

Piotr A Mieczkowski

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.

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	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
120	The Shu complex prevents mutagenesis and cytotoxicity of single-strand specific alkylation lesions. <i>ELife</i> , 2021 , 10,	8.9	1
119	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021 , 39, 1115-1128	44.5	31
118	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
117	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
116	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
115	<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
114	Extreme physiology: Biomass and transcriptional profiling of three abandoned Agave cultivars. <i>Industrial Crops and Products</i> , 2021 , 172, 114043	5.9	4
113	Atypical UV Photoproducts Induce Non-canonical Mutation Classes Associated with Driver Mutations in Melanoma. <i>Cell Reports</i> , 2020 , 33, 108401	10.6	4
112	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
111	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
110	Mutation signatures specific to DNA alkylating agents in yeast and cancers. <i>Nucleic Acids Research</i> , 2020 , 48, 3692-3707	20.1	13
109	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
108	Tn-Seq Analysis Identifies Genes Important for <i>Yersinia pestis</i> Adherence during Primary Pneumonic Plague. <i>MSphere</i> , 2020 , 5,	5	3
107	Adaptation and selection shape clonal evolution of tumors during residual disease and recurrence. <i>Nature Communications</i> , 2020 , 11, 5017	17.4	9
106	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
105	Repair of multiple simultaneous double-strand breaks causes bursts of genome-wide clustered hypermutation. <i>PLoS Biology</i> , 2019 , 17, e3000464	9.7	19

104	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
103	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
102	Unraveling the complex genome of <i>Saccharum spontaneum</i> using Polyploid Gene Assembler. <i>DNA Research</i> , 2019 , 26, 205-216	4.5	6
101	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
100	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
99	Repair of multiple simultaneous double-strand breaks causes bursts of genome-wide clustered hypermutation 2019 , 17, e3000464		
98	Repair of multiple simultaneous double-strand breaks causes bursts of genome-wide clustered hypermutation 2019 , 17, e3000464		
97	Repair of multiple simultaneous double-strand breaks causes bursts of genome-wide clustered hypermutation 2019 , 17, e3000464		
96	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018 , 173, 305-320.e10	56.2	166
95	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018 , 33, 244-258.e10	24.3	150
94	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018 , 33, 721-735.e8	24.3	228
93	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018 , 33, 690-705.e9	24.3	277
92	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
91	A Case Study of Genomic Instability in an Industrial Strain of <i>G3: Genes, Genomes, Genetics</i> , 2018 , 8, 3703-3713	3.7	9
90	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
89	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
88	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017 , 31, 181-193	24.3	350
87	<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

86	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017 , 169, 1327-1341.e23	56.2	1125
85	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
84	APOBEC3B cytidine deaminase targets the non-transcribed strand of tRNA genes in yeast. <i>DNA Repair</i> , 2017 , 53, 4-14	4.3	23
83	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017 , 31, 411-423	24.3	210
82	Root microbiota drive direct integration of phosphate stress and immunity. <i>Nature</i> , 2017 , 543, 513-518	50.4	369
81	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
80	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017 , 32, 204-220.e15	24.3	391
79	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017 , 32, 185-203.e15	24.3	13896
78	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017 , 171, 950-965.e28	56.2	451
77	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
76	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
75	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
74	Essential Roles for Polymerase β -Mediated End Joining in the Repair of Chromosome Breaks. <i>Molecular Cell</i> , 2016 , 63, 662-673	17.6	135
73	APOBEC3A and APOBEC3B Preferentially Deaminate the Lagging Strand Template during DNA Replication. <i>Cell Reports</i> , 2016 , 14, 1273-1282	10.6	118
72	The Impact of Environmental and Endogenous Damage on Somatic Mutation Load in Human Skin Fibroblasts. <i>PLoS Genetics</i> , 2016 , 12, e1006385	6	55
71	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
70	Multiplex amplicon sequencing for microbe identification in community-based culture collections. <i>Scientific Reports</i> , 2016 , 6, 29543	4.9	26
69	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016 , 29, 723-736	24.3	324

68	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
67	<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
66	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
65	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
64	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
63	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
62	Cavitation Enhancing Nanodroplets Mediate Efficient DNA Fragmentation in a Bench Top Ultrasonic Water Bath. <i>PLoS ONE</i> , 2015 , 10, e0133014	3.7	18
61	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
60	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
59	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
58	Evidence for local regulatory control of escape from imprinted X chromosome inactivation. <i>Genetics</i> , 2014 , 197, 715-23	4	13
57	Heterogeneous polymerase fidelity and mismatch repair bias genome variation and composition. <i>Genome Research</i> , 2014 , 24, 1751-64	9.7	111
56	Antifungal drug resistance evoked via RNAi-dependent epimutations. <i>Nature</i> , 2014 , 513, 555-8	50.4	98
55	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
54	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
53	Break-induced replication is a source of mutation clusters underlying kataegis. <i>Cell Reports</i> , 2014 , 7, 1640-1648	12.1	121
52	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
51	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

50	Cryptococcus gattii 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
49	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	6	260
48	Unisexual reproduction drives meiotic recombination and phenotypic and karyotypic plasticity in <i>Cryptococcus neoformans</i> . <i>PLoS Genetics</i> , 2014 , 10, e1004849	6	46
47	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
46	fourSig: a method for determining chromosomal interactions in 4C-Seq data. <i>Nucleic Acids Research</i> , 2014 , 42, e68	20.1	32
45	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
44	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
43	Practical innovations for high-throughput amplicon sequencing. <i>Nature Methods</i> , 2013 , 10, 999-1002	21.6	461
42	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
41	Genomic insights into the atopic eczema-associated skin commensal yeast <i>Malassezia sympodialis</i> . <i>MBio</i> , 2013 , 4, e00572-12	7.8	89
40	Fragile DNA motifs trigger mutagenesis at distant chromosomal loci in <i>saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2013 , 9, e1003551	6	23
39	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
38	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
37	Site-specific silencing of regulatory elements as a mechanism of X inactivation. <i>Cell</i> , 2012 , 151, 951-63	56.2	141
36	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
35	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
34	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
33	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

32	Polyglutamine toxicity is controlled by prion composition and gene dosage in yeast. <i>PLoS Genetics</i> , 2012 , 8, e1002634	6	39
31	Chromatin architectures at fission yeast transcriptional promoters and replication origins. <i>Nucleic Acids Research</i> , 2012 , 40, 7176-89	20.1	32
30	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
29	MAP3K4/CBP-regulated H2B acetylation controls epithelial-mesenchymal transition in trophoblast stem cells. <i>Cell Stem Cell</i> , 2011 , 8, 525-37	18	84
28	Damage-induced localized hypermutability. <i>Cell Cycle</i> , 2011 , 10, 1073-85	4.7	34
27	Tup1 stabilizes promoter nucleosome positioning and occupancy at transcriptionally plastic genes. <i>Nucleic Acids Research</i> , 2011 , 39, 8803-19	20.1	33
26	A map of open chromatin in human pancreatic islets. <i>Nature Genetics</i> , 2010 , 42, 255-9	36.3	435
25	Nucleosome dynamics define transcriptional enhancers. <i>Nature Genetics</i> , 2010 , 42, 343-7	36.3	382
24	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
23	MapSplice: accurate mapping of RNA-seq reads for splice junction discovery. <i>Nucleic Acids Research</i> , 2010 , 38, e178	20.1	762
22	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
21	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
20	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
19	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
18	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
17	UVA generates pyrimidine dimers in DNA directly. <i>Biophysical Journal</i> , 2009 , 96, 1151-8	2.9	118
16	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
15	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

14	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
13	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
12	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
11	Nanoscale detection of ionizing radiation damage to DNA by atomic force microscopy. <i>Small</i> , 2008 , 4, 288-94	11	20
10	Detecting ultraviolet damage in single DNA molecules by atomic force microscopy. <i>Biophysical Journal</i> , 2007 , 93, 1758-67	2.9	45
9	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
8	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
7	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
6	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
5	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
4	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
3	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
2	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
1	Mitotic systemic genomic instability in yeast		2