

# Brnice A Benayoun

## List of Publications by Citations

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58  
papers

3,608  
citations

31  
h-index

60  
g-index

73  
ext. papers

4,608  
ext. citations

12.5  
avg, IF

5.83  
L-index

#	Paper	IF	Citations
58	Transgenerational epigenetic inheritance of longevity in <i>Caenorhabditis elegans</i> . <i>Nature</i> , <b>2011</b> , 479, 365-371	56.4	462
57	Epigenetic regulation of ageing: linking environmental inputs to genomic stability. <i>Nature Reviews Molecular Cell Biology</i> , <b>2015</b> , 16, 593-610	48.7	362
56	H3K4me3 breadth is linked to cell identity and transcriptional consistency. <i>Cell</i> , <b>2014</b> , 158, 673-88	56.2	278
55	Forkhead transcription factors: key players in health and disease. <i>Trends in Genetics</i> , <b>2011</b> , 27, 224-32	8.5	200
54	A platform for rapid exploration of aging and diseases in a naturally short-lived vertebrate. <i>Cell</i> , <b>2015</b> , 160, 1013-1026	56.2	133
53	The African Turquoise Killifish Genome Provides Insights into Evolution and Genetic Architecture of Lifespan. <i>Cell</i> , <b>2015</b> , 163, 1539-54	56.2	121
52	Inhibition of pluripotency networks by the Rb tumor suppressor restricts reprogramming and tumorigenesis. <i>Cell Stem Cell</i> , <b>2015</b> , 16, 39-50	18	119
51	Males shorten the life span of <i>C. elegans</i> hermaphrodites via secreted compounds. <i>Science</i> , <b>2014</b> , 343, 541-4	33.3	112
50	Identification of AMPK Phosphorylation Sites Reveals a Network of Proteins Involved in Cell Invasion and Facilitates Large-Scale Substrate Prediction. <i>Cell Metabolism</i> , <b>2015</b> , 22, 907-21	24.6	110
49	Remodeling of epigenome and transcriptome landscapes with aging in mice reveals widespread induction of inflammatory responses. <i>Genome Research</i> , <b>2019</b> , 29, 697-709	9.7	104
48	The Mitochondrial-Encoded Peptide MOTS-c Translocates to the Nucleus to Regulate Nuclear Gene Expression in Response to Metabolic Stress. <i>Cell Metabolism</i> , <b>2018</b> , 28, 516-524.e7	24.6	100
47	A post-translational modification code for transcription factors: sorting through a sea of signals. <i>Trends in Cell Biology</i> , <b>2009</b> , 19, 189-97	18.3	94
46	The transcription factor encyclopedia. <i>Genome Biology</i> , <b>2012</b> , 13, R24	18.3	86
45	Heterogeneity in old fibroblasts is linked to variability in reprogramming and wound healing. <i>Nature</i> , <b>2019</b> , 574, 553-558	50.4	84
44	Histone variant H2A.J accumulates in senescent cells and promotes inflammatory gene expression. <i>Nature Communications</i> , <b>2017</b> , 8, 14995	17.4	80
43	IMMUNITY AND AGING IN THE HUMAN FACE. <i>Innovation in Aging</i> , <b>2019</b> , 3, S768-S768	0.1	78
42	SEX-DIMORPHISM IN THE GENOMIC REGULATION OF AGING. <i>Innovation in Aging</i> , <b>2019</b> , 3, S768-S769	0.1	78

41	INVESTIGATING THE ROLE OF AHR IN MEDIATING SEX DIFFERENCES OF AGING MACROPHAGES. <i>Innovation in Aging</i> , <b>2019</b> , 3, S836-S836	0.1	78
40	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> , <b>2011</b> , 20, 1673-86	5.6	69
39	Generic binding sites, generic DNA-binding domains: where does specific promoter recognition come from?. <i>FASEB Journal</i> , <b>2010</b> , 24, 346-56	0.9	66
38	The mutations and potential targets of the forkhead transcription factor FOXL2. <i>Molecular and Cellular Endocrinology</i> , <b>2008</b> , 282, 2-11	4.4	63
37	Functional exploration of the adult ovarian granulosa cell tumor-associated somatic FOXL2 mutation p.Cys134Trp (c.402C>G). <i>PLoS ONE</i> , <b>2010</b> , 5, e8789	3.7	59
36	The transcription factor FOXL2: at the crossroads of ovarian physiology and pathology. <i>Molecular and Cellular Endocrinology</i> , <b>2012</b> , 356, 55-64	4.4	54
35	The identification and characterization of a FOXL2 response element provides insights into the pathogenesis of mutant alleles. <i>Human Molecular Genetics</i> , <b>2008</b> , 17, 3118-27	5.6	54
34	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> , <b>2009</b> , 18, 632-44	5.6	53
33	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> , <b>2009</b> , 46, 455-7	5.8	51
32	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> , <b>2013</b> , 32, 2739-46	9.2	44
31	High telomerase is a hallmark of undifferentiated spermatogonia and is required for maintenance of male germline stem cells. <i>Genes and Development</i> , <b>2015</b> , 29, 2420-34	12.6	39
30	Towards a functional classification of pathogenic FOXL2 mutations using transactivation reporter systems. <i>Human Molecular Genetics</i> , <b>2009</b> , 18, 3324-33	5.6	37
29	Discovery of novel protein partners of the transcription factor FOXL2 provides insights into its physiopathological roles. <i>Human Molecular Genetics</i> , <b>2012</b> , 21, 3264-74	5.6	34
28	MOTS-c is an exercise-induced mitochondrial-encoded regulator of age-dependent physical decline and muscle homeostasis. <i>Nature Communications</i> , <b>2021</b> , 12, 470	17.4	32
27	The microbiome: An emerging key player in aging and longevity. <i>Translational Medicine of Aging</i> , <b>2020</b> , 4, 103-116	2.7	31
26	Widespread sex dimorphism in aging and age-related diseases. <i>Human Genetics</i> , <b>2020</b> , 139, 333-356	6.3	28
25	Multi-level remodeling of transcriptional landscapes in aging and longevity. <i>BMB Reports</i> , <b>2019</b> , 52, 86-108	9.5	25
24	SUMOylation of the Forkhead transcription factor FOXL2 promotes its stabilization/activation through transient recruitment to PML bodies. <i>PLoS ONE</i> , <b>2011</b> , 6, e25463	3.7	21

23	Differential functional effects of novel mutations of the transcription factor FOXL2 in BPES patients. <i>Human Mutation</i> , <b>2008</b> , 29, E123-31	4.7	21
22	The post-translational modification profile of the forkhead transcription factor FOXL2 suggests the existence of parallel processive/concerted modification pathways. <i>Proteomics</i> , <b>2008</b> , 8, 3118-23	4.8	20
21	The new molecular biology of granulosa cell tumors of the ovary. <i>Genome Medicine</i> , <b>2009</b> , 1, 81	14.4	17
20	FOXL2: at the crossroads of female sex determination and ovarian function. <i>Advances in Experimental Medicine and Biology</i> , <b>2009</b> , 665, 207-26	3.6	16
19	The microbiome: an emerging key player in aging and longevity. <i>Translational Medicine of Aging</i> , <b>2020</b> , 4, 103-116	2.7	15
18	Epigenetic memory of longevity in <i>Caenorhabditis elegans</i> . <i>Worm</i> , <b>2012</b> , 1, 77-81		10
17	Transposable elements, circular RNAs and mitochondrial transcription in age-related genomic regulation. <i>Development (Cambridge)</i> , <b>2020</b> , 147,	6.6	9
16	MOTS-c: A Mitochondrial-Encoded Regulator of the Nucleus. <i>BioEssays</i> , <b>2019</b> , 41, e1900046	4.1	9
15	The forkhead factor FOXL2: a novel tumor suppressor?. <i>Biochimica Et Biophysica Acta: Reviews on Cancer</i> , <b>2010</b> , 1805, 1-5	11.2	9
14	Remodeling of the H3 nucleosomal landscape during mouse aging. <i>Translational Medicine of Aging</i> , <b>2020</b> , 4, 22-31	2.7	8
13	Multi-omic profiling of primary mouse neutrophils predicts a pattern of sex and age-related functional regulation. <i>Nature Aging</i> , <b>2021</b> , 1, 715-733		7
12	Computational inference of a genomic pluripotency signature in human and mouse stem cells. <i>Biology Direct</i> , <b>2016</b> , 11, 47	7.2	5
11	Functional genomics of inflamm-aging and immunosenescence. <i>Briefings in Functional Genomics</i> , <b>2021</b> ,	4.9	4
10	Aging Epigenetics: Changes and Challenges <b>2018</b> , 3-32		3
9	A regulatory domain is required for Foxn4 activity during retinogenesis. <i>Journal of Molecular Neuroscience</i> , <b>2012</b> , 46, 315-23	3.3	3
8	Mitochondrial-Encoded Peptide MOTS-c is an Exercise-Induced Regulator of Aging Metabolic Homeostasis and Physical Capacity		3
7	Old fibroblasts secrete inflammatory cytokines that drive variability in reprogramming efficiency and may affect wound healing between old individuals		3
6	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> , <b>2021</b> , 118,	11.5	2

5	Endogenous Retroviral Elements Generate Pathologic Neutrophils and Elastase Rich Exosomes in Pulmonary Arterial Hypertension		2
4	Measuring Phagocytosis in Bone Marrow-Derived Macrophages and Peritoneal Macrophages with Aging. <i>Methods in Molecular Biology</i> , <b>2020</b> , 2144, 161-170	1.4	2
3	NHR-8 and P-glycoproteins uncouple xenobiotic resistance from longevity in chemosensory mutants. <i>ELife</i> , <b>2021</b> , 10,	8.9	1
2	Protocol for analysis of mouse neutrophil NETosis by flow cytometry. <i>STAR Protocols</i> , <b>2021</b> , 2, 100948	1.4	0
1	Protocol for isolation of adult mouse ear pinnae-derived primary fibroblasts. <i>STAR Protocols</i> , <b>2021</b> , 2, 100406	1.4	