Joao Pedro de Magalhaes

List of Publications by Year
in descending order

157 papers	12,505 citations	26630 56 h-index	32842 100 g-index
175 all docs	175 docs citations	175 times ranked	15809 citing authors

#	Article	IF	Citations
1	Gene co-expression analysis for functional classification and geneâ€“disease predictions. Briefings in Bioinformatics, 2018, 19, bbw139.	6.5	718
2	Meta-analysis of age-related gene expression profiles identifies common signatures of aging. Bioinformatics, 2009, 25, 875-881.	4.1	651
3	RNA-Seq Signatures Normalized by mRNA Abundance Allow Absolute Deconvolution of Human Immune Cell Types. Cell Reports, 2019, 26, 1627-1640.e7.	6.4	590
4	Human Ageing Genomic Resources: new and updated databases. Nucleic Acids Research, 2018, 46, D1083-D1090.	14.5	511
5	Human Ageing Genomic Resources: Integrated databases and tools for the biology and genetics of ageing. Nucleic Acids Research, 2012, 41, D1027-D1033.	14.5	467
6	A database of vertebrate longevity records and their relation to other lifeâ€history traits. Journal of Evolutionary Biology, 2009, 22, 1770-1774.	1.7	444
7	The Role of DNA Methylation in Aging, Rejuvenation, and Age-Related Disease. Rejuvenation Research, 2012, 15, 483-494.	1.8	307
8	An Analysis of the Relationship Between Metabolism, Developmental Schedules, and Longevity Using Phylogenetic Independent Contrasts. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2007, 62, 149-160.	3.6	293
9	Subcytotoxic H2O2 Stress Triggers a Release of Transforming Growth Factor-Î²1, Which Induces Biomarkers of Cellular Senescence of Human Diploid Fibroblasts. Journal of Biological Chemistry, 2001, 276, 2531-2537.	3.4	284
10	How ageing processes influence cancer. Nature Reviews Cancer, 2013, 13, 357-365.	28.4	280
11	Insights into the Evolution of Longevity from the Bowhead Whale Genome. Cell Reports, 2015, 10, 112-122.	6.4	280
12	Longer lifespan in male mice treated with a weakly estrogenic agonist, an antioxidant, an Î±â€glucosidase inhibitor or a Nrf2â€inducer. Aging Cell, 2016, 15, 872-884.	6.7	277
13	Stress, cell senescence and organismal ageing. Mechanisms of Ageing and Development, 2018, 170, 2-9.	4.6	234
14	m6A-Atlas: a comprehensive knowledgebase for unraveling the<i>N</i>6-methyladenosine (m6A) epitranscriptome. Nucleic Acids Research, 2021, 49, D134-D143.	14.5	185
15	A review and appraisal of the DNA damage theory of ageing. Mutation Research - Reviews in Mutation Research, 2011, 728, 12-22.	5.5	177
16	WHISTLE: a high-accuracy map of the human N6-methyladenosine (m6A) epitranscriptome predicted using a machine learning approach. Nucleic Acids Research, 2019, 47, e41-e41.	14.5	177
17	A multidimensional systems biology analysis of cellular senescence in aging and disease. Genome Biology, 2020, 21, 91.	8.8	177
18	The Human Ageing Genomic Resources: online databases and tools for biogerontologists. Aging Cell, 2009, 8, 65-72.	6.7	173

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19	flowAI: automatic and interactive anomaly discerning tools for flow cytometry data. Bioinformatics, 2016, 32, 2473-2480.	4.1	166
20	HAGR: the Human Ageing Genomic Resources. Nucleic Acids Research, 2004, 33, D537-D543.	14.5	147
21	The Business of Anti-Aging Science. Trends in Biotechnology, 2017, 35, 1062-1073.	9.3	127
22	The DrugAge database of aging-related drugs. Aging Cell, 2017, 16, 594-597.	6.7	121
23	Genome-Environment Interactions That Modulate Aging: Powerful Targets for Drug Discovery. Pharmacological Reviews, 2012, 64, 88-101.	16.0	118
24	GenAge: a genomic and proteomic network map of human ageing. FEBS Letters, 2004, 571, 243-247.	2.8	116
25	GeneFriends: a human RNA-seq-based gene and transcript co-expression database. Nucleic Acids Research, 2015, 43, D1124-D1132.	14.5	108
26	Programmatic features of aging originating in development: aging mechanisms beyond molecular damage?. FASEB Journal, 2012, 26, 4821-4826.	0.5	106
27	A review of supervised machine learning applied to ageing research. Biogerontology, 2017, 18, 171-188.	3.9	101
28	Biohorology and biomarkers of aging: Current state-of-the-art, challenges and opportunities. Ageing Research Reviews, 2020, 60, 101050.	10.9	101
29	Genomes Optimize Reproduction: Aging as a Consequence of the Developmental Program. Physiology, 2005, 20, 252-259.	3.1	100
30	Next-generation sequencing in aging research: Emerging applications, problems, pitfalls and possible solutions. Ageing Research Reviews, 2010, 9, 315-323.	10.9	98
31	The Influence of Genes on the Aging Process of Mice. Genetics, 2005, 169, 265-274.	2.9	97
32	From humans to hydra: patterns of cancer across the tree of life. Biological Reviews, 2018, 93, 1715-1734.	10.4	97
33	A human tissueâ€specific transcriptomic analysis reveals a complex relationship between aging, cancer, and cellular senescence. Aging Cell, 2019, 18, e13041.	6.7	97
34	From cells to ageing: a review of models and mechanisms of cellular senescence and their impact on human ageing. Experimental Cell Research, 2004, 300, 1-10.	2.6	96
35	Cells discover fire: Employing reactive oxygen species in developmentand consequences for aging. Experimental Gerontology, 2006, 41, 1-10.	2.8	96
36	Whole transcriptome sequencing of the aging rat brain reveals dynamic RNA changes in the dark matter of the genome. Age, 2013, 35, 763-776.	3.0	94

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37	Being cool: how body temperature influences ageing and longevity. Biogerontology, 2015, 16, 383-397.	3.9	94
38	Geroprotectors.org: a new, structured and curated database of current therapeutic interventions in aging and age-related disease. Aging, 2015, 7, 616-628.	3.1	93
39	LongevityMap: a database of human genetic variants associated with longevity. Trends in Genetics, 2013, 29, 559-560.	6.7	92
40	RNA Sequencing Reveals Differential Expression of Mitochondrial and Oxidation Reduction Genes in the Long-Lived Naked Mole-Rat When Compared to Mice. PLoS ONE, 2011, 6, e26729.	2.5	91
41	A comparison of human and mouse gene co-expression networks reveals conservation and divergence at the tissue, pathway and disease levels. BMC Evolutionary Biology, 2015, 15, 259.	3.2	89
42	A network pharmacology approach reveals new candidate caloric restriction mimetics in <i>C. elegans</i>. Aging Cell, 2016, 15, 256-266.	6.7	86
43	m7GHub: deciphering the location, regulation and pathogenesis of internal mRNA N7-methylguanosine (m7G) sites in human. Bioinformatics, 2020, 36, 3528-3536.	4.1	85
44	From the Hayflick mosaic to the mosaics of ageing.. International Journal of Biochemistry and Cell Biology, 2002, 34, 1415-1429.	2.8	84
45	The Digital Ageing Atlas: integrating the diversity of age-related changes into a unified resource. Nucleic Acids Research, 2015, 43, D873-D878.	14.5	83
46	UVB-induced premature senescence of human diploid skin fibroblasts. International Journal of Biochemistry and Cell Biology, 2002, 34, 1331-1339.	2.8	80
47	A meta-analysis of caloric restriction gene expression profiles to infer common signatures and regulatory mechanisms. Molecular BioSystems, 2012, 8, 1339.	2.9	80
48	Stress-induced premature senescence in BJ and hTERT-BJ1 human foreskin fibroblasts. FEBS Letters, 2002, 523, 157-162.	2.8	76
49	Systems Biology and Longevity: An Emerging Approach to Identify Innovative Anti- Aging Targets and Strategies. Current Pharmaceutical Design, 2010, 16, 802-813.	1.9	76
50	Targeting immune dysfunction in aging. Ageing Research Reviews, 2021, 70, 101410.	10.9	76
51	Systematic analysis of the gerontome reveals links between aging and age-related diseases. Human Molecular Genetics, 2016, 25, ddw307.	2.9	74
52	The Naked Mole Rat Genome Resource: facilitating analyses of cancer and longevity-related adaptations. Bioinformatics, 2014, 30, 3558-3560.	4.1	71
53	Gene expression and regulation in H2O2-induced premature senescence of human foreskin fibroblasts expressing or not telomerase. Experimental Gerontology, 2004, 39, 1379-1389.	2.8	68
54	GeneFriends: An online co-expression analysis tool to identify novel gene targets for aging and complex diseases. BMC Genomics, 2012, 13, 535.	2.8	67

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55	Naked mole rats can undergo developmental, oncogene-induced and DNA damage-induced cellular senescence. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 1801-1806.	7.1	67
56	Gene Size Matters: An Analysis of Gene Length in the Human Genome. Frontiers in Genetics, 2021, 12, 559998.	2.3	67
57	The hoverfly and the wasp: A critique of the hallmarks of aging as a paradigm. Ageing Research Reviews, 2021, 70, 101407.	10.9	67
58	Cell divisions and mammalian aging: integrative biology insights from genes that regulate longevity. BioEssays, 2008, 30, 567-578.	2.5	66
59	RMDisease: a database of genetic variants that affect RNA modifications, with implications for epitranscriptome pathogenesis. Nucleic Acids Research, 2021, 49, D1396-D1404.	14.5	65
60	Winter is coming: the future of cryopreservation. BMC Biology, 2021, 19, 56.	3.8	64
61	Vive la radiorÃ©sistance!: converging research in radiobiology and biogerontology to enhance human radioresistance for deep space exploration and colonization. Oncotarget, 2018, 9, 14692-14722.	1.8	62
62	Attention-based multi-label neural networks for integrated prediction and interpretation of twelve widely occurring RNA modifications. Nature Communications, 2021, 12, 4011.	12.8	61
63	The effects of donor age on organ transplants: A review and implications for aging research. Experimental Gerontology, 2018, 110, 230-240.	2.8	60
64	Dissecting the Gene Network of Dietary Restriction to Identify Evolutionarily Conserved Pathways and New Functional Genes. PLoS Genetics, 2012, 8, e1002834.	3.5	58
65	Biological Processes Modulating Longevity across Primates: A Phylogenetic Genome-Phenome Analysis. Molecular Biology and Evolution, 2018, 35, 1990-2004.	8.9	58
66	miRNA-31 Improves Cognition and Abolishes Amyloid-Î² Pathology by Targeting APP and BACE1 in an Animal Model of Alzheimerâ€™s Disease. Molecular Therapy - Nucleic Acids, 2020, 19, 1219-1236.	5.1	56
67	Accelerated protein evolution analysis reveals genes and pathways associated with the evolution of mammalian longevity. Age, 2013, 35, 301-314.	3.0	54
68	An integrative analysis of the age-associated multi-omic landscape across cancers. Nature Communications, 2021, 12, 2345.	12.8	54
69	m5C-Atlas: a comprehensive database for decoding and annotating the 5-methylcytosine (m5C) epitranscriptome. Nucleic Acids Research, 2022, 50, D196-D203.	14.5	53
70	A data mining approach for classifying DNA repair genes into ageing-related or non-ageing-related. BMC Genomics, 2011, 12, 27.	2.8	52
71	Molecular damage in aging. Nature Aging, 2021, 1, 1096-1106.	11.6	51
72	Why genes extending lifespan in model organisms have not been consistently associated with human longevity and what it means to translation research. Cell Cycle, 2014, 13, 2671-2673.	2.6	50

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73	Targeting aging mechanisms: pharmacological perspectives. Trends in Endocrinology and Metabolism, 2022, 33, 266-280.	7.1	50
74	Transcriptome analysis in calorie-restricted rats implicates epigenetic and post-translational mechanisms in neuroprotection and aging. Genome Biology, 2015, 16, 285.	8.8	49
75	Prediction of C. elegans Longevity Genes by Human and Worm Longevity Networks. PLoS ONE, 2012, 7, e48282.	2.5	49
76	Mitochondrially encoded methionine is inversely related to longevity in mammals. Aging Cell, 2011, 10, 198-207.	6.7	48
77	Open-minded scepticism: inferring the causal mechanisms of human ageing from genetic perturbations. Ageing Research Reviews, 2005, 4, 1-22.	10.9	44
78	Cognitive aging as an extension of brain development: A model linking learning, brain plasticity, and neurodegeneration. Mechanisms of Ageing and Development, 2005, 126, 1026-1033.	4.6	43
79	A new approach for interpreting Random Forest models and its application to the biology of ageing. Bioinformatics, 2018, 34, 2449-2456.	4.1	43
80	To help aging populations, classify organismal senescence. Science, 2019, 366, 576-578.	12.6	42
81	Growth kinetics rather than stress accelerate telomere shortening in cultures of human diploid fibroblasts in oxidative stress-induced premature senescence. FEBS Letters, 2001, 502, 109-112.	2.8	40
82	Age-related gene-specific changes of A-to-I mRNA editing in the human brain. Mechanisms of Ageing and Development, 2010, 131, 445-447.	4.6	40
83	Ageing transcriptome meta-analysis reveals similarities and differences between key mammalian tissues. Aging, 2021, 13, 3313-3341.	3.1	40
84	Cell resilience in species life spans: a link to inflammation?. Aging Cell, 2010, 9, 519-526.	6.7	39
85	The Scientific Quest for Lasting Youth: Prospects for Curing Aging. Rejuvenation Research, 2014, 17, 458-467.	1.8	39
86	Bioinformatics approaches for deciphering the epitranscriptome: Recent progress and emerging topics. Computational and Structural Biotechnology Journal, 2020, 18, 1587-1604.	4.1	38
87	Sexâ€specific aging in animals: Perspective and future directions. Aging Cell, 2022, 21, e13542.	6.7	36
88	The evolution of mammalian aging. Experimental Gerontology, 2002, 37, 769-775.	2.8	34
89	Analyses of humanâ€“chimpanzee orthologous gene pairs to explore evolutionary hypotheses of aging. Mechanisms of Ageing and Development, 2007, 128, 355-364.	4.6	34
90	Predicting the Pro-Longevity or Anti-Longevity Effect of Model Organism Genes with New Hierarchical Feature Selection Methods. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2015, 12, 262-275.	3.0	34

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91	Machine learning for predicting lifespan-extending chemical compounds. Aging, 2017, 9, 1721-1737.	3.1	34
92	The genomics of ecological flexibility, large brains, and long lives in capuchin monkeys revealed with fecalFACS. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	34
93	ConsRM: collection and large-scale prediction of the evolutionarily conserved RNA methylation sites, with implications for the functional epitranscriptome. Briefings in Bioinformatics, 2021, 22, .	6.5	34
94	Hallmarks of aging-based dual-purpose disease and age-associated targets predicted using PandaOmics AI-powered discovery engine. Aging, 2022, 14, 2475-2506.	3.1	33
95	Positive selection and gene duplications in tumour suppressor genes reveal clues about how cetaceans resist cancer. Proceedings of the Royal Society B: Biological Sciences, 2021, 288, 20202592.	2.6	32
96	Fish oil supplements, longevity and aging. Aging, 2016, 8, 1578-1582.	3.1	30
97	Telomeres and Telomerase: A Modern Fountain of Youth?. Rejuvenation Research, 2004, 7, 126-133.	1.8	27
98	Ageing-associated changes in the expression of lncRNAs in human tissues reflect a transcriptional modulation in ageing pathways. Mechanisms of Ageing and Development, 2020, 185, 111177.	4.6	27
99	Every gene can (and possibly will) be associated with cancer. Trends in Genetics, 2022, 38, 216-217.	6.7	27
100	Age-associated differences in the cancer molecular landscape. Trends in Cancer, 2022, 8, 962-971.	7.4	24
101	Stress-induced premature senescence as alternative toxicological method for testing the long-term effects of molecules under development in the industry. Biogerontology, 2000, 1, 179-183.	3.9	22
102	Circulating MicroRNAs in Young Patients with Acute Coronary Syndrome. International Journal of Molecular Sciences, 2018, 19, 1467.	4.1	22
103	Insights on cryoprotectant toxicity from gene expression profiling of endothelial cells exposed to ethylene glycol. Cryobiology, 2015, 71, 405-412.	0.7	21
104	Analysis of the FGF gene family provides insights into aquatic adaptation in cetaceans. Scientific Reports, 2017, 7, 40233.	3.3	21
105	Human Disease-Associated Mitochondrial Mutations Fixed in Nonhuman Primates. Journal of Molecular Evolution, 2005, 61, 491-497.	1.8	20
106	Vulnerability of progeroid smooth muscle cells to biomechanical forces is mediated by MMP13. Nature Communications, 2020, 11, 4110.	12.8	20
107	Longevity pharmacology comes of age. Drug Discovery Today, 2021, 26, 1559-1562.	6.4	20
108	How bioinformatics can help reverse engineer human aging. Ageing Research Reviews, 2004, 3, 125-141.	10.9	19

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109	The biology of ageing. , 2011, , 21-47.		18
110	Gathering insights on disease etiology from gene expression profiles of healthy tissues. Bioinformatics, 2011, 27, 3300-3305.	4.1	18
111	A review of the biomedical innovations for healthy longevity. Aging, 2017, 9, 7-25.	3.1	18
112	Has gene duplication impacted the evolution of Eutherian longevity?. Aging Cell, 2016, 15, 978-980.	6.7	17
113	Topological Characterization of Human and Mouse m⁵C Epitranscriptome Revealed by Bisulfite Sequencing. International Journal of Genomics, 2018, 2018, 1-19.	1.6	17
114	Is mammalian aging genetically controlled?. Biogerontology, 2003, 4, 119-120.	3.9	16
115	A Reassessment of Genes Modulating Aging in Mice Using Demographic Measurements of the Rate of Aging. Genetics, 2018, 208, 1617-1630.	2.9	16
116	A scan for genes associated with cancer mortality and longevity in pedigree dog breeds. Mammalian Genome, 2020, 31, 215-227.	2.2	16
117	SynergyAge, a curated database for synergistic and antagonistic interactions of longevity-associated genes. Scientific Data, 2020, 7, 366.	5.3	16
118	Aliceâ€™s dilemma. Futures, 2004, 36, 85-89.	2.5	15
119	Mutational Bias Plays an Important Role in Shaping Longevity-Related Amino Acid Content in Mammalian mtDNA-Encoded Proteins. Journal of Molecular Evolution, 2012, 74, 332-341.	1.8	15
120	A-to-I RNA editing does not change with age in the healthy male rat brain. Biogerontology, 2013, 14, 395-400.	3.9	15
121	A mathematical model of mortality dynamics across the lifespan combining heterogeneity and stochastic effects. Experimental Gerontology, 2013, 48, 801-811.	2.8	15
122	Comparing enrichment analysis and machine learning for identifying gene properties that discriminate between gene classes. Briefings in Bioinformatics, 2020, 21, 803-814.	6.5	15
123	Cellular reprogramming and the rise of rejuvenation biotech. Trends in Biotechnology, 2022, 40, 639-642.	9.3	15
124	Ecological, biomedical and epidemiological approaches to understanding oxidative balance and ageing: what they can teach each other. Functional Ecology, 2010, 24, 997-1006.	3.6	14
125	Evolution, structure and emerging roles of C1ORF112 in DNA replication, DNA damage responses, and cancer. Cellular and Molecular Life Sciences, 2021, 78, 4365-4376.	5.4	14
126	Positive Selection and Enhancer Evolution Shaped Lifespan and Body Mass in Great Apes. Molecular Biology and Evolution, 2022, 39, .	8.9	14

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127	Trans cohort metabolic reprogramming towards glutaminolysis in long-term successfully treated HIV-infection. Communications Biology, 2022, 5, 27.	4.4	13
128	Species Selection in Comparative Studies of Aging and Antiaging Research. , 2006, , 9-20.		12
129	Genomeâ€Wide Patterns of Genetic Distances Reveal Candidate Loci Contributing to Human Populationâ€Specific Traits. Annals of Human Genetics, 2012, 76, 142-158.	0.8	12
130	Endless paces of degenerationâ€"applying comparative genomics to study evolution's moulding of longevity. EMBO Reports, 2013, 14, 661-662.	4.5	12
131	The big, the bad and the ugly. EMBO Reports, 2015, 16, 771-776.	4.5	11
132	Using deep learning to associate human genes with age-related diseases. Bioinformatics, 2020, 36, 2202-2208.	4.1	11
133	The fog of genetics: what is known, unknown and unknowable in the genetics of complex traits and diseases. EMBO Reports, 2019, 20, e48054.	4.5	11
134	Reductions in hypothalamic Gfap expression, glial cells and Î±-tanycytes in lean and hypermetabolic Gnasxl-deficient mice. Molecular Brain, 2016, 9, 39.	2.6	10
135	Enhancing Epitranscriptome Module Detection from m6A-Seq Data Using Threshold-Based Measurement Weighting Strategy. BioMed Research International, 2018, 2018, 1-15.	1.9	10
136	Histone Variant macroH2A1.1 Enhances Nonhomologous End Joining-dependent DNA Double-strand-break Repair and Reprogramming Efficiency of Human iPSCs. Stem Cells, 2022, 40, 35-48.	3.2	9
137	No Increase in Senescence-Associated Î²-Galactosidase Activity in Werner Syndrome Fibroblasts after Exposure to H2O2. Annals of the New York Academy of Sciences, 2004, 1019, 375-378.	3.8	8
138	In memory of Dr. Olivier Toussaint. Biogerontology, 2017, 18, 1-1.	3.9	8
139	Identification of polymorphisms in cancer patients that differentially affect survival with age. Aging, 2017, 9, 2117-2136.	3.1	8
140	A Proposal to Sequence Genomes of Unique Interest for Research on Aging. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2007, 62, 583-584.	3.6	7
141	Paternal genome effects on aging: Evidence for a role of Rasgrf1 in longevity determination?. Mechanisms of Ageing and Development, 2011, 132, 72-73.	4.6	7
142	MYCN/LIN28B/Let-7/HMGA2 pathway implicated by meta-analysis of GWAS in suppression of post-natal proliferation thereby potentially contributing to aging. Mechanisms of Ageing and Development, 2013, 134, 346-348.	4.6	7
143	Machine learning-based predictions of dietary restriction associations across ageing-related genes. BMC Bioinformatics, 2022, 23, 10.	2.6	7
144	Identifying Novel Osteoarthritis-Associated Genes in Human Cartilage Using a Systematic Meta-Analysis and a Multi-Source Integrated Network. International Journal of Molecular Sciences, 2022, 23, 4395.	4.1	7

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145	Integrative Genomics of Aging. , 2016, , 263-285.		6
146	Hormesis: a quest for virtuality?. Human and Experimental Toxicology, 2001, 20, 311-314.	2.2	5
147	A role for Ras signaling in modulating mammalian aging by the GH/IGF1 axis. Aging, 2011, 3, 336-337.	3.1	5
148	Ethical Perspectives in Biogerontology. Ethics and Health Policy, 2013, , 173-188.	0.4	5
149	An analysis and validation pipeline for large-scale RNAi-based screens. Scientific Reports, 2013, 3, 1076.	3.3	5
150	A direct communication proposal to test the Zoo Hypothesis. Space Policy, 2016, 38, 22-26.	1.5	5
151	The inherent challenges of classifying senescenceâ€”Response. Science, 2020, 368, 595-596.	12.6	5
152	Skin Aging in Long-Lived Naked Mole-Rats Is Accompanied by Increased Expression of Longevity-Associated and Tumor Suppressor Genes. Journal of Investigative Dermatology, 2022, 142, 2853-2863.e4.	0.7	5
153	Osh6 links yeast vacuolar functions to lifespan extension and TOR. Cell Cycle, 2012, 11, 2419-2419.	2.6	2
154	Integrative genomics of aging. , 2021, , 151-171.		1
155	Ageing research in the post-genome era: new technologies for an old problem. SEB Experimental Biology Series, 2009, 62, 99-115.	0.1	1
156	A method for the permeabilization of live <i>Drosophila melanogaster</i> larvae to small molecules and cryoprotectants. Fly, 2020, 14, 29-33.	1.7	0
157	Single-cell gene regulation across aging tissues. Nature Aging, 2022, 2, 468-470.	11.6	0