

Piotr A Mieczkowski

List of Publications by Citations

Source: <https://exaly.com/author-pdf/8338556/piotr-a-mieczkowski-publications-by-citations.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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

121
papers

13,196
citations

56
h-index

114
g-index

135
ext. papers

16,864
ext. citations

13.6
avg, IF

5.67
L-index

#	Paper	IF	Citations
121	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
120	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017 , 32, 185-203.e13	24.3	13896
119	MapSplice: accurate mapping of RNA-seq reads for splice junction discovery. <i>Nucleic Acids Research</i> , 2010 , 38, e178	20.1	762
118	Practical innovations for high-throughput amplicon sequencing. <i>Nature Methods</i> , 2013 , 10, 999-1002	21.6	461
117	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28	56.2	451
116	A map of open chromatin in human pancreatic islets. <i>Nature Genetics</i> , 2010 , 42, 255-9	36.3	435
115	Genetic heterogeneity of diffuse large B-cell lymphoma. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013 , 110, 1398-403	11.5	419
114	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017 , 32, 204-220.e15	24.3	391
113	Nucleosome dynamics define transcriptional enhancers. <i>Nature Genetics</i> , 2010 , 42, 343-7	36.3	382
112	Root microbiota drive direct integration of phosphate stress and immunity. <i>Nature</i> , 2017 , 543, 513-518	50.4	369
111	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193	24.3	350
110	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016 , 29, 723-736	24.3	324
109	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
108	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018 , 33, 690-705.e9	24.3	277
107	Analysis of the genome and transcriptome of <i>Cryptococcus neoformans</i> var. <i>grubii</i> reveals complex RNA expression and microevolution leading to virulence attenuation. <i>PLoS Genetics</i> , 2014 , 10, e1004261 ⁶		260
106	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
105	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228

104	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017 , 31, 411-423	24.3	210
103	Genome structure of a <i>Saccharomyces cerevisiae</i> strain widely used in bioethanol production. <i>Genome Research</i> , 2009 , 19, 2258-70	9.7	186
102	Double-strand breaks associated with repetitive DNA can reshape the genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008 , 105, 11845-50	11.5	183
101	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
100	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018 , 33, 244-258.e10	24.3	150
99	Site-specific silencing of regulatory elements as a mechanism of X inactivation. <i>Cell</i> , 2012 , 151, 951-63	56.2	141
98	Genus-Wide Comparative Genomics of <i>Malassezia</i> Delineates Its Phylogeny, Physiology, and Niche Adaptation on Human Skin. <i>PLoS Genetics</i> , 2015 , 11, e1005614	6	140
97	Essential Roles for Polymerase δ -Mediated End Joining in the Repair of Chromosome Breaks. <i>Molecular Cell</i> , 2016 , 63, 662-673	17.6	135
96	Tracking replication enzymology in vivo by genome-wide mapping of ribonucleotide incorporation. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 185-91	17.6	127
95	The pattern of gene amplification is determined by the chromosomal location of hairpin-capped breaks. <i>Cell</i> , 2006 , 125, 1283-96	56.2	127
94	Break-induced replication is a source of mutation clusters underlying kataegis. <i>Cell Reports</i> , 2014 , 7, 1640-1648	16.48	121
93	Gene expression divergence in yeast is coupled to evolution of DNA-encoded nucleosome organization. <i>Nature Genetics</i> , 2009 , 41, 438-45	36.3	121
92	APOBEC3A and APOBEC3B Preferentially Deaminate the Lagging Strand Template during DNA Replication. <i>Cell Reports</i> , 2016 , 14, 1273-1282	10.6	118
91	UVA generates pyrimidine dimers in DNA directly. <i>Biophysical Journal</i> , 2009 , 96, 1151-8	2.9	118
90	Unisexual and heterosexual meiotic reproduction generate aneuploidy and phenotypic diversity de novo in the yeast <i>Cryptococcus neoformans</i> . <i>PLoS Biology</i> , 2013 , 11, e1001653	9.7	113
89	Heterogeneous polymerase fidelity and mismatch repair bias genome variation and composition. <i>Genome Research</i> , 2014 , 24, 1751-64	9.7	111
88	Recombination between retrotransposons as a source of chromosome rearrangements in the yeast <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2006 , 5, 1010-20	4.3	107
87	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. <i>American Journal of Human Genetics</i> , 2016 , 98, 1051-1066	11	107

86	Antifungal drug resistance evoked via RNAi-dependent epimutations. <i>Nature</i> , 2014 , 513, 555-8	50.4	98
85	Genomic insights into the atopic eczema-associated skin commensal yeast <i>Malassezia sympodialis</i> . <i>MBio</i> , 2013 , 4, e00572-12	7.8	89
84	Primer ID Validates Template Sampling Depth and Greatly Reduces the Error Rate of Next-Generation Sequencing of HIV-1 Genomic RNA Populations. <i>Journal of Virology</i> , 2015 , 89, 8540-55	6.6	85
83	A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- β Superfamily. <i>Cell Systems</i> , 2018 , 7, 422-437.e7	10.6	85
82	MAP3K4/CBP-regulated H2B acetylation controls epithelial-mesenchymal transition in trophoblast stem cells. <i>Cell Stem Cell</i> , 2011 , 8, 525-37	18	84
81	High-resolution transcript profiling of the atypical biotrophic interaction between <i>Theobroma cacao</i> and the fungal pathogen <i>Moniliophthora perniciosa</i> . <i>Plant Cell</i> , 2014 , 26, 4245-69	11.6	83
80	Genetic regulation of telomere-telomere fusions in the yeast <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003 , 100, 10854-9	11.5	83
79	Analysis of a food-borne fungal pathogen outbreak: virulence and genome of a <i>Mucor circinelloides</i> isolate from yogurt. <i>MBio</i> , 2014 , 5, e01390-14	7.8	82
78	Chromosome fragility at GAA tracts in yeast depends on repeat orientation and requires mismatch repair. <i>EMBO Journal</i> , 2008 , 27, 2896-906	13	81
77	The genome sequence of <i>Leishmania (Leishmania) amazonensis</i> : functional annotation and extended analysis of gene models. <i>DNA Research</i> , 2013 , 20, 567-81	4.5	79
76	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
75	<i>Pseudomonas syringae</i> Type III Effector HopBB1 Promotes Host Transcriptional Repressor Degradation to Regulate Phytohormone Responses and Virulence. <i>Cell Host and Microbe</i> , 2017 , 21, 156-168	23.4	74
74	Genome and secretome analysis of the hemibiotrophic fungal pathogen, <i>Moniliophthora roreri</i> , which causes frosty pod rot disease of cacao: mechanisms of the biotrophic and necrotrophic phases. <i>BMC Genomics</i> , 2014 , 15, 164	4.5	69
73	<i>Cryptococcus gattii</i> VGIII isolates causing infections in HIV/AIDS patients in Southern California: identification of the local environmental source as arboreal. <i>PLoS Pathogens</i> , 2014 , 10, e1004285	7.6	65
72	The oncogenic potential of BK-polyomavirus is linked to viral integration into the human genome. <i>Journal of Pathology</i> , 2015 , 237, 379-89	9.4	64
71	Loss of a histone deacetylase dramatically alters the genomic distribution of Spo11p-catalyzed DNA breaks in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 3955-60	11.5	64
70	Highly recombinant VGII <i>Cryptococcus gattii</i> population develops clonal outbreak clusters through both sexual macroevolution and asexual microevolution. <i>MBio</i> , 2014 , 5, e01494-14	7.8	63
69	Elucidation of the calcineurin-Crz1 stress response transcriptional network in the human fungal pathogen <i>Cryptococcus neoformans</i> . <i>PLoS Genetics</i> , 2017 , 13, e1006667	6	60

68	Genome-wide maps of alkylation damage, repair, and mutagenesis in yeast reveal mechanisms of mutational heterogeneity. <i>Genome Research</i> , 2017 , 27, 1674-1684	9.7	58
67	High-resolution genome-wide analysis of irradiated (UV and F-rays) diploid yeast cells reveals a high frequency of genomic loss of heterozygosity (LOH) events. <i>Genetics</i> , 2012 , 190, 1267-84	4	56
66	Global analysis of the relationship between the binding of the Bas1p transcription factor and meiosis-specific double-strand DNA breaks in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2006 , 26, 1014-27	4.8	56
65	The Impact of Environmental and Endogenous Damage on Somatic Mutation Load in Human Skin Fibroblasts. <i>PLoS Genetics</i> , 2016 , 12, e1006385	6	55
64	The fidelity of the ligation step determines how ends are resolved during nonhomologous end joining. <i>Nature Communications</i> , 2014 , 5, 4286	17.4	52
63	Gene copy-number variation in haploid and diploid strains of the yeast <i>Saccharomyces cerevisiae</i> . <i>Genetics</i> , 2013 , 193, 785-801	4	52
62	Essential role for polymerase specialization in cellular nonhomologous end joining. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, E4537-45	11.5	50
61	Unisexual reproduction drives meiotic recombination and phenotypic and karyotypic plasticity in <i>Cryptococcus neoformans</i> . <i>PLoS Genetics</i> , 2014 , 10, e1004849	6	46
60	Intercellular Communication between Airway Epithelial Cells Is Mediated by Exosome-Like Vesicles. <i>American Journal of Respiratory Cell and Molecular Biology</i> , 2019 , 60, 209-220	5.7	46
59	Detecting ultraviolet damage in single DNA molecules by atomic force microscopy. <i>Biophysical Journal</i> , 2007 , 93, 1758-67	2.9	45
58	<i>Saccharomyces cerevisiae</i> transcriptional reprogramming due to bacterial contamination during industrial scale bioethanol production. <i>Microbial Cell Factories</i> , 2015 , 14, 13	6.4	42
57	The compact chromatin structure of a Ty repeated sequence suppresses recombination hotspot activity in <i>Saccharomyces cerevisiae</i> . <i>Molecular Cell</i> , 2004 , 15, 221-31	17.6	40
56	Polyglutamine toxicity is controlled by prion composition and gene dosage in yeast. <i>PLoS Genetics</i> , 2012 , 8, e1002634	6	39
55	The product of the DNA damage-inducible gene of <i>Saccharomyces cerevisiae</i> , DIN7, specifically functions in mitochondria. <i>Genetics</i> , 2000 , 154, 73-81	4	38
54	The histone methylase Set2p and the histone deacetylase Rpd3p repress meiotic recombination at the HIS4 meiotic recombination hotspot in <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2008 , 7, 1298-308	4.3	37
53	Global analysis of genomic instability caused by DNA replication stress in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016 , 113, E8114-E8121	11.5	36
52	Dengue type 1 viruses circulating in humans are highly infectious and poorly neutralized by human antibodies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019 , 116, 227-232	11.5	35
51	Damage-induced localized hypermutability. <i>Cell Cycle</i> , 2011 , 10, 1073-85	4.7	34

50	Chronic oxidative DNA damage due to DNA repair defects causes chromosomal instability in <i>Saccharomyces cerevisiae</i> . <i>Molecular and Cellular Biology</i> , 2008 , 28, 5432-45	4.8	34
49	Top1 stabilizes promoter nucleosome positioning and occupancy at transcriptionally plastic genes. <i>Nucleic Acids Research</i> , 2011 , 39, 8803-19	20.1	33
48	fourSig: a method for determining chromosomal interactions in 4C-Seq data. <i>Nucleic Acids Research</i> , 2014 , 42, e68	20.1	32
47	Chromatin architectures at fission yeast transcriptional promoters and replication origins. <i>Nucleic Acids Research</i> , 2012 , 40, 7176-89	20.1	32
46	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021 , 39, 1115-1128	44.5	31
45	Genes acquired by horizontal transfer are potentially involved in the evolution of phytopathogenicity in <i>Moniliophthora perniciosa</i> and <i>Moniliophthora roreri</i> , two of the major pathogens of cacao. <i>Journal of Molecular Evolution</i> , 2010 , 70, 85-97	3.1	30
44	Quantitative analysis of focused a-to-I RNA editing sites by ultra-high-throughput sequencing in psychiatric disorders. <i>PLoS ONE</i> , 2012 , 7, e43227	3.7	29
43	Assessing serotonin receptor mRNA editing frequency by a novel ultra high-throughput sequencing method. <i>Nucleic Acids Research</i> , 2010 , 38, e118	20.1	29
42	The fungal pathogen <i>Moniliophthora perniciosa</i> has genes similar to plant PR-1 that are highly expressed during its interaction with cacao. <i>PLoS ONE</i> , 2012 , 7, e45929	3.7	26
41	Multiplex amplicon sequencing for microbe identification in community-based culture collections. <i>Scientific Reports</i> , 2016 , 6, 29543	4.9	26
40	Xylem transcription profiles indicate potential metabolic responses for economically relevant characteristics of <i>Eucalyptus</i> species. <i>BMC Genomics</i> , 2013 , 14, 201	4.5	25
39	APOBEC3B cytidine deaminase targets the non-transcribed strand of tRNA genes in yeast. <i>DNA Repair</i> , 2017 , 53, 4-14	4.3	23
38	Fragile DNA motifs trigger mutagenesis at distant chromosomal loci in <i>saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2013 , 9, e1003551	6	23
37	Low levels of DNA polymerase alpha induce mitotic and meiotic instability in the ribosomal DNA gene cluster of <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2008 , 4, e1000105	6	21
36	Nanoscale detection of ionizing radiation damage to DNA by atomic force microscopy. <i>Small</i> , 2008 , 4, 288-94	11	20
35	Repair of multiple simultaneous double-strand breaks causes bursts of genome-wide clustered hypermutation. <i>PLoS Biology</i> , 2019 , 17, e3000464	9.7	19
34	The mitochondrial genome of <i>Moniliophthora roreri</i> , the frosty pod rot pathogen of cacao. <i>Fungal Biology</i> , 2012 , 116, 551-62	2.8	19
33	Cavitation Enhancing Nanodroplets Mediate Efficient DNA Fragmentation in a Bench Top Ultrasonic Water Bath. <i>PLoS ONE</i> , 2015 , 10, e0133014	3.7	18

32	Specific modulation of the root immune system by a community of commensal bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021 , 118,	11.5	17
31	A Mutation in the Borcs7 Subunit of the Lysosome Regulatory BORC Complex Results in Motor Deficits and Dystrophic Axonopathy in Mice. <i>Cell Reports</i> , 2018 , 24, 1254-1265	10.6	16
30	Repair of base damage within break-induced replication intermediates promotes kataegis associated with chromosome rearrangements. <i>Nucleic Acids Research</i> , 2019 , 47, 9666-9684	20.1	14
29	Expression of UMP1 is inducible by DNA damage and required for resistance of <i>S. cerevisiae</i> cells to UV light. <i>Current Genetics</i> , 2000 , 38, 53-9	2.9	14
28	Mutation signatures specific to DNA alkylating agents in yeast and cancers. <i>Nucleic Acids Research</i> , 2020 , 48, 3692-3707	20.1	13
27	A native and an invasive dune grass share similar, patchily distributed, root-associated fungal communities. <i>Fungal Ecology</i> , 2016 , 23, 141-155	4.1	13
26	Evidence for local regulatory control of escape from imprinted X chromosome inactivation. <i>Genetics</i> , 2014 , 197, 715-23	4	13
25	Long transposon-rich centromeres in an oomycete reveal divergence of centromere features in Stramenopila-Alveolata-Rhizaria lineages. <i>PLoS Genetics</i> , 2020 , 16, e1008646	6	12
24	Separating DNA with different topologies by atomic force microscopy in comparison with gel electrophoresis. <i>Journal of Physical Chemistry B</i> , 2010 , 114, 12162-5	3.4	10
23	The two-faced nature of BK polyomavirus: lytic infection or non-lytic large-T-positive carcinoma. <i>Journal of Pathology</i> , 2018 , 246, 7-11	9.4	10
22	Adaptation and selection shape clonal evolution of tumors during residual disease and recurrence. <i>Nature Communications</i> , 2020 , 11, 5017	17.4	9
21	A Case Study of Genomic Instability in an Industrial Strain of. <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 3703-3713	3.7	9
20	Scattered far and wide: A broadly distributed temperate dune grass finds familiar fungal root associates in its invasive range. <i>Soil Biology and Biochemistry</i> , 2017 , 112, 177-190	7.5	6
19	Whole Genome Sequence Analysis of Mutations Accumulated in Yeast Strains with Defects in the Processing of Okazaki Fragments Indicates Template-Switching Events. <i>G3: Genes, Genomes, Genetics</i> , 2017 , 7, 3775-3787	3.2	6
18	Flavonoid supplementation affects the expression of genes involved in cell wall formation and lignification metabolism and increases sugar content and saccharification in the fast-growing eucalyptus hybrid <i>E. urophylla</i> x <i>E. grandis</i> . <i>BMC Plant Biology</i> , 2014 , 14, 301	5.3	6
17	Characterization of systemic genomic instability in budding yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 28221-28231	11.5	6
16	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021 , 22, 109	18.3	6
15	Unraveling the complex genome of <i>Saccharum spontaneum</i> using Polyploid Gene Assembler. <i>DNA Research</i> , 2019 , 26, 205-216	4.5	6

14	Atypical UV Photoproducts Induce Non-canonical Mutation Classes Associated with Driver Mutations in Melanoma. <i>Cell Reports</i> , 2020 , 33, 108401	10.6	4
13	Congenital Midline Cervical Cleft: First Report and Genetic Analysis of Two Related Patients. <i>Annals of Otolaryngology, Rhinology and Laryngology</i> , 2020 , 129, 653-656	2.1	4
12	Extreme physiology: Biomass and transcriptional profiling of three abandoned Agave cultivars. <i>Industrial Crops and Products</i> , 2021 , 172, 114043	5.9	4
11	Identification of a Locus in Mice that Regulates the Collateral Damage and Lethality of Virus Infection. <i>Cell Reports</i> , 2019 , 27, 1387-1396.e5	10.6	3
10	BK polyomavirus nephropathy with systemic viral spread: Whole genome sequencing data from a fatal case of BKPyV infection. <i>Transplant Infectious Disease</i> , 2020 , 22, e13269	2.7	3
9	Tn-Seq Analysis Identifies Genes Important for <i>Yersinia pestis</i> Adherence during Primary Pneumonic Plague. <i>MSphere</i> , 2020 , 5,	5	3
8	<i>Moniliophthora perniciosa</i> , the causal agent of witches broom disease of cacao, interferes with cytokinin metabolism during infection of Micro-Tom tomato and promotes symptom development. <i>New Phytologist</i> , 2021 , 231, 365-381	9.8	3
7	Mitotic systemic genomic instability in yeast		2
6	The Shu complex prevents mutagenesis and cytotoxicity of single-strand specific alkylation lesions. <i>ELife</i> , 2021 , 10,	8.9	1
5	Internode elongation in energy cane shows remarkable clues on lignocellulosic biomass biosynthesis in <i>Saccharum</i> hybrids.. <i>Gene</i> , 2022 , 146476	3.8	1
4	The fidelity of DNA replication, particularly on GC-rich templates, is reduced by defects of the Fe-S cluster in DNA polymerase β <i>Nucleic Acids Research</i> , 2021 , 49, 5623-5636	20.1	0
3	Repair of multiple simultaneous double-strand breaks causes bursts of genome-wide clustered hypermutation 2019 , 17, e3000464		
2	Repair of multiple simultaneous double-strand breaks causes bursts of genome-wide clustered hypermutation 2019 , 17, e3000464		
1	Repair of multiple simultaneous double-strand breaks causes bursts of genome-wide clustered hypermutation 2019 , 17, e3000464		