

Dmitry A Gordenin

List of Publications by Year in descending order

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Version: 2024-02-01

94
papers

22,393
citations

36203

51
h-index

49773

87
g-index

106
all docs

106
docs citations

106
times ranked

30273
citing authors

#	ARTICLE	IF	CITATIONS
1	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , 2013, 499, 214-218.	13.7	4,761
2	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014, 507, 315-322.	13.7	2,496
3	The repertoire of mutational signatures in human cancer. <i>Nature</i> , 2020, 578, 94-101.	13.7	2,104
4	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	13.5	1,742
5	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017, 543, 378-384.	13.7	1,158
6	An APOBEC cytidine deaminase mutagenesis pattern is widespread in human cancers. <i>Nature Genetics</i> , 2013, 45, 970-976.	9.4	1,023
7	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	7.7	665
8	Cadmium is a mutagen that acts by inhibiting mismatch repair. <i>Nature Genetics</i> , 2003, 34, 326-329.	9.4	440
9	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020, 52, 331-341.	9.4	431
10	Division of Labor at the Eukaryotic Replication Fork. <i>Molecular Cell</i> , 2008, 30, 137-144.	4.5	412
11	Clustered Mutations in Yeast and in Human Cancers Can Arise from Damaged Long Single-Strand DNA Regions. <i>Molecular Cell</i> , 2012, 46, 424-435.	4.5	379
12	The Mre11 Complex Is Required for Repair of Hairpin-Capped Double-Strand Breaks and Prevention of Chromosome Rearrangements. <i>Cell</i> , 2002, 108, 183-193.	13.5	359
13	Hypermutation in human cancer genomes: footprints and mechanisms. <i>Nature Reviews Cancer</i> , 2014, 14, 786-800.	12.8	354
14	An APOBEC3A hypermutation signature is distinguishable from the signature of background mutagenesis by APOBEC3B in human cancers. <i>Nature Genetics</i> , 2015, 47, 1067-1072.	9.4	354
15	Hypermutable Homonucleotide Runs in Mismatch Repair and DNA Polymerase Proofreading Yeast Mutants. <i>Molecular and Cellular Biology</i> , 1997, 17, 2859-2865.	1.1	309
16	Genomic Subtypes of Non-invasive Bladder Cancer with Distinct Metabolic Profile and Female Gender Bias in KDM6A Mutation Frequency. <i>Cancer Cell</i> , 2017, 32, 701-715.e7.	7.7	224
17	Okazaki Fragment Maturation in Yeast. <i>Journal of Biological Chemistry</i> , 2003, 278, 1618-1625.	1.6	208
18	Repeat expansion "all in flap". <i>Nature Genetics</i> , 1997, 16, 116-118.	9.4	201

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19	The 3'→5' Exonucleases of DNA Polymerases δ and ϵ and the 5'→3' Exonuclease Exo1 Have Major Roles in Postreplication Mutation Avoidance in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 1999, 19, 2000-2007.	1.1	196
20	RNA-templated DNA repair. <i>Nature</i> , 2007, 447, 338-341.	13.7	194
21	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. <i>Cancer Cell</i> , 2018, 34, 996-1011.e8.	7.7	190
22	Destabilization of Yeast Micro- and Minisatellite DNA Sequences by Mutations Affecting a Nuclease Involved in Okazaki Fragment Processing (<i>rad27</i>) and DNA Polymerase δ (<i>pol3-t</i>). <i>Molecular and Cellular Biology</i> , 1998, 18, 2779-2788.	1.1	189
23	Chromosomal site-specific double-strand breaks are efficiently targeted for repair by oligonucleotides in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 14994-14999.	3.3	176
24	The 3'→5' exonuclease of DNA polymerase δ can substitute for the 5' flap endonuclease Rad27/Fen1 in processing Okazaki fragments and preventing genome instability. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 5122-5127.	3.3	147
25	Break-Induced Replication Is a Source of Mutation Clusters Underlying Kataegis. <i>Cell Reports</i> , 2014, 7, 1640-1648.	2.9	143
26	Heterogeneous polymerase fidelity and mismatch repair bias genome variation and composition. <i>Genome Research</i> , 2014, 24, 1751-1764.	2.4	141
27	Inverted Alu repeats unstable in yeast are excluded from the human genome. <i>EMBO Journal</i> , 2000, 19, 3822-3830.	3.5	133
28	Okazaki Fragment Maturation in Yeast. <i>Journal of Biological Chemistry</i> , 2003, 278, 1626-1633.	1.6	130
29	Hypermutable of Damaged Single-Strand DNA Formed at Double-Strand Breaks and Uncapped Telomeres in Yeast <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2008, 4, e1000264.	1.5	130
30	Factors Affecting Inverted Repeat Stimulation of Recombination and Deletion in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 1998, 148, 1507-1524.	1.2	123
31	Clusters of Multiple Mutations: Incidence and Molecular Mechanisms. <i>Annual Review of Genetics</i> , 2015, 49, 243-267.	3.2	116
32	Biased Distribution of Inverted and Direct Alus in the Human Genome: Implications for Insertion, Exclusion, and Genome Stability. <i>Genome Research</i> , 2001, 11, 12-27.	2.4	114
33	Flexibility of Eukaryotic Okazaki Fragment Maturation through Regulated Strand Displacement Synthesis. <i>Journal of Biological Chemistry</i> , 2008, 283, 34129-34140.	1.6	114
34	APOBEC3-dependent kataegis and TREX1-driven chromothripsis during telomere crisis. <i>Nature Genetics</i> , 2020, 52, 884-890.	9.4	106
35	A Novel Role in DNA Metabolism for the Binding of Fen1/Rad27 to PCNA and Implications for Genetic Risk. <i>Molecular and Cellular Biology</i> , 1999, 19, 5373-5382.	1.1	100
36	Conservative Repair of a Chromosomal Double-Strand Break by Single-Strand DNA through Two Steps of Annealing. <i>Molecular and Cellular Biology</i> , 2006, 26, 7645-7657.	1.1	98

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37	Genome-wide model for the normal eukaryotic DNA replication fork. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 17674-17679.	3.3	88
38	Yeast ARMs (DNA at-risk motifs) can reveal sources of genome instability. Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis, 1998, 400, 45-58.	0.4	87
39	Mutator phenotypes of yeast strains heterozygous for mutations in the MSH2 gene. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 2970-2975.	3.3	86
40	The Impact of Environmental and Endogenous Damage on Somatic Mutation Load in Human Skin Fibroblasts. PLoS Genetics, 2016, 12, e1006385.	1.5	82
41	Cohesin Is Limiting for the Suppression of DNA Damage-Induced Recombination between Homologous Chromosomes. PLoS Genetics, 2010, 6, e1001006.	1.5	81
42	Genomic and evolutionary classification of lung cancer in never smokers. Nature Genetics, 2021, 53, 1348-1359.	9.4	81
43	APOBEC-Induced Cancer Mutations Are Uniquely Enriched in Early-Replicating, Gene-Dense, and Active Chromatin Regions. Cell Reports, 2015, 13, 1103-1109.	2.9	80
44	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. Nature Genetics, 2020, 52, 1178-1188.	9.4	79
45	Base Damage within Single-Strand DNA Underlies In Vivo Hypermutability Induced by a Ubiquitous Environmental Agent. PLoS Genetics, 2012, 8, e1003149.	1.5	76
46	The Multiple Biological Roles of the 3'→5' Exonuclease of Saccharomyces cerevisiae DNA Polymerase Î require Switching between the Polymerase and Exonuclease Domains. Molecular and Cellular Biology, 2005, 25, 461-471.	1.1	71
47	The choice of nucleotide inserted opposite abasic sites formed within chromosomal DNA reveals the polymerase activities participating in translesion DNA synthesis. DNA Repair, 2013, 12, 878-889.	1.3	68
48	The Prevention of Repeat-Associated Deletions in <i>Saccharomyces cerevisiae</i> by Mismatch Repair Depends on Size and Origin of Deletions. Genetics, 1996, 143, 1579-1587.	1.2	68
49	Apn1 and Apn2 endonucleases prevent accumulation of repair-associated DNA breaks in budding yeast as revealed by direct chromosomal analysis. Nucleic Acids Research, 2008, 36, 1836-1846.	6.5	62
50	Oxidative stress-induced mutagenesis in single-strand DNA occurs primarily at cytosines and is DNA polymerase zeta-dependent only for adenines and guanines. Nucleic Acids Research, 2013, 41, 8995-9005.	6.5	58
51	Infectious vaccine-derived rubella viruses emerge, persist, and evolve in cutaneous granulomas of children with primary immunodeficiencies. PLoS Pathogens, 2019, 15, e1008080.	2.1	58
52	Functional analysis of human MutSÂ and MutSÂ complexes in yeast. Nucleic Acids Research, 1999, 27, 736-742.	6.5	57
53	Similarity between mutation spectra in hypermutated genomes of rubella virus and in SARS-CoV-2 genomes accumulated during the COVID-19 pandemic. PLoS ONE, 2020, 15, e0237689.	1.1	53
54	Alkylation Base Damage Is Converted into Repairable Double-Strand Breaks and Complex Intermediates in G2 Cells Lacking AP Endonuclease. PLoS Genetics, 2011, 7, e1002059.	1.5	52

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55	Genetic Factors Affecting the Impact of DNA Polymerase α , Proofreading Activity on Mutation Avoidance in Yeast. <i>Genetics</i> , 1999, 152, 47-59.	1.2	51
56	A single-strand specific lesion drives MMS-induced hyper-mutability at a double-strand break in yeast. <i>DNA Repair</i> , 2010, 9, 914-921.	1.3	48
57	Clustered and genome-wide transient mutagenesis in human cancers: Hypermutation without permanent mutators or loss of fitness. <i>BioEssays</i> , 2014, 36, 382-393.	1.2	48
58	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. <i>Microbial Cell</i> , 2019, 6, 1-64.	1.4	47
59	Mutator Specificity and Disease: Looking over the FENce. <i>Cell</i> , 1997, 88, 155-158.	13.5	45
60	Functional Analysis of Human FEN1 in <i>Saccharomyces Cerevisiae</i> and Its Role in Genome Stability. <i>Human Molecular Genetics</i> , 1999, 8, 2263-2273.	1.4	41
61	The flexible loop of human FEN1 endonuclease is required for flap cleavage during DNA replication and repair. <i>EMBO Journal</i> , 2002, 21, 5930-5942.	3.5	40
62	The Transition of Closely Opposed Lesions to Double-Strand Breaks during Long-Patch Base Excision Repair Is Prevented by the Coordinated Action of DNA Polymerase β and Rad27/Fen1. <i>Molecular and Cellular Biology</i> , 2009, 29, 1212-1221.	1.1	38
63	Damage-induced localized hypermutability. <i>Cell Cycle</i> , 2011, 10, 1073-1085.	1.3	38
64	APOBEC3B cytidine deaminase targets the non-transcribed strand of tRNA genes in yeast. <i>DNA Repair</i> , 2017, 53, 4-14.	1.3	37
65	Repair of multiple simultaneous double-strand breaks causes bursts of genome-wide clustered hypermutation. <i>PLoS Biology</i> , 2019, 17, e3000464.	2.6	35
66	The Sister Chromatid Cohesion Pathway Suppresses Multiple Chromosome Gain and Chromosome Amplification. <i>Genetics</i> , 2014, 196, 373-384.	1.2	34
67	Who Is Leading the Replication Fork, Pol δ or Pol ϵ ? <i>Molecular Cell</i> , 2016, 61, 492-493.	4.5	34
68	Mutation signatures specific to DNA alkylating agents in yeast and cancers. <i>Nucleic Acids Research</i> , 2020, 48, 3692-3707.	6.5	32
69	Mutational signatures of redox stress in yeast single-strand DNA and of aging in human mitochondrial DNA share a common feature. <i>PLoS Biology</i> , 2019, 17, e3000263.	2.6	29
70	Hypermutation in single-stranded DNA. <i>DNA Repair</i> , 2020, 91-92, 102868.	1.3	28
71	UV-exposure, endogenous DNA damage, and DNA replication errors shape the spectra of genome changes in human skin. <i>PLoS Genetics</i> , 2021, 17, e1009302.	1.5	26
72	Analysis of APOBEC-induced mutations in yeast strains with low levels of replicative DNA polymerases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 9440-9450.	3.3	22

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73	Precise excision of bacterial transposon Tn 5 in yeast. <i>Molecular Genetics and Genomics</i> , 1988, 213, 388-393.	2.4	21
74	Understanding the origins of UV-induced recombination through manipulation of sister chromatid cohesion. <i>Cell Cycle</i> , 2012, 11, 3937-3944.	1.3	21
75	Somatic mutation load and spectra: A record of DNA damage and repair in healthy human cells. <i>Environmental and Molecular Mutagenesis</i> , 2018, 59, 672-686.	0.9	19
76	From RNA World to SARS-CoV-2: The Edited Story of RNA Viral Evolution. <i>Cells</i> , 2021, 10, 1557.	1.8	18
77	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. <i>American Journal of Epidemiology</i> , 2021, 190, 962-976.	1.6	16
78	Mitotic intragenic recombination in the yeast <i>Saccharomyces</i> : marker-effects on conversion and reciprocity of recombination. <i>Current Genetics</i> , 1984, 9, 31-37.	0.8	11
79	RAD53 is limiting in double-strand break repair and in protection against toxicity associated with ribonucleotide reductase inhibition. <i>DNA Repair</i> , 2012, 11, 317-323.	1.3	8
80	Rapid genetic test for discrimination between haploid and polyploid transformants in <i>Saccharomyces</i> . <i>Current Genetics</i> , 1984, 8, 341-344.	0.8	5
81	Comprehensive molecular characterization and analysis of muscle-invasive urothelial carcinomas.. <i>Journal of Clinical Oncology</i> , 2017, 35, 4500-4500.	0.8	4
82	Suppression of Allelic Recombination and Aneuploidy by Cohesin Is Independent of Chk1 in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2014, 9, e113435.	1.1	4
83	Michael Ter-Avanesyan (1949-2018) – Advent of the scientist. <i>Prion</i> , 2019, 13, 33-36.	0.9	1
84	Comprehensive molecular profiling of urothelial bladder cancer at the DNA, RNA, and protein levels: A TCGA project.. <i>Journal of Clinical Oncology</i> , 2014, 32, 4509-4509.	0.8	1
85	Thread 1: Mutational drivers. <i>Nature Genetics</i> , 2013, , .	9.4	0
86	Thread 3: Environmental exposure and pathogens. <i>Nature Genetics</i> , 2013, , .	9.4	0
87	Hypermutable Associated with Double-Strand Break Repair. <i>NATO Science for Peace and Security Series C: Environmental Security</i> , 2012, , 1-11.	0.1	0
88	Title is missing!. , 2019, 17, e3000464.		0
89	Title is missing!. , 2019, 17, e3000464.		0
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91	Title is missing!. , 2020, 15, e0237689.		0
92	Title is missing!. , 2020, 15, e0237689.		0
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