

Dmitry A Gordenin

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

95
papers

15,884
citations

47
h-index

106
g-index

106
ext. papers

19,840
ext. citations

15.3
avg, IF

6.95
L-index

#	Paper	IF	Citations
95	From RNA World to SARS-CoV-2: The Edited Story of RNA Viral Evolution. <i>Cells</i> , 2021 , 10,	7.9	4
94	Tracing Lung Cancer Risk Factors Through Mutational Signatures in Never-Smokers. <i>American Journal of Epidemiology</i> , 2021 , 190, 962-976	3.8	4
93	Genomic and evolutionary classification of lung cancer in never smokers. <i>Nature Genetics</i> , 2021 , 53, 1348-1359	13.59	14
92	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	6	10
91	Mutation signatures specific to DNA alkylating agents in yeast and cancers. <i>Nucleic Acids Research</i> , 2020 , 48, 3692-3707	20.1	13
90	The repertoire of mutational signatures in human cancer. <i>Nature</i> , 2020 , 578, 94-101	50.4	849
89	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020 , 52, 331-341	36.3	168
88	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	11.5	13
87	Similarity between mutation spectra in hypermutated genomes of rubella virus and in SARS-CoV-2 genomes accumulated during the COVID-19 pandemic. <i>PLoS ONE</i> , 2020 , 15, e0237689	3.7	31
86	Hypermutation in single-stranded DNA. <i>DNA Repair</i> , 2020 , 91-92, 102868	4.3	7
85	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. <i>Nature Genetics</i> , 2020 , 52, 1178-1188	36.3	25
84	APOBEC3-dependent kataegis and TREX1-driven chromothripsis during telomere crisis. <i>Nature Genetics</i> , 2020 , 52, 884-890	36.3	43
83	Similarity between mutation spectra in hypermutated genomes of rubella virus and in SARS-CoV-2 genomes accumulated during the COVID-19 pandemic 2020 , 15, e0237689		
82	Similarity between mutation spectra in hypermutated genomes of rubella virus and in SARS-CoV-2 genomes accumulated during the COVID-19 pandemic 2020 , 15, e0237689		
81	Similarity between mutation spectra in hypermutated genomes of rubella virus and in SARS-CoV-2 genomes accumulated during the COVID-19 pandemic 2020 , 15, e0237689		
80	Similarity between mutation spectra in hypermutated genomes of rubella virus and in SARS-CoV-2 genomes accumulated during the COVID-19 pandemic 2020 , 15, e0237689		
79	Repair of multiple simultaneous double-strand breaks causes bursts of genome-wide clustered hypermutation. <i>PLoS Biology</i> , 2019 , 17, e3000464	9.7	19

78	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	9.7	13
77	Guidelines for DNA recombination and repair studies: Cellular assays of DNA repair pathways. <i>Microbial Cell</i> , 2019 , 6, 1-64	3.9	27
76	Infectious vaccine-derived rubella viruses emerge, persist, and evolve in cutaneous granulomas of children with primary immunodeficiencies. <i>PLoS Pathogens</i> , 2019 , 15, e1008080	7.6	33
75	Michael Ter-Avanesyan (1949-2018) - Advent of the scientist. <i>Prion</i> , 2019 , 13, 33-36	2.3	1
74	Repair of multiple simultaneous double-strand breaks causes bursts of genome-wide clustered hypermutation 2019 , 17, e3000464		
73	Repair of multiple simultaneous double-strand breaks causes bursts of genome-wide clustered hypermutation 2019 , 17, e3000464		
72	Repair of multiple simultaneous double-strand breaks causes bursts of genome-wide clustered hypermutation 2019 , 17, e3000464		
71	Molecular Evolution of Early-Onset Prostate Cancer Identifies Molecular Risk Markers and Clinical Trajectories. <i>Cancer Cell</i> , 2018 , 34, 996-1011.e8	24.3	89
70	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	3.2	14
69	Integrated genomic and molecular characterization of cervical cancer. <i>Nature</i> , 2017 , 543, 378-384	50.4	755
68	APOBEC3B cytidine deaminase targets the non-transcribed strand of tRNA genes in yeast. <i>DNA Repair</i> , 2017 , 53, 4-14	4.3	23
67	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017 , 171, 540-556.e75	25.2	961
66	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	24.3	141
65	Comprehensive molecular characterization and analysis of muscle-invasive urothelial carcinomas. <i>Journal of Clinical Oncology</i> , 2017 , 35, 4500-4500	2.2	4
64	Who Is Leading the Replication Fork, Pol δ or Pol ϵ ? <i>Molecular Cell</i> , 2016 , 61, 492-493	17.6	30
63	The Impact of Environmental and Endogenous Damage on Somatic Mutation Load in Human Skin Fibroblasts. <i>PLoS Genetics</i> , 2016 , 12, e1006385	6	55
62	An APOBEC3A hypermutation signature is distinguishable from the signature of background mutagenesis by APOBEC3B in human cancers. <i>Nature Genetics</i> , 2015 , 47, 1067-72	36.3	238
61	APOBEC-Induced Cancer Mutations Are Uniquely Enriched in Early-Replicating, Gene-Dense, and Active Chromatin Regions. <i>Cell Reports</i> , 2015 , 13, 1103-1109	10.6	57

60	Clusters of Multiple Mutations: Incidence and Molecular Mechanisms. <i>Annual Review of Genetics</i> , 2015 , 49, 243-67	14.5	75
59	Comprehensive molecular characterization of urothelial bladder carcinoma. <i>Nature</i> , 2014 , 507, 315-22	50.4	1963
58	Clustered and genome-wide transient mutagenesis in human cancers: Hypermutation without permanent mutators or loss of fitness. <i>BioEssays</i> , 2014 , 36, 382-393	4.1	39
57	Heterogeneous polymerase fidelity and mismatch repair bias genome variation and composition. <i>Genome Research</i> , 2014 , 24, 1751-64	9.7	111
56	The somatic genomic landscape of chromophobe renal cell carcinoma. <i>Cancer Cell</i> , 2014 , 26, 319-330	24.3	521
55	The sister chromatid cohesion pathway suppresses multiple chromosome gain and chromosome amplification. <i>Genetics</i> , 2014 , 196, 373-84	4	26
54	Break-induced replication is a source of mutation clusters underlying kataegis. <i>Cell Reports</i> , 2014 , 7, 1640-1648	12.1	121
53	Hypermutation in human cancer genomes: footprints and mechanisms. <i>Nature Reviews Cancer</i> , 2014 , 14, 786-800	31.3	274
52	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	2.2	1
51	Suppression of allelic recombination and aneuploidy by cohesin is independent of Chk1 in <i>Saccharomyces cerevisiae</i> . <i>PLoS ONE</i> , 2014 , 9, e113435	3.7	4
50	An APOBEC cytidine deaminase mutagenesis pattern is widespread in human cancers. <i>Nature Genetics</i> , 2013 , 45, 970-6	36.3	774
49	The choice of nucleotide inserted opposite abasic sites formed within chromosomal DNA reveals the polymerase activities participating in translesion DNA synthesis. <i>DNA Repair</i> , 2013 , 12, 878-89	4.3	47
48	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , 2013 , 499, 214-218	50.4	3616
47	Oxidative stress-induced mutagenesis in single-strand DNA occurs primarily at cytosines and is DNA polymerase zeta-dependent only for adenines and guanines. <i>Nucleic Acids Research</i> , 2013 , 41, 8995-9005	20.1	36
46	RAD53 is limiting in double-strand break repair and in protection against toxicity associated with ribonucleotide reductase inhibition. <i>DNA Repair</i> , 2012 , 11, 317-23	4.3	8
45	Understanding the origins of UV-induced recombination through manipulation of sister chromatid cohesion. <i>Cell Cycle</i> , 2012 , 11, 3937-44	4.7	9
44	Clustered mutations in yeast and in human cancers can arise from damaged long single-strand DNA regions. <i>Molecular Cell</i> , 2012 , 46, 424-35	17.6	302
43	Base damage within single-strand DNA underlies in vivo hypermutability induced by a ubiquitous environmental agent. <i>PLoS Genetics</i> , 2012 , 8, e1003149	6	49

42	Hypermutability Associated with Double-Strand Break Repair. <i>NATO Science for Peace and Security Series C: Environmental Security</i> , 2012 , 1-11	0.3	
41	Damage-induced localized hypermutability. <i>Cell Cycle</i> , 2011 , 10, 1073-85	4.7	34
40	Alkylation base damage is converted into repairable double-strand breaks and complex intermediates in G2 cells lacking AP endonuclease. <i>PLoS Genetics</i> , 2011 , 7, e1002059	6	41
39	Genome-wide model for the normal eukaryotic DNA replication fork. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 17674-9	11.5	76
38	Cohesin Is limiting for the suppression of DNA damage-induced recombination between homologous chromosomes. <i>PLoS Genetics</i> , 2010 , 6, e1001006	6	65
37	A single-strand specific lesion drives MMS-induced hyper-mutability at a double-strand break in yeast. <i>DNA Repair</i> , 2010 , 9, 914-21	4.3	42
36	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 delta and Rad27/Fen1. <i>Molecular and Cellular Biology</i> , 2009 , 29, 1212-21	4.8	33
35	Division of labor at the eukaryotic replication fork. <i>Molecular Cell</i> , 2008 , 30, 137-44	17.6	353
34	Flexibility of eukaryotic Okazaki fragment maturation through regulated strand displacement synthesis. <i>Journal of Biological Chemistry</i> , 2008 , 283, 34129-40	5.4	104
33	Hypermutability 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	6	115
32	Apn1 and Apn2 endonucleases prevent accumulation of repair-associated DNA breaks in budding yeast as revealed by direct chromosomal analysis. <i>Nucleic Acids Research</i> , 2008 , 36, 1836-46	20.1	54
31	RNA-templated DNA repair. <i>Nature</i> , 2007 , 447, 338-41	50.4	161
30	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, 7645-57	4.8	83
29	The multiple biological roles of the 3F->5Texonuclease of <i>Saccharomyces cerevisiae</i> DNA polymerase delta require switching between the polymerase and exonuclease domains. <i>Molecular and Cellular Biology</i> , 2005 , 25, 461-71	4.8	59
28	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, 14994-9	11.5	154
27	Okazaki fragment maturation in yeast. II. Cooperation between the polymerase and 3F5Texonuclease activities of Pol delta in the creation of a ligatable nick. <i>Journal of Biological Chemistry</i> , 2003 , 278, 1626-33	5.4	122
26	Cadmium is a mutagen that acts by inhibiting mismatch repair. <i>Nature Genetics</i> , 2003 , 34, 326-9	36.3	374
25	Okazaki fragment maturation in yeast. I. Distribution of functions between FEN1 AND DNA2. <i>Journal of Biological Chemistry</i> , 2003 , 278, 1618-25	5.4	187

24	The flexible loop of human FEN1 endonuclease is required for flap cleavage during DNA replication and repair. <i>EMBO Journal</i> , 2002 , 21, 5930-42	13	37
23	The Mre11 complex is required for repair of hairpin-capped double-strand breaks and prevention of chromosome rearrangements. <i>Cell</i> , 2002 , 108, 183-93	56.2	319
22	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	9.7	97
21	The 3F->5Texonuclease of DNA polymerase delta can substitute for the 5Tflap 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, 5122-7	11.5	131
20	Inverted Alu repeats unstable in yeast are excluded from the human genome. <i>EMBO Journal</i> , 2000 , 19, 3822-30	13	111
19	Mutator phenotypes of yeast strains heterozygous for mutations in the MSH2 gene. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1999 , 96, 2970-5	11.5	77
18	Functional analysis of human MutSalpha and MutSbeta complexes in yeast. <i>Nucleic Acids Research</i> , 1999 , 27, 736-42	20.1	53
17	Functional analysis of human FEN1 in <i>Saccharomyces cerevisiae</i> and its role in genome stability. <i>Human Molecular Genetics</i> , 1999 , 8, 2263-73	5.6	35
16	The 3F->5Texonucleases of DNA polymerases delta and epsilon and the 5T->3Texonuclease Exo1 have major roles in postreplication mutation avoidance in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 1999 , 19, 2000-7	4.8	181
15	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, 5373-82	4.8	87
14	Genetic factors affecting the impact of DNA polymerase delta proofreading activity on mutation avoidance in yeast. <i>Genetics</i> , 1999 , 152, 47-59	4	42
13	Yeast ARMs (DNA at-risk motifs) can reveal sources of genome instability. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 1998 , 400, 45-58	3.3	76
12	Destabilization of yeast micro- and minisatellite DNA sequences by mutations affecting a nuclease involved in Okazaki fragment processing (rad27) and DNA polymerase delta (pol3-t). <i>Molecular and Cellular Biology</i> , 1998 , 18, 2779-88	4.8	169
11	Factors affecting inverted repeat stimulation of recombination and deletion in <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 1998 , 148, 1507-24	4	107
10	Hypermutability of homonucleotide runs in mismatch repair and DNA polymerase proofreading yeast mutants. <i>Molecular and Cellular Biology</i> , 1997 , 17, 2859-65	4.8	273
9	Mutator specificity and disease: looking over the FENce. <i>Cell</i> , 1997 , 88, 155-8	56.2	43
8	The prevention of repeat-associated deletions in <i>Saccharomyces cerevisiae</i> by mismatch repair depends on size and origin of deletions. <i>Genetics</i> , 1996 , 143, 1579-87	4	55
7	Precise excision of bacterial transposon Tn5 in yeast. <i>Molecular Genetics and Genomics</i> , 1988 , 213, 388-93		14

6	Mitotic intragenic recombination in the yeast <i>Saccharomyces</i> : marker-effects on conversion and reciprocity of recombination. <i>Current Genetics</i> , 1984 , 9, 31-7	2.9	10
5	Rapid genetic test for discrimination between haploid and polyploid transformants in <i>Saccharomyces</i> . <i>Current Genetics</i> , 1984 , 8, 341-4	2.9	4
4	Germline determinants of the somatic mutation landscape in 2,642 cancer genomes		13
3	The Repertoire of Mutational Signatures in Human Cancer		67
2	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing		12
1	Clustered Mutations in Human Cancer		2