Jan Vijg

List of Publications by Year in descending order

158 papers	13,945 citations	25034 57 h-index	24258 110 g-index
164 all docs	164 docs citations	164 times ranked	16074 citing authors

#	Article	IF	Citations
1	SomaMutDB: a database of somatic mutations in normal human tissues. Nucleic Acids Research, 2022, 50, D1100-D1108.	14.5	21
2	Single-cell analysis of somatic mutation burden in mammary epithelial cells of pathogenic BRCA1/2 mutation carriers. Journal of Clinical Investigation, 2022, 132, .	8.2	7
3	Meeting Report: Aging Research and Drug Discovery. Aging, 2022, 14, 530-543.	3.1	4
4	Single-cell analysis of somatic mutations in human bronchial epithelial cells in relation to aging and smoking. Nature Genetics, 2022, 54, 492-498.	21.4	47
5	Single-molecule, quantitative detection of low-abundance somatic mutations by high-throughput sequencing. Science Advances, 2022, 8, eabm3259.	10.3	11
6	Genome Maintenance in Aging and Lung Carcinogenesis. , 2022, , .		0
7	Bronchial Field Progenitor Basal Cells Show Methylome-Wide Characteristics Reflective of Lung Cancer Case-Control, Age, and Smoking Status. , 2022, , .		0
8	The central role of DNA damage in the ageing process. Nature, 2021, 592, 695-703.	27.8	340
9	Somatic Mutations at Single Base Resolution in Single Bronchial Progenitor Cells Collected from Human Lung. , 2021, , .		0
10	Ageâ€related telomere attrition causes aberrant gene expression in subâ€telomeric regions. Aging Cell, 2021, 20, e13357.	6.7	11
11	Bronchial Field Progenitor Basal Cells Show Methylome-Wide Characteristics Reflective of Lung Cancer Case-Control, Age, and Smoking Status of the Donor. , 2021, , .		0
12	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.	1.0	4
13	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.	2.3	3
14	From DNA damage to mutations: All roads lead to aging. Ageing Research Reviews, 2021, 68, 101316.	10.9	55
15	Einstein-Nathan Shock Center: translating the hallmarks of aging to extend human health span. GeroScience, 2021, 43, 2167-2182.	4.6	5
16	Rare genetic coding variants associated with human longevity and protection against age-related diseases. Nature Aging, 2021, 1, 783-794.	11.6	22
17	Maintenance of genome sequence integrity in long- and short-lived rodent species. Science Advances, 2021, 7, eabj3284.	10.3	29
18	Genomic expansion of Aldh1a1 protects beavers against high metabolic aldehydes from lipid oxidation. Cell Reports, 2021, 37, 109965.	6.4	7

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19	SCCNV: A Software Tool for Identifying Copy Number Variation From Single-Cell Whole-Genome Sequencing. Frontiers in Genetics, 2020, 11, 505441.	2.3	7
20	FOXO3a acts to suppress DNA doubleâ€strand breakâ€induced mutations. Aging Cell, 2020, 19, e13184.	6.7	18
21	Genetics of extreme human longevity to guide drug discovery for healthy ageing. Nature Metabolism, 2020, 2, 663-672.	11.9	32
22	Loss of gene coordination as a stochastic cause of ageing. Nature Metabolism, 2020, 2, 1188-1189.	11.9	2
23	Inducible aging in Hydra oligactis implicates sexual reproduction, loss of stem cells, and genome maintenance as major pathways. GeroScience, 2020, 42, 1119-1132.	4.6	13
24	Pathogenic Mechanisms of Somatic Mutation and Genome Mosaicism in Aging. Cell, 2020, 182, 12-23.	28.9	128
25	Single-cell analysis reveals different age-related somatic mutation profiles between stem and differentiated cells in human liver. Science Advances, 2020, 6, eaax2659.	10.3	79
26	ARDD 2020: from aging mechanisms to interventions. Aging, 2020, 12, 24484-24503.	3.1	32
27	New Insights into Bioactive Compounds of Traditional Chinese Medicines for Insulin Resistance Based on Signaling Pathways. Chemistry and Biodiversity, 2019, 16, e1900176.	2.1	5
28	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.	3.3	18
29	Age is in the nucleus. Nature Metabolism, 2019, 1, 931-932.	11.9	9
30	SIRT6 Is Responsible for More Efficient DNA Double-Strand Break Repair in Long-Lived Species. Cell, 2019, 177, 622-638.e22.	28.9	225
31	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.	7.1	174
32	Global, integrated analysis of methylomes and transcriptomes from laser capture microdissected bronchial and alveolar cells in human lung. Epigenetics, 2018, 13, 264-274.	2.7	7
33	Mechanisms of cancer resistance in long-lived mammals. Nature Reviews Cancer, 2018, 18, 433-441.	28.4	195
34	Cell Replacement to Reverse Brain Aging: Challenges, Pitfalls, and Opportunities. Trends in Neurosciences, 2018, 41, 267-279.	8.6	16
35	Bleomycin-induced genome structural variations in normal, non-tumor cells. Scientific Reports, 2018, 8, 16523.	3.3	14
36	Somatic Mutagenesis in Mammals and Its Implications for Human Disease and Aging. Annual Review of Genetics, 2018, 52, 397-419.	7.6	83

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37	Intratissue DNA Methylation Heterogeneity in Aging. , 2018, , 201-209.		1
38	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.	2.3	20
39	Nuclear Genomic Instability and Aging. Annual Review of Biochemistry, 2018, 87, 295-322.	11.1	178
40	Mechanisms and consequences of aneuploidy and chromosome instability in the aging brain. Mechanisms of Ageing and Development, 2017, 161, 19-36.	4.6	42
41	Mutation and catastrophe in the aging genome. Experimental Gerontology, 2017, 94, 34-40.	2.8	28
42	Aging and the Inevitable Limit to Human Life Span. Gerontology, 2017, 63, 432-434.	2.8	33
43	Differences between germline and somatic mutation rates in humans and mice. Nature Communications, 2017, 8, 15183.	12.8	309
44	Accurate identification of single-nucleotide variants in whole-genome-amplified single cells. Nature Methods, 2017, 14, 491-493.	19.0	191
45	Genome instability and aging: Cause or effect?. Translational Medicine of Aging, 2017, 1, 5-11.	1.3	22
46	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.	2.4	6
47	Analysis of individual cells identifies cellâ€toâ€cell variability following induction of cellular senescence. Aging Cell, 2017, 16, 1043-1050.	6.7	182
48	Ageing: Biomarkers get physical. Nature Biomedical Engineering, 2017, 1, .	22.5	0
49	Genome-wide, Single-Cell DNA Methylomics Reveals Increased Non-CpG Methylation during Human Oocyte Maturation. Stem Cell Reports, 2017, 9, 397-407.	4.8	77
50	Dong et al. reply. Nature, 2017, 546, E7-E7.	27.8	3
51	Dong et al. reply. Nature, 2017, 546, E9-E10.	27.8	3
52	Dong et al. reply. Nature, 2017, 546, E12-E12.	27.8	4
53	Dong et al. reply. Nature, 2017, 546, E14-E15.	27.8	4
54	Dong et al. reply. Nature, 2017, 546, E21-E21.	27.8	1

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55	Genome instability: a conserved mechanism of ageing?. Essays in Biochemistry, 2017, 61, 305-315.	4.7	37
56	A review of the biomedical innovations for healthy longevity. Aging, 2017, 9, 7-25.	3.1	18
57	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.	1.8	25
58	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.	1.8	4
59	Deep biomarkers of human aging: Application of deep neural networks to biomarker development. Aging, 2016, 8, 1021-1033.	3.1	266
60	The Essence of Aging. Gerontology, 2016, 62, 381-385.	2.8	31
61	Evidence for a limit to human lifespan. Nature, 2016, 538, 257-259.	27.8	341
62	The dark side of circulating nucleic acids. Aging Cell, 2016, 15, 398-399.	6.7	45
63	Do DNA Double-Strand Breaks Drive Aging?. Molecular Cell, 2016, 63, 729-738.	9.7	172
64	Restricted diet delays accelerated ageing and genomic stress in DNA-repair-deficient mice. Nature, 2016, 537, 427-431.	27.8	228
65	In silico Pathway Activation Network Decomposition Analysis (iPANDA) as a method for biomarker development. Nature Communications, 2016, 7, 13427.	12.8	126
66	Single-cell genome-wide bisulfite sequencing uncovers extensive heterogeneity in the mouse liver methylome. Genome Biology, 2016, 17, 150.	8.8	104
67	Whole Chromosome Instability induces senescence and promotes SASP. Scientific Reports, 2016, 6, 35218.	3.3	117
68	Quantitative detection of low-abundance somatic structural variants in normal cells by high-throughput sequencing. Nature Methods, 2016, 13, 584-586.	19.0	17
69	Whole chromosome aneuploidy in the brain of Bub1bH/Hand Ercc1â^'/Î”7mice. Human Molecular Genetics, 2016, 25, 755-765.	2.9	17
70	Sensitivity of primary fibroblasts in culture to atmospheric oxygen does not correlate with species lifespan. Aging, 2016, 8, 841-847.	3.1	10
71	Interventions to Slow Aging in Humans: Are We Ready?. Aging Cell, 2015, 14, 497-510.	6.7	481
72	Genetic evidence for common pathways in human ageâ€related diseases. Aging Cell, 2015, 14, 809-817.	6.7	70

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73	Improved transposon-based library preparation for the Ion Torrent platform. BioTechniques, 2015, 58, 200-2.	1.8	12
74	Age-related somatic mutations in the cancer genome. Oncotarget, 2015, 6, 24627-24635.	1.8	104
75	DNA repair in species with extreme lifespan differences. Aging, 2015, 7, 1171-1182.	3.1	132
76	Development of a Targeted Multi-Disorder High-Throughput Sequencing Assay for the Effective Identification of Disease-Causing Variants. PLoS ONE, 2015, 10, e0133742.	2.5	15
77	Single-cell transcriptogenomics reveals transcriptional exclusion of ENU-mutated alleles. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 772, 55-62.	1.0	27
78	Comprehensive transcriptional landscape of aging mouse liver. BMC Genomics, 2015, 16, 899.	2.8	98
79	Comparative analysis of genome maintenance genes in naked mole rat, mouse, and human. Aging Cell, 2015, 14, 288-291.	6.7	58
80	Single-cell, locus-specific bisulfite sequencing (SLBS) for direct detection of epimutations in DNA methylation patterns. Nucleic Acids Research, 2015, 43, e93-e93.	14.5	36
81	INK4 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.	7.1	92
82	High-throughput sequencing in mutation detection: A new generation of genotoxicity tests?. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2015, 776, 136-143.	1.0	34
83	Controlled induction of DNA double-strand breaks in the mouse liver induces features of tissue ageing. Nature Communications, 2015, 6, 6790.	12.8	90
84	Deletion of Individual Ku Subunits in Mice Causes an NHEJ-Independent Phenotype Potentially by Altering Apurinic/Apyrimidinic Site Repair. PLoS ONE, 2014, 9, e86358.	2.5	21
85	The Progeroid Phenotype of Ku80 Deficiency Is Dominant over DNA-PKCS Deficiency. PLoS ONE, 2014, 9, e93568.	2.5	13
86	An Essential Role for Senescent Cells in Optimal Wound Healing through Secretion of PDGF-AA. Developmental Cell, 2014, 31, 722-733.	7.0	1,376
87	Aging genomes: A necessary evil in the logic of life. BioEssays, 2014, 36, 282-292.	2.5	20
88	Genome-wide quantitative analysis of DNA methylation from bisulfite sequencing data. Bioinformatics, 2014, 30, 1933-1934.	4.1	17
89	Editorial overview: Molecular and genetic bases of disease: The double life of DNA. Current Opinion in Genetics and Development, 2014, 26, v-vii.	3.3	5
90	Somatic mutations, genome mosaicism, cancer and aging. Current Opinion in Genetics and Development, 2014, 26, 141-149.	3.3	111

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91	Whole genome sequencing of glioblastoma multiforme identifies multiple structural variations involved in EGFR activation. Mutagenesis, 2014, 29, 341-350.	2.6	16
92	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.	1.0	8
93	Comparative genetics of longevity and cancer: insights from long-lived rodents. Nature Reviews Genetics, 2014, 15, 531-540.	16.3	169
94	Innovating Aging: Promises and Pitfalls on the Road to Life Extension. Gerontology, 2014, 60, 373-380.	2.8	21
95	Four-Color FISH for the Detection of Low-Level Aneuploidy in Interphase Cells. Methods in Molecular Biology, 2014, 1136, 291-305.	0.9	15
96	<scp>DNA</scp> damage in normally and prematurely aged mice. Aging Cell, 2013, 12, 467-477.	6.7	50
97	Genome Instability and Aging. Annual Review of Physiology, 2013, 75, 645-668.	13.1	314
98	Life spanning murine gene expression profiles in relation to chronological and pathological aging in multiple organs. Aging Cell, 2013, 12, 901-909.	6.7	58
99	High Preservation of CpG Cytosine Methylation Patterns at Imprinted Gene Loci in Liver and Brain of Aged Mice. PLoS ONE, 2013, 8, e73496.	2.5	4
100	Myc-Dependent Genome Instability and Lifespan in Drosophila. PLoS ONE, 2013, 8, e74641.	2.5	40
101	Aging on a different scale â€“ chronological versus pathology-related aging. Aging, 2013, 5, 782-788.	3.1	20
102	Measuring Genome Instability in Aging â€“ A Mini-Review. Gerontology, 2012, 58, 129-138.	2.8	31
103	Chromosome-specific accumulation of aneuploidy in the aging mouse brain. Human Molecular Genetics, 2012, 21, 5246-5253.	2.9	83
104	5-Aza-2â€²-deoxycytidine-induced genome rearrangements are mediated by DNMT1. Oncogene, 2012, 31, 5172-5179.	5.9	54
105	Direct, genome-wide assessment of DNA mutations in single cells. Nucleic Acids Research, 2012, 40, 2032-2040.	14.5	68
106	Comprehensive microRNA profiling in B-cells of human centenarians by massively parallel sequencing. BMC Genomics, 2012, 13, 353.	2.8	69
107	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.	1.0	75
108	Broad segmental progeroid changes in short-lived Ercc1 ^{â^'/Î”7} mice. Pathobiology of Aging & Age Related Diseases, 2011, 1, 7219.	1.1	79

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109	Chromosomal aneuploidy in the aging brain. Mechanisms of Ageing and Development, 2011, 132, 429-436.	4.6	50
110	Epigenetic factors in aging and longevity. Pflugers Archiv European Journal of Physiology, 2010, 459, 247-258.	2.8	278
111	Age- and Temperature-Dependent Somatic Mutation Accumulation in Drosophila melanogaster. PLoS Genetics, 2010, 6, e1000950.	3.5	58
112	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.	1.8	4
113	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.	3.6	86
114	Mitochondrial DNA mutations and aging: devils in the details?. Trends in Genetics, 2009, 25, 91-98.	6.7	99
115	Genome instability, cancer and aging. Biochimica Et Biophysica Acta - General Subjects, 2009, 1790, 963-969.	2.4	102
116	SNP'ing for longevity. Aging, 2009, 1, 442-443.	3.1	3
117	DNA damage and ageing: new-age ideas for an age-old problem. Nature Cell Biology, 2008, 10, 1241-1247.	10.3	325
118	Turning anti-ageing genes against cancer. Nature Reviews Molecular Cell Biology, 2008, 9, 903-910.	37.0	36
119	Aging: A Sirtuin Shake-Up?. Cell, 2008, 135, 797-798.	28.9	18
120	Mutation Frequencies and Spectra in DNA Polymerase Î·â€“Deficient Mice. Cancer Research, 2008, 68, 2081-2084.	0.9	21
121	Effect of Ku80 Deficiency on Mutation Frequencies and Spectra at a LacZ Reporter Locus in Mouse Tissues and Cells. PLoS ONE, 2008, 3, e3458.	2.5	13
122	Genome dynamics and transcriptional deregulation in aging. Neuroscience, 2007, 145, 1341-1347.	2.3	42
123	Intra-Organ Variation in Age-Related Mutation Accumulation in the Mouse. PLoS ONE, 2007, 2, e876.	2.5	55
124	A model system for analyzing somatic mutations in Drosophila melanogaster. Nature Methods, 2007, 4, 401-403.	19.0	22
125	Detection and Analysis of Somatic Mutations at a lacZ Reporter Locus in Higher Organisms. Methods in Molecular Biology, 2007, 371, 267-287.	0.9	23
126	Increased cell-to-cell variation in gene expression in ageing mouse heart. Nature, 2006, 441, 1011-1014.	27.8	537

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127	A new progeroid syndrome reveals that genotoxic stress suppresses the somatotroph axis. Nature, 2006, 444, 1038-1043.	27.8	601
128	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.	1.0	100
129	Aging and p53: getting it straight A commentary on a recent paper by Gentry and Venkatachalam. Aging Cell, 2005, 4, 331-333.	6.7	16
130	Genetics of Longevity and Aging. Annual Review of Medicine, 2005, 56, 193-212.	12.2	143
131	Transcripts of aging. Trends in Genetics, 2004, 20, 221-224.	6.7	26
132	Oxygen accelerates the accumulation of mutations during the senescence and immortalization of murine cells in culture. Aging Cell, 2003, 2, 287-294.	6.7	176
133	Aging and Genome Maintenance: Lessons from the Mouse?. Science, 2003, 299, 1355-1359.	12.6	538
134	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.	3.2	7
135	Mutational fingerprints of aging. Nucleic Acids Research, 2002, 30, 545-549.	14.5	83
136	Genome Dynamics in Aging Mice. Genome Research, 2002, 12, 1732-1738.	5.5	60
137	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.	1.7	37
138	Large genome rearrangements as a primary cause of aging. Mechanisms of Ageing and Development, 2002, 123, 907-915.	4.6	134
139	Mutation frequency and type during ageing in mouse seminiferous tubules. Mechanisms of Ageing and Development, 2001, 122, 1321-1331.	4.6	17
140	Somatic mutations and aging: a re-evaluation. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 2000, 447, 117-135.	1.0	225
141	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.	7.1	231
142	Mutation Accumulation In Vivo and the Importance of Genome Stability in Aging and Cancer. Results and Problems in Cell Differentiation, 2000, 29, 165-180.	0.7	8
143	Transgenic assays for mutations and cancer: current status and future perspectives. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 1998, 400, 337-354.	1.0	25
144	Siblings of centenarians live longer. Lancet, The, 1998, 351, 1560.	13.7	172

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145	Genetic testing: The problems and the promise. Nature Biotechnology, 1997, 15, 422-426.	17.5	94
146	Rapid accumulation of genome rearrangements in liver but not in brain of old mice. Nature Genetics, 1997, 17, 431-434.	21.4	245
147	Evaluation of a plasmid-based transgenic mouse model for detecting in vivo mutations. Mutagenesis, 1996, 11, 111-118.	2.6	78
148	Understanding the Biology of Aging: The Key To Prevention and Therapy. Journal of the American Geriatrics Society, 1995, 43, 426-434.	2.6	51
149	Detecting Individual Genetic Variation. Nature Biotechnology, 1995, 13, 137-139.	17.5	4
150	Plasmid-based transgenic mouse model for studying in vivomutations. Nature, 1995, 377, 657-659.	27.8	143
151	Two-dimensional DNA typing. Molecular Biotechnology, 1995, 4, 275-295.	2.4	13
152	Spontaneous DNA breaks in the rat brain during development and aging. Mutation Research - DNAging, 1990, 237, 9-15.	3.2	32
153	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.	4.0	11
154	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.	7.1	466
155	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.	4.6	38
156	UV-induced unscheduled DNA synthesis in fibroblasts of aging inbred rats. Mutation Research - DNA Repair Reports, 1985, 146, 197-204.	1.8	14
157	Kinetics of ultraviolet induced DNA excision repair in rat and human fibroblasts. Mutation Research - DNA Repair Reports, 1984, 132, 129-138.	1.8	47
158	Single-Cell Whole-Genome Sequencing Reveals B Lymphocyte Mutational Landscapes Across the Human Lifespan. SSRN Electronic Journal, 0, , .	0.4	0