Jan Vijg

List of Publications by Year
in descending order

158 papers	13,945 citations	24978 57 h-index	24179 110 g-index
164 all docs	164 docs citations	164 times ranked	16074 citing authors

#	Article	IF	Citations
1	An Essential Role for Senescent Cells in Optimal Wound Healing through Secretion of PDGF-AA. Developmental Cell, 2014, 31, 722-733.	3.1	1,376
2	A new progeroid syndrome reveals that genotoxic stress suppresses the somatotroph axis. Nature, 2006, 444, 1038-1043.	13.7	601
3	Aging and Genome Maintenance: Lessons from the Mouse?. Science, 2003, 299, 1355-1359.	6.0	538
4	Increased cell-to-cell variation in gene expression in ageing mouse heart. Nature, 2006, 441, 1011-1014.	13.7	537
5	Interventions to Slow Aging in Humans: Are We Ready?. Aging Cell, 2015, 14, 497-510.	3.0	481
6	Efficient rescue of integrated shuttle vectors from transgenic mice: a model for studying mutations in vivo.. Proceedings of the National Academy of Sciences of the United States of America, 1989, 86, 7971-7975.	3.3	466
7	Evidence for a limit to human lifespan. Nature, 2016, 538, 257-259.	13.7	341
8	The central role of DNA damage in the ageing process. Nature, 2021, 592, 695-703.	13.7	340
9	DNA damage and ageing: new-age ideas for an age-old problem. Nature Cell Biology, 2008, 10, 1241-1247.	4.6	325
10	Genome Instability and Aging. Annual Review of Physiology, 2013, 75, 645-668.	5.6	314
11	Differences between germline and somatic mutation rates in humans and mice. Nature Communications, 2017, 8, 15183.	5.8	309
12	Epigenetic factors in aging and longevity. Pflugers Archiv European Journal of Physiology, 2010, 459, 247-258.	1.3	278
13	Deep biomarkers of human aging: Application of deep neural networks to biomarker development. Aging, 2016, 8, 1021-1033.	1.4	266
14	Rapid accumulation of genome rearrangements in liver but not in brain of old mice. Nature Genetics, 1997, 17, 431-434.	9.4	245
15	Distinct spectra of somatic mutations accumulated with age in mouse heart and small intestine. Proceedings of the National Academy of Sciences of the United States of America, 2000, 97, 8403-8408.	3.3	231
16	Restricted diet delays accelerated ageing and genomic stress in DNA-repair-deficient mice. Nature, 2016, 537, 427-431.	13.7	228
17	Somatic mutations and aging: a re-evaluation. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2000, 447, 117-135.	0.4	225
18	SIRT6 Is Responsible for More Efficient DNA Double-Strand Break Repair in Long-Lived Species. Cell, 2019, 177, 622-638.e22.	13.5	225

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19	Mechanisms of cancer resistance in long-lived mammals. Nature Reviews Cancer, 2018, 18, 433-441.	12.8	195
20	Accurate identification of single-nucleotide variants in whole-genome-amplified single cells. Nature Methods, 2017, 14, 491-493.	9.0	191
21	Analysis of individual cells identifies cellâ€toâ€cell variability following induction of cellular senescence. Aging Cell, 2017, 16, 1043-1050.	3.0	182
22	Nuclear Genomic Instability and Aging. Annual Review of Biochemistry, 2018, 87, 295-322.	5.0	178
23	Oxygen accelerates the accumulation of mutations during the senescence and immortalization of murine cells in culture. Aging Cell, 2003, 2, 287-294.	3.0	176
24	Single-cell whole-genome sequencing reveals the functional landscape of somatic mutations in B lymphocytes across the human lifespan. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 9014-9019.	3.3	174
25	Siblings of centenarians live longer. Lancet, The, 1998, 351, 1560.	6.3	172
26	Do DNA Double-Strand Breaks Drive Aging?. Molecular Cell, 2016, 63, 729-738.	4.5	172
27	Comparative genetics of longevity and cancer: insights from long-lived rodents. Nature Reviews Genetics, 2014, 15, 531-540.	7.7	169
28	Plasmid-based transgenic mouse model for studying in vivomutations. Nature, 1995, 377, 657-659.	13.7	143
29	Genetics of Longevity and Aging. Annual Review of Medicine, 2005, 56, 193-212.	5.0	143
30	Large genome rearrangements as a primary cause of aging. Mechanisms of Ageing and Development, 2002, 123, 907-915.	2.2	134
31	DNA repair in species with extreme lifespan differences. Aging, 2015, 7, 1171-1182.	1.4	132
32	Pathogenic Mechanisms of Somatic Mutation and Genome Mosaicism in Aging. Cell, 2020, 182, 12-23.	13.5	128
33	In silico Pathway Activation Network Decomposition Analysis (iPANDA) as a method for biomarker development. Nature Communications, 2016, 7, 13427.	5.8	126
34	Whole Chromosome Instability induces senescence and promotes SASP. Scientific Reports, 2016, 6, 35218.	1.6	117
35	Somatic mutations, genome mosaicism, cancer and aging. Current Opinion in Genetics and Development, 2014, 26, 141-149.	1.5	111
36	Age-related somatic mutations in the cancer genome. Oncotarget, 2015, 6, 24627-24635.	0.8	104

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37	Single-cell genome-wide bisulfite sequencing uncovers extensive heterogeneity in the mouse liver methylome. Genome Biology, 2016, 17, 150.	3.8	104
38	Genome instability, cancer and aging. Biochimica Et Biophysica Acta - General Subjects, 2009, 1790, 963-969.	1.1	102
39	Increased genomic instability is not a prerequisite for shortened lifespan in DNA repair deficient mice. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2006, 596, 22-35.	0.4	100
40	Mitochondrial DNA mutations and aging: devils in the details?. Trends in Genetics, 2009, 25, 91-98.	2.9	99
41	Comprehensive transcriptional landscape of aging mouse liver. BMC Genomics, 2015, 16, 899.	1.2	98
42	Genetic testing: The problems and the promise. Nature Biotechnology, 1997, 15, 422-426.	9.4	94
43	<i>INK4</i> locus of the tumor-resistant rodent, the naked mole rat, expresses a functional p15/p16 hybrid isoform. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1053-1058.	3.3	92
44	Controlled induction of DNA double-strand breaks in the mouse liver induces features of tissue ageing. Nature Communications, 2015, 6, 6790.	5.8	90
45	Does Damage to DNA and Other Macromolecules Play a Role in Aging? If So, How?. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2009, 64A, 175-178.	1.7	86
46	Mutational fingerprints of aging. Nucleic Acids Research, 2002, 30, 545-549.	6.5	83
47	Chromosome-specific accumulation of aneuploidy in the aging mouse brain. Human Molecular Genetics, 2012, 21, 5246-5253.	1.4	83
48	Somatic Mutagenesis in Mammals and Its Implications for Human Disease and Aging. Annual Review of Genetics, 2018, 52, 397-419.	3.2	83
49	Broad segmental progeroid changes in short-lived <i>Ercc1</i> ^{â^'/Î"7} mice. Pathobiology of Aging & Age Related Diseases, 2011, 1, 7219.	1.1	79
50	Single-cell analysis reveals different age-related somatic mutation profiles between stem and differentiated cells in human liver. Science Advances, 2020, 6, eaax2659.	4.7	79
51	Evaluation of a plasmid-based transgenic mouse model for detecting in vivo mutations. Mutagenesis, 1996, 11, 111-118.	1.0	78
52	Genome-wide, Single-Cell DNA Methylomics Reveals Increased Non-CpG Methylation during Human Oocyte Maturation. Stem Cell Reports, 2017, 9, 397-407.	2.3	77
53	Direct mutation analysis by high-throughput sequencing: From germline to low-abundant, somatic variants. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2012, 729, 1-15.	0.4	75
54	Genetic evidence for common pathways in human ageâ€related diseases. Aging Cell, 2015, 14, 809-817.	3.0	70

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55	Comprehensive microRNA profiling in B-cells of human centenarians by massively parallel sequencing. BMC Genomics, 2012, 13, 353.	1.2	69
56	Direct, genome-wide assessment of DNA mutations in single cells. Nucleic Acids Research, 2012, 40, 2032-2040.	6.5	68
57	Genome Dynamics in Aging Mice. Genome Research, 2002, 12, 1732-1738.	2.4	60
58	Age- and Temperature-Dependent Somatic Mutation Accumulation in Drosophila melanogaster. PLoS Genetics, 2010, 6, e1000950.	1.5	58
59	Life spanning murine gene expression profiles in relation to chronological and pathological aging in multiple organs. Aging Cell, 2013, 12, 901-909.	3.0	58
60	Comparative analysis of genome maintenance genes in naked mole rat, mouse, and human. Aging Cell, 2015, 14, 288-291.	3.0	58
61	Intra-Organ Variation in Age-Related Mutation Accumulation in the Mouse. PLoS ONE, 2007, 2, e876.	1.1	55
62	From DNA damage to mutations: All roads lead to aging. Ageing Research Reviews, 2021, 68, 101316.	5.0	55
63	5-Aza-2â€²-deoxycytidine-induced genome rearrangements are mediated by DNMT1. Oncogene, 2012, 31, 5172-5179.	2.6	54
64	Understanding the Biology of Aging: The Key To Prevention and Therapy. Journal of the American Geriatrics Society, 1995, 43, 426-434.	1.3	51
65	Chromosomal aneuploidy in the aging brain. Mechanisms of Ageing and Development, 2011, 132, 429-436.	2.2	50
66	<scp>DNA</scp> damage in normally and prematurely aged mice. Aging Cell, 2013, 12, 467-477.	3.0	50
67	Kinetics of ultraviolet induced DNA excision repair in rat and human fibroblasts. Mutation Research - DNA Repair Reports, 1984, 132, 129-138.	1.9	47
68	Single-cell analysis of somatic mutations in human bronchial epithelial cells in relation to aging and smoking. Nature Genetics, 2022, 54, 492-498.	9.4	47
69	The dark side of circulating nucleic acids. Aging Cell, 2016, 15, 398-399.	3.0	45
70	Genome dynamics and transcriptional deregulation in aging. Neuroscience, 2007, 145, 1341-1347.	1.1	42
71	Mechanisms and consequences of aneuploidy and chromosome instability in the aging brain. Mechanisms of Ageing and Development, 2017, 161, 19-36.	2.2	42
72	Myc-Dependent Genome Instability and Lifespan in Drosophila. PLoS ONE, 2013, 8, e74641.	1.1	40

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73	Age-dependent accumulation of alkali-labile sites in DNA of post-mitotic but not in that of mitotic rat liver cells. Mechanisms of Ageing and Development, 1988, 45, 41-49.	2.2	38
74	Age-related mutation accumulation at a lacZ reporter locus in normal and tumor tissues of Trp53-deficient mice. Mutation Research - Genetic Toxicology and Environmental Mutagenesis, 2002, 514, 153-163.	0.9	37
75	Genome instability: a conserved mechanism of ageing?. Essays in Biochemistry, 2017, 61, 305-315.	2.1	37
76	Turning anti-ageing genes against cancer. Nature Reviews Molecular Cell Biology, 2008, 9, 903-910.	16.1	36
77	Single-cell, locus-specific bisulfite sequencing (SLBS) for direct detection of epimutations in DNA methylation patterns. Nucleic Acids Research, 2015, 43, e93-e93.	6.5	36
78	High-throughput sequencing in mutation detection: A new generation of genotoxicity tests?. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 776, 136-143.	0.4	34
79	Aging and the Inevitable Limit to Human Life Span. Gerontology, 2017, 63, 432-434.	1.4	33
80	Spontaneous DNA breaks in the rat brain during development and aging. Mutation Research - DNAging, 1990, 237, 9-15.	3.3	32
81	Genetics of extreme human longevity to guide drug discovery for healthy ageing. Nature Metabolism, 2020, 2, 663-672.	5.1	32
82	ARDD 2020: from aging mechanisms to interventions. Aging, 2020, 12, 24484-24503.	1.4	32
83	Measuring Genome Instability in Aging â€“ A Mini-Review. Gerontology, 2012, 58, 129-138.	1.4	31
84	The Essence of Aging. Gerontology, 2016, 62, 381-385.	1.4	31
85	Maintenance of genome sequence integrity in long- and short-lived rodent species. Science Advances, 2021, 7, eabj3284.	4.7	29
86	Mutation and catastrophe in the aging genome. Experimental Gerontology, 2017, 94, 34-40.	1.2	28
87	Single-cell transcriptogenomics reveals transcriptional exclusion of ENU-mutated alleles. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 772, 55-62.	0.4	27
88	Transcripts of aging. Trends in Genetics, 2004, 20, 221-224.	2.9	26
89	Transgenic assays for mutations and cancer: current status and future perspectives. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 1998, 400, 337-354.	0.4	25
90	Development and validation of a targeted next generation DNA sequencing panel outperforming whole exome sequencing for the identification of clinically relevant genetic variants. Oncotarget, 2017, 8, 102033-102045.	0.8	25

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91	Detection and Analysis of Somatic Mutations at a lacZ Reporter Locus in Higher Organisms. Methods in Molecular Biology, 2007, 371, 267-287.	0.4	23
92	A model system for analyzing somatic mutations in Drosophila melanogaster. Nature Methods, 2007, 4, 401-403.	9.0	22
93	Genome instability and aging: Cause or effect?. Translational Medicine of Aging, 2017, 1, 5-11.	0.6	22
94	Rare genetic coding variants associated with human longevity and protection against age-related diseases. Nature Aging, 2021, 1, 783-794.	5.3	22
95	Mutation Frequencies and Spectra in DNA Polymerase Î·â€"Deficient Mice. Cancer Research, 2008, 68, 2081-2084.	0.4	21
96	Deletion of Individual Ku Subunits in Mice Causes an NHEJ-Independent Phenotype Potentially by Altering Apurinic/Apyrimidinic Site Repair. PLoS ONE, 2014, 9, e86358.	1.1	21
97	Innovating Aging: Promises and Pitfalls on the Road to Life Extension. Gerontology, 2014, 60, 373-380.	1.4	21
98	SomaMutDB: a database of somatic mutations in normal human tissues. Nucleic Acids Research, 2022, 50, D1100-D1108.	6.5	21
99	Aging genomes: A necessary evil in the logic of life. BioEssays, 2014, 36, 282-292.	1.2	20
100	Development of a Method to Implement Whole-Genome Bisulfite Sequencing of cfDNA from Cancer Patients and a Mouse Tumor Model. Frontiers in Genetics, 2018, 9, 6.	1.1	20
101	Aging on a different scale â€" chronological versus pathology-related aging. Aging, 2013, 5, 782-788.	1.4	20
102	Aging: A Sirtuin Shake-Up?. Cell, 2008, 135, 797-798.	13.5	18
103	A review of the biomedical innovations for healthy longevity. Aging, 2017, 9, 7-25.	1.4	18
104	A direct comparison of interphase FISH versus low-coverage single cell sequencing to detect aneuploidy reveals respective strengths and weaknesses. Scientific Reports, 2019, 9, 10508.	1.6	18
105	FOXO3a acts to suppress DNA doubleâ€strand breakâ€induced mutations. Aging Cell, 2020, 19, e13184.	3.0	18
106	Mutation frequency and type during ageing in mouse seminiferous tubules. Mechanisms of Ageing and Development, 2001, 122, 1321-1331.	2.2	17
107	Genome-wide quantitative analysis of DNA methylation from bisulfite sequencing data. Bioinformatics, 2014, 30, 1933-1934.	1.8	17
108	Quantitative detection of low-abundance somatic structural variants in normal cells by high-throughput sequencing. Nature Methods, 2016, 13, 584-586.	9.0	17

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109	Whole chromosome aneuploidy in the brain of Bub1bH/Hand Ercc1â[^]'/Î"7mice. Human Molecular Genetics, 2016, 25, 755-765.	1.4	17
110	Aging and p53: getting it straight A commentary on a recent paper by Gentry and Venkatachalam. Aging Cell, 2005, 4, 331-333.	3.0	16
111	Whole genome sequencing of glioblastoma multiforme identifies multiple structural variations involved in EGFR activation. Mutagenesis, 2014, 29, 341-350.	1.0	16
112	Cell Replacement to Reverse Brain Aging: Challenges, Pitfalls, and Opportunities. Trends in Neurosciences, 2018, 41, 267-279.	4.2	16
113	Development of a Targeted Multi-Disorder High-Throughput Sequencing Assay for the Effective Identification of Disease-Causing Variants. PLoS ONE, 2015, 10, e0133742.	1.1	15
114	Four-Color FISH for the Detection of Low-Level Aneuploidy in Interphase Cells. Methods in Molecular Biology, 2014, 1136, 291-305.	0.4	15
115	UV-induced unscheduled DNA synthesis in fibroblasts of aging inbred rats. Mutation Research - DNA Repair Reports, 1985, 146, 197-204.	1.9	14
116	Bleomycin-induced genome structural variations in normal, non-tumor cells. Scientific Reports, 2018, 8, 16523.	1.6	14
117	Two-dimensional DNA typing. Molecular Biotechnology, 1995, 4, 275-295.	1.3	13
118	Effect of Ku80 Deficiency on Mutation Frequencies and Spectra at a LacZ Reporter Locus in Mouse Tissues and Cells. PLoS ONE, 2008, 3, e3458.	1.1	13
119	The Progeroid Phenotype of Ku80 Deficiency Is Dominant over DNA-PKCS Deficiency. PLoS ONE, 2014, 9, e93568.	1.1	13
120	Inducible aging in Hydra oligactis implicates sexual reproduction, loss of stem cells, and genome maintenance as major pathways. GeroScience, 2020, 42, 1119-1132.	2.1	13
121	Improved transposon-based library preparation for the Ion Torrent platform. BioTechniques, 2015, 58, 200-2.	0.8	12
122	Age-related induction and disappearance of carcinogen-DNA-adducts in livers of rats exposed to low levels of 2-acetylaminofluorene. Chemico-Biological Interactions, 1989, 69, 373-384.	1.7	11
123	Ageâ€related telomere attrition causes aberrant gene expression in subâ€telomeric regions. Aging Cell, 2021, 20, e13357.	3.0	11
124	Single-molecule, quantitative detection of low-abundance somatic mutations by high-throughput sequencing. Science Advances, 2022, 8, eabm3259.	4.7	11
125	Sensitivity of primary fibroblasts in culture to atmospheric oxygen does not correlate with species lifespan. Aging, 2016, 8, 841-847.	1.4	10
126	Age is in the nucleus. Nature Metabolism, 2019, 1, 931-932.	5.1	9

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127	Deficiency of the DNA repair protein nibrin increases the basal but not the radiation induced mutation frequency in vivo. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2014, 769, 11-16.	0.4	8
128	Mutation Accumulation In Vivo and the Importance of Genome Stability in Aging and Cancer. Results and Problems in Cell Differentiation, 2000, 29, 165-180.	0.2	8
129	Rapid, inexpensive scanning for all possible BRCA1 and BRCA2 gene sequence variants in a single assay: implications for genetic testing. Journal of Medical Genetics, 2003, 40, 33e-33.	1.5	7
130	Global, integrated analysis of methylomes and transcriptomes from laser capture microdissected bronchial and alveolar cells in human lung. Epigenetics, 2018, 13, 264-274.	1.3	7
131	SCCNV: A Software Tool for Identifying Copy Number Variation From Single-Cell Whole-Genome Sequencing. Frontiers in Genetics, 2020, 11, 505441.	1.1	7
132	Genomic expansion of Aldh1a1 protects beavers against high metabolic aldehydes from lipid oxidation. Cell Reports, 2021, 37, 109965.	2.9	7
133	Single-cell analysis of somatic mutation burden in mammary epithelial cells of pathogenic BRCA1/2 mutation carriers. Journal of Clinical Investigation, 2022, 132, .	3.9	7
134	A high-fidelity method for genomic sequencing of single somatic cells reveals a very high mutational burden. Experimental Biology and Medicine, 2017, 242, 1318-1324.	1.1	6
135	Editorial overview: Molecular and genetic bases of disease: The double life of DNA. Current Opinion in Genetics and Development, 2014, 26, v-vii.	1.5	5
136	New Insights into Bioactive Compounds of Traditional Chinese Medicines for Insulin Resistance Based on Signaling Pathways. Chemistry and Biodiversity, 2019, 16, e1900176.	1.0	5
137	Einstein-Nathan Shock Center: translating the hallmarks of aging to extend human health span. GeroScience, 2021, 43, 2167-2182.	2.1	5
138	Detecting Individual Genetic Variation. Nature Biotechnology, 1995, 13, 137-139.	9.4	4
139	A dual-activation, adenoviral-based system for the controlled induction of DNA double-strand breaks by the restriction endonuclease SacI. BioTechniques, 2009, 47, 847-854.	0.8	4
140	Dong et al. reply. Nature, 2017, 546, E12-E12.	13.7	4
141	Dong et al. reply. Nature, 2017, 546, E14-E15.	13.7	4
142	A workflow for simultaneous DNA copy number and methylome analysis of inner cell mass and trophectoderm cells from human blastocysts. Fertility and Sterility, 2021, 115, 1533-1540.	0.5	4
143	â€œBest-Guessâ€•MRAD Provides Robust Evidence for a Limit to Human Lifespan: Reply to de Grey (Rejuvenation Res. 2017;20:261â€“262). Rejuvenation Research, 2017, 20, 437-440.	0.9	4
144	High Preservation of CpG Cytosine Methylation Patterns at Imprinted Gene Loci in Liver and Brain of Aged Mice. PLoS ONE, 2013, 8, e73496.	1.1	4

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145	Meeting Report: Aging Research and Drug Discovery. Aging, 2022, 14, 530-543.	1.4	4
146	Dong et al. reply. Nature, 2017, 546, E7-E7.	13.7	3
147	Dong et al. reply. Nature, 2017, 546, E9-E10.	13.7	3
148	A Compendium of Age-Related PheWAS and GWAS Traits for Human Genetic Association Studies, Their Networks and Genetic Correlations. Frontiers in Genetics, 2021, 12, 680560.	1.1	3
149	SNP'ing for longevity. Aging, 2009, 1, 442-443.	1.4	3
150	Loss of gene coordination as a stochastic cause of ageing. Nature Metabolism, 2020, 2, 1188-1189.	5.1	2
151	Dong et al. reply. Nature, 2017, 546, E21-E21.	13.7	1
152	Intratissue DNA Methylation Heterogeneity in Aging. , 2018, , 201-209.		1
153	Ageing: Biomarkers get physical. Nature Biomedical Engineering, 2017, 1, .	11.6	0
154	Somatic Mutations at Single Base Resolution in Single Bronchial Progenitor Cells Collected from Human Lung. , 2021, , .		0
155	Bronchial Field Progenitor Basal Cells Show Methylome-Wide Characteristics Reflective of Lung Cancer Case-Control, Age, and Smoking Status of the Donor. , 2021, , .		0
156	Single-Cell Whole-Genome Sequencing Reveals B Lymphocyte Mutational Landscapes Across the Human Lifespan. SSRN Electronic Journal, 0, , .	0.4	0
157	Genome Maintenance in Aging and Lung Carcinogenesis. , 2022, , .		0
158	Bronchial Field Progenitor Basal Cells Show Methylome-Wide Characteristics Reflective of Lung Cancer Case-Control, Age, and Smoking Status. , 2022, , .		0