

# BÃ©rÃ©nice A Benayoun

## List of Publications by Year in descending order

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Version: 2024-02-01

60  
papers

4,959  
citations

136740

32  
h-index

168136

53  
g-index

73  
all docs

73  
docs citations

73  
times ranked

8441  
citing authors

#	ARTICLE	IF	CITATIONS
1	Functional genomics of inflamm-aging and immunosenescence. <i>Briefings in Functional Genomics</i> , 2022, 21, 43-55.	1.3	16
2	Time isnâ€™t kind to female T cells. <i>Nature Aging</i> , 2022, 2, 189-191.	5.3	2
3	Sex as a Biological Variable in Nutrition Research: From Human Studies to Animal Models. <i>Annual Review of Nutrition</i> , 2022, 42, 227-250.	4.3	13
4	Endogenous Retroviral Elements Generate Pathologic Neutrophils in Pulmonary Arterial Hypertension. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2022, 206, 1019-1034.	2.5	10
5	A multiomic atlas for the exploration of healthy aging in human monocytes. <i>Nature Aging</i> , 2021, 1, 19-21.	5.3	0
6	Protocol for isolation of adult mouse ear pinnae-derived primary fibroblasts. <i>STAR Protocols</i> , 2021, 2, 100406.	0.5	2
7	Multi-omic profiling of primary mouse neutrophils predicts a pattern of sex- and age-related functional regulation. <i>Nature Aging</i> , 2021, 1, 715-733.	5.3	55
8	NHR-8 and P-glycoproteins uncouple xenobiotic resistance from longevity in chemosensory <i>C. elegans</i> mutants. <i>ELife</i> , 2021, 10, .	2.8	8
9	MOTS-c is an exercise-induced mitochondrial-encoded regulator of age-dependent physical decline and muscle homeostasis. <i>Nature Communications</i> , 2021, 12, 470.	5.8	97
10	Genome-wide surveillance of transcription errors in response to genotoxic stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	19
11	Protocol for analysis of mouse neutrophil NETosis by flow cytometry. <i>STAR Protocols</i> , 2021, 2, 100948.	0.5	11
12	Widespread sex dimorphism in aging and age-related diseases. <i>Human Genetics</i> , 2020, 139, 333-356.	1.8	76
13	The microbiome: An emerging key player in aging and longevity. <i>Translational Medicine of Aging</i> , 2020, 4, 103-116.	0.6	76
14	Transposable elements, circular RNAs and mitochondrial transcription in age-related genomic regulation. <i>Development (Cambridge)</i> , 2020, 147, .	1.2	25
15	Remodeling of the H3 nucleosomal landscape during mouse aging. <i>Translational Medicine of Aging</i> , 2020, 4, 22-31.	0.6	22
16	Special issue on â€œMolecular genetics of aging and longevityâ€ a critical time in the field of geroscience. <i>Human Genetics</i> , 2020, 139, 275-276.	1.8	0
17	Measuring Phagocytosis in Bone Marrow-Derived Macrophages and Peritoneal Macrophages with Aging. <i>Methods in Molecular Biology</i> , 2020, 2144, 161-170.	0.4	4
18	The microbiome: an emerging key player in aging and longevity. <i>Translational Medicine of Aging</i> , 2020, 4, 103-116.	0.6	23

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19	MOTSâ€œ: A Mitochondrialâ€œEncoded Regulator of the Nucleus. <i>BioEssays</i> , 2019, 41, e1900046.	1.2	19
20	Multi-level remodeling of transcriptional landscapes in aging and longevity. <i>BMB Reports</i> , 2019, 52, 86-108.	1.1	42
21	Remodeling of epigenome and transcriptome landscapes with aging in mice reveals widespread induction of inflammatory responses. <i>Genome Research</i> , 2019, 29, 697-709.	2.4	234
22	IMMUNITY AND AGINGâ€œTHE HUMAN FACE. <i>Innovation in Aging</i> , 2019, 3, S768-S768.	0.0	0
23	SEX-DIMORPHISM IN THE GENOMIC REGULATION OF AGING. <i>Innovation in Aging</i> , 2019, 3, S768-S769.	0.0	0
24	INVESTIGATING THE ROLE OF AHR IN MEDIATING SEX DIFFERENCES OF AGING MACROPHAGES. <i>Innovation in Aging</i> , 2019, 3, S836-S836.	0.0	0
25	Heterogeneity in old fibroblasts is linked to variability in reprogramming and wound healing. <i>Nature</i> , 2019, 574, 553-558.	13.7	187
26	Aging Epigenetics. , 2018, , 3-32.		7
27	The Mitochondrial-Encoded Peptide MOTS-c Translocates to the Nucleus to Regulate Nuclear Gene Expression in Response to Metabolic Stress. <i>Cell Metabolism</i> , 2018, 28, 516-524.e7.	7.2	181
28	Histone variant H2A.J accumulates in senescent cells and promotes inflammatory gene expression. <i>Nature Communications</i> , 2017, 8, 14995.	5.8	131
29	Computational inference of a genomic pluripotency signature in human and mouse stem cells. <i>Biology Direct</i> , 2016, 11, 47.	1.9	5
30	The African Turquoise Killifish Genome Provides Insights into Evolution and Genetic Architecture of Lifespan. <i>Cell</i> , 2015, 163, 1539-1554.	13.5	200
31	A Platform for Rapid Exploration of Aging and Diseases in a Naturally Short-Lived Vertebrate. <i>Cell</i> , 2015, 160, 1013-1026.	13.5	199
32	Identification of AMPK Phosphorylation Sites Reveals a Network of Proteins Involved in Cell Invasion and Facilitates Large-Scale Substrate Prediction. <i>Cell Metabolism</i> , 2015, 22, 907-921.	7.2	149
33	Epigenetic regulation of ageing: linking environmental inputs to genomic stability. <i>Nature Reviews Molecular Cell Biology</i> , 2015, 16, 593-610.	16.1	515
34	High telomerase is a hallmark of undifferentiated spermatogonia and is required for maintenance of male germline stem cells. <i>Genes and Development</i> , 2015, 29, 2420-2434.	2.7	56
35	Inhibition of Pluripotency Networks by the Rb Tumor Suppressor Restricts Reprogramming and Tumorigenesis. <i>Cell Stem Cell</i> , 2015, 16, 39-50.	5.2	166
36	Males Shorten the Life Span of <i>C. elegans</i> Hermaphrodites via Secreted Compounds. <i>Science</i> , 2014, 343, 541-544.	6.0	150

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37	H3K4me3 Breadth Is Linked to Cell Identity and Transcriptional Consistency. <i>Cell</i> , 2014, 158, 673-688.	13.5	404
38	Adult ovarian granulosa cell tumor transcriptomics: prevalence of FOXL2 target genes misregulation gives insights into the pathogenic mechanism of the p.Cys134Trp somatic mutation. <i>Oncogene</i> , 2013, 32, 2739-2746.	2.6	49
39	Epigenetic memory of longevity in <i>Caenorhabditis elegans</i> . <i>Worm</i> , 2012, 1, 77-81.	1.0	13
40	Discovery of novel protein partners of the transcription factor FOXL2 provides insights into its physiopathological roles. <i>Human Molecular Genetics</i> , 2012, 21, 3264-3274.	1.4	41
41	The Transcription Factor Encyclopedia. <i>Genome Biology</i> , 2012, 13, R24.	13.9	103
42	The transcription factor FOXL2: At the crossroads of ovarian physiology and pathology. <i>Molecular and Cellular Endocrinology</i> , 2012, 356, 55-64.	1.6	67
43	A Regulatory Domain Is Required for Foxn4 Activity During Retinogenesis. <i>Journal of Molecular Neuroscience</i> , 2012, 46, 315-323.	1.1	6
44	SUMOylation of the Forkhead Transcription Factor FOXL2 Promotes Its Stabilization/Activation through Transient Recruitment to PML Bodies. <i>PLoS ONE</i> , 2011, 6, e25463.	1.1	24
45	Forkhead transcription factors: key players in health and disease. <i>Trends in Genetics</i> , 2011, 27, 224-232.	2.9	267
46	Transgenerational epigenetic inheritance of longevity in <i>Caenorhabditis elegans</i> . <i>Nature</i> , 2011, 479, 365-371.	13.7	562
47	Transcription factor FOXL2 protects granulosa cells from stress and delays cell cycle: role of its regulation by the SIRT1 deacetylase. <i>Human Molecular Genetics</i> , 2011, 20, 1673-1686.	1.4	81
48	The forkhead factor FOXL2: A novel tumor suppressor?. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , 2010, 1805, 1-5.	3.3	13
49	Generic binding sites, generic DNA-binding domains: where does specific promoter recognition come from?. <i>FASEB Journal</i> , 2010, 24, 346-356.	0.2	74
50	Functional Exploration of the Adult Ovarian Granulosa Cell Tumor-Associated Somatic FOXL2 Mutation p.Cys134Trp (c.402C>G). <i>PLoS ONE</i> , 2010, 5, e8789.	1.1	67
51	Towards a functional classification of pathogenic FOXL2 mutations using transactivation reporter systems. <i>Human Molecular Genetics</i> , 2009, 18, 3324-3333.	1.4	41
52	Positive and negative feedback regulates the transcription factor FOXL2 in response to cell stress: evidence for a regulatory imbalance induced by disease-causing mutations. <i>Human Molecular Genetics</i> , 2009, 18, 632-644.	1.4	56
53	Functional evidence implicating FOXL2 in non-syndromic premature ovarian failure and in the regulation of the transcription factor OSR2. <i>Journal of Medical Genetics</i> , 2009, 46, 455-457.	1.5	55
54	A post-translational modification code for transcription factors: sorting through a sea of signals. <i>Trends in Cell Biology</i> , 2009, 19, 189-197.	3.6	109

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55	The new molecular biology of granulosa cell tumors of the ovary. <i>Genome Medicine</i> , 2009, 1, 81.	3.6	22
56	FOXL2: At the Crossroads of Female Sex Determination and Ovarian Function. <i>Advances in Experimental Medicine and Biology</i> , 2009, 665, 207-226.	0.8	18
57	The postâ€translational modification profile of the forkhead transcription factor FOXL2 suggests the existence of parallel processive/concerted modification pathways. <i>Proteomics</i> , 2008, 8, 3118-3123.	1.3	21
58	Differential functional effects of novel mutations of the transcription factor FOXL2 in BPES patients. <i>Human Mutation</i> , 2008, 29, E123-E131.	1.1	27
59	The mutations and potential targets of the forkhead transcription factor FOXL2. <i>Molecular and Cellular Endocrinology</i> , 2008, 282, 2-11.	1.6	68
60	The identification and characterization of a FOXL2 response element provides insights into the pathogenesis of mutant alleles. <i>Human Molecular Genetics</i> , 2008, 17, 3118-3127.	1.4	58