been analyzed using a standardized protocol in a single attempt without further efforts to optimize the procedure and therefore it cannot be excluded that certain observed binding properties are due to technical rather than biological reasons and that further optimization could result in a different outcome. Submission of antibodies: The Swedish Human Proteome Atlas (HPA) program, invites submission of antibodies from both academic and commercial sources to be included in the human protein atlas. All antibodies will be validated by the HPA-program by a standard procedure and antibodies that are accepted will be use in the tissue- profiling program to generate high-resolution immunohistochemistry images representing a wide spectrum of normal tissues and cancer types.

**Abbreviations:** HPA

**Synonyms:** Human Protein Atlas, HPA antibody, HPA antibody, Human Protein Atlas
**Resource Type:** storage service resource, material storage repository, database, service resource, atlas, biospecimen repository, data or information resource

**Defining Citation:** PMID:21139605, PMID:16127175, PMID:18669619, PMID:18853439

**Keywords:** expression profile, protein, immunohistochemistry, subcellular localization, expression level, transcript, immunofluorescence, western blot, protein array, rna, epithelial, gene, antibody, cancer tissue, cell line, confocal imaging protocol, glioma, hematoxylin, human, mesenchymal tumor, microarray, normal, tissue section, tumor, western blot, molecular neuroanatomy resource, proteomics, proteome, differential expression, protein expression, image collection, organ, cell, tissue, kidney, liver, heart, brain, pancreas, protein profile, chromosome, annotation, bio.tools, FASEB list

**Related Condition:** Cancer, Tumor, Breast cancer, Colorectal cancer, Lung cancer, Prostate cancer, Normal

**Funding Agency:** Knut and Alice Wallenberg Foundation

**Availability:** Public, Free, For informational purposes, Non-commercial, Acknowledgement required

**Resource Name:** HPA

**Resource ID:** SCR_006710

**Alternate IDs:** nif-0000-00204, biotools:proteinatlas

**Alternate URLs:** https://bio.tools/proteinatlas

---

**Ratings and Alerts**

No rating or validation information has been found for HPA.

No alerts have been found for HPA.

---

**Data and Source Information**

**Source:** SciCrunch Registry

---

**Usage and Citation Metrics**

We found 4587 mentions in open access literature.

**Listed below are recent publications.** The full list is available at RRID.

Radford RAW, et al. (2023) Identification of phosphorylated tau protein interactors in


Christians A, et al. (2023) Heterozygous variants in the DVL2 interaction region of DACT1 cause CAKUT and features of Townes-Brocks syndrome 2. Human genetics, 142(1), 73.


Wang Z, et al. (2023) ARHGAP21 Is Involved in the Carcinogenic Mechanism of Cholangiocarcinoma: A Study Based on Bioinformatic Analyses and Experimental Validation. Medicina (Kaunas, Lithuania), 59(1).


Fan L, et al. (2023) Increased expression of TBC1D10B as a potential prognostic and immunotherapy relevant biomarker in liver hepatocellular carcinoma. Scientific reports, 13(1), 335.


Liu Y, et al. (2023) SPOCK2 and SPRED1 function downstream of EZH2 to impede the malignant progression of lung adenocarcinoma in vitro and in vivo. Human cell, 36(2), 812.