

Resource Summary Report

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Human Ageing Genomic Resources

RRID:SCR_007700

Type: Tool

Proper Citation

Human Ageing Genomic Resources (RRID:SCR_007700)

Resource Information

URL: <http://genomics.senescence.info/>

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Description: Collection of databases and tools designed to help researchers study the genetics of human ageing using modern approaches such as functional genomics, network analyses, systems biology and evolutionary analyses. A major resource in HAGR is GenAge, which includes a curated database of genes related to human aging and a database of ageing- and longevity-associated genes in model organisms. Another major database in HAGR is AnAge. Featuring over 4,000 species, AnAge provides a compilation of data on aging, longevity, and life history that is ideal for the comparative biology of aging. GenDR is a database of genes associated with dietary restriction based on genetic manipulation experiments and gene expression profiling. Other projects include evolutionary studies, genome sequencing, cancer genomics, and gene expression analyses. The latter allowed them to identify a set of genes commonly altered during mammalian aging which represents a conserved molecular signature of aging. Software, namely in the form of scripts for Perl and SPSS, is made available for users to perform a variety of bioinformatic analyses potentially relevant for studying aging. The Perl toolkit, entitled the Ageing Research Computational Tools (ARCT), provides modules for parsing files, data-mining, searching and downloading data from the Internet, etc. Also available is an SPSS script that can be used to determine the demographic rate of aging for a given population. An extensive list of links regarding computational biology, genomics, gerontology, and comparative biology is also available.

Abbreviations: HAGR

Resource Type: data or information resource, database, software resource, software toolkit

Defining Citation: [PMID:23193293](#)

Keywords: gene, gerontology, human, model, senescence, genomics, longevity, genetics, perl, spss, demographic analysis, genome, evolution, gene expression, model

organism, human aging, dietary restriction, genetic manipulation

Related Condition: Aging, Cancer

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Availability: GNU General Public License, Creative Commons Attribution v3 Unported License

Resource Name: Human Ageing Genomic Resources

Resource ID: SCR_007700

Alternate IDs: nif-0000-02938, r3d100011871

Alternate URLs: <https://doi.org/10.17616/R34W81>

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Record Last Update: 20260905T132614+0000

Ratings and Alerts

No rating or validation information has been found for Human Ageing Genomic Resources.

No alerts have been found for Human Ageing Genomic Resources.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 107 mentions in open access literature.

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

Tu Y, et al. (2026) Rhein protects against renal aging and fibrotic injury by multiple targets through inhibition of TNF-??-mediated autophagy and necroptosis crosstalk. *Frontiers in pharmacology*, 17, 1693000.

Zhang X, et al. (2026) Aging-dependent expression of vascular endothelial growth factor receptor-1 is associated with T-cell immune senescence in carotid atherosclerosis. *Brain circulation*, 12(1), 31.

Juan G, et al. (2026) Identification of cell senescence-related genes in spontaneous preterm birth based on bioinformatics analysis and machine learning. *PloS one*, 21(1), e0340809.

Liu Y, et al. (2026) Integrated UPLC, bioinformatics, and in vitro analyses reveal Yiqihuoxue decoction (GSC) alleviates vascular aging by promoting autophagy. *Scientific reports*, 16(1).

Huang JN, et al. (2026) Multi-omics analyses related to mitochondria and ageing in triple-negative breast cancer implicate PYCR1 potentiates tumor progression. *Cancer cell international*, 26(1).

Li Q, et al. (2026) Age-associated methionine sulfoxide reductase A protects against valvular interstitial cell senescence and valvular calcification. *GeroScience*, 48(1), 807.

Liu C, et al. (2026) Integrated bioinformatics and experimental validation identify aging-related prognostic genes in clear cell renal cell carcinoma. *Medicine*, 105(20), e48809.

He C, et al. (2026) A prognostic senescence-related long non-coding RNA signature identifies cold and hot tumors of stomach adenocarcinoma. *Oncology letters*, 32(2), 350.

Cox K, et al. (2025) Rapid Colonisation of Synanthropic Stone Martens in a Highly Urbanised Region: Insights From Temporal and Spatial Analysis. *Ecology and evolution*, 15(5), e71392.

Lopez-Teros M, et al. (2025) Palmitate-Induced Primary Rat Senescent Astrocytes Exhibit Higher Inflammatory Activity and a Distinct Transcriptomic Profile Compared to Reactive Astrocytes. *Journal of neurochemistry*, 169(7), e70164.

Yao J, et al. (2025) PSMA5 as a modulator of glioblastoma senescence and prognosis. *BMC cancer*, 25(1), 1079.

Li CL, et al. (2025) Unveiling the role of EGR1 and hub senescence-related genes in type II alveolar epithelial cells senescence for obstructive sleep apnea. *BMC biotechnology*, 26(1), 8.

Du J, et al. (2025) Identification and validation of aging related genes in osteoarthritis. *Frontiers in genetics*, 16, 1561644.

Lian K, et al. (2025) The role of senescence-related genes in major depressive disorder: insights from machine learning and single cell analysis. *BMC psychiatry*, 25(1), 188.

Huang K, et al. (2025) Genetic targets related to aging for the treatment of coronary artery disease. *BMC medical genomics*, 18(1), 66.

Xiang M, et al. (2025) Machine learning-enabled identification of nucleus pulposus senescence-associated genes as potential biomarkers for intervertebral disc degeneration. *European journal of medical research*, 30(1), 887.

Mavaddatiyan L, et al. (2025) Exploring the involvement of ferroptosis-associated genes and pathways in mesenchymal stem cell aging through bioinformatics analysis. *Frontiers in aging*, 6, 1509267.

Chen Z, et al. (2025) Investigating biomarkers of mitochondrial and aging-related genes in major depressive disorder through bioinformatics analysis. *Frontiers in psychiatry*, 16, 1653998.

Xie X, et al. (2025) Identifying aging-related biomarkers in adipose tissue using integrative bioinformatics and machine-learning approaches: discovery of ELN, MXD1, and FGF21 as key genes. *Frontiers in endocrinology*, 16, 1638343.

Karimi I, et al. (2025) The anti-aging potential of antihypertensive peptides of *Pariset*, a dataset of algal peptides. *Frontiers in aging*, 6, 1618082.