

Piotr A Mieczkowski

List of Publications by Year in descending order

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Version: 2024-02-01

123
papers

19,215
citations

20797

60
h-index

17090

122
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135
all docs

135
docs citations

135
times ranked

34286
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive and Integrative Genomic Characterization of Hepatocellular Carcinoma. <i>Cell</i> , 2017, 169, 1327-1341.e23.	13.5	1,794
2	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	7.7	1,428
3	MapSplice: Accurate mapping of RNA-seq reads for splice junction discovery. <i>Nucleic Acids Research</i> , 2010, 38, e178-e178.	6.5	946
4	Practical innovations for high-throughput amplicon sequencing. <i>Nature Methods</i> , 2013, 10, 999-1002.	9.0	787
5	Comprehensive and Integrated Genomic Characterization of Adult Soft Tissue Sarcomas. <i>Cell</i> , 2017, 171, 950-965.e28.	13.5	738
6	Root microbiota drive direct integration of phosphate stress and immunity. <i>Nature</i> , 2017, 543, 513-518.	13.7	669
7	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	7.7	642
8	Comprehensive Molecular Characterization of Pheochromocytoma and Paraganglioma. <i>Cancer Cell</i> , 2017, 31, 181-193.	7.7	532
9	A map of open chromatin in human pancreatic islets. <i>Nature Genetics</i> , 2010, 42, 255-259.	9.4	515
10	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, 1398-1403.	3.3	494
11	Comprehensive Pan-Genomic Characterization of Adrenocortical Carcinoma. <i>Cancer Cell</i> , 2016, 29, 723-736.	7.7	482
12	A Comprehensive Pan-Cancer Molecular Study of Gynecologic and Breast Cancers. <i>Cancer Cell</i> , 2018, 33, 690-705.e9.	7.7	478
13	Nucleosome dynamics define transcriptional enhancers. <i>Nature Genetics</i> , 2010, 42, 343-347.	9.4	426
14	Comparative Molecular Analysis of Gastrointestinal Adenocarcinomas. <i>Cancer Cell</i> , 2018, 33, 721-735.e8.	7.7	396
15	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
16	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
17	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.	1.5	336
18	Integrated Molecular Characterization of Uterine Carcinosarcoma. <i>Cancer Cell</i> , 2017, 31, 411-423.	7.7	309

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19	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	13.5	272
20	The Integrated Genomic Landscape of Thymic Epithelial Tumors. <i>Cancer Cell</i> , 2018, 33, 244-258.e10.	7.7	270
21	Genome structure of a <i>Saccharomyces cerevisiae</i> strain widely used in bioethanol production. <i>Genome Research</i> , 2009, 19, 2258-2270.	2.4	237
22	Essential Roles for Polymerase λ -Mediated End Joining in the Repair of Chromosome Breaks. <i>Molecular Cell</i> , 2016, 63, 662-673.	4.5	229
23	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, 11845-11850.	3.3	216
24	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.	1.5	198
25	Site-Specific Silencing of Regulatory Elements as a Mechanism of X Inactivation. <i>Cell</i> , 2012, 151, 951-963.	13.5	176
26	APOBEC3A and APOBEC3B Preferentially Deaminate the Lagging Strand Template during DNA Replication. <i>Cell Reports</i> , 2016, 14, 1273-1282.	2.9	173
27	Tracking replication enzymology in vivo by genome-wide mapping of ribonucleotide incorporation. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 185-191.	3.6	167
28	Antifungal drug resistance evoked via RNAi-dependent epimutations. <i>Nature</i> , 2014, 513, 555-558.	13.7	147
29	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.	2.6	145
30	The Pattern of Gene Amplification Is Determined by the Chromosomal Location of Hairpin-Capped Breaks. <i>Cell</i> , 2006, 125, 1283-1296.	13.5	144
31	Break-Induced Replication Is a Source of Mutation Clusters Underlying Kataegis. <i>Cell Reports</i> , 2014, 7, 1640-1648.	2.9	143
32	Heterogeneous polymerase fidelity and mismatch repair bias genome variation and composition. <i>Genome Research</i> , 2014, 24, 1751-1764.	2.4	141
33	Clinical Sequencing Exploratory Research Consortium: Accelerating Evidence-Based Practice of Genomic Medicine. <i>American Journal of Human Genetics</i> , 2016, 98, 1051-1066.	2.6	137
34	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.	2.9	134
35	Gene expression divergence in yeast is coupled to evolution of DNA-encoded nucleosome organization. <i>Nature Genetics</i> , 2009, 41, 438-445.	9.4	132
36	UVA Generates Pyrimidine Dimers in DNA Directly. <i>Biophysical Journal</i> , 2009, 96, 1151-1158.	0.2	132

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37	Recombination between retrotransposons as a source of chromosome rearrangements in the yeast <i>Saccharomyces cerevisiae</i> . <i>DNA Repair</i> , 2006, 5, 1010-1020.	1.3	129
38	Evaluating the analytical validity of circulating tumor DNA sequencing assays for precision oncology. <i>Nature Biotechnology</i> , 2021, 39, 1115-1128.	9.4	126
39	Genomic Insights into the Atopic Eczema-Associated Skin Commensal Yeast <i>Malassezia sympodialis</i> . <i>MBio</i> , 2013, 4, e00572-12.	1.8	118
40	<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.	5.1	115
41	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, 8540-8555.	1.5	111
42	The Genome Sequence of <i>Leishmania (Leishmania) amazonensis</i> : Functional Annotation and Extended Analysis of Gene Models. <i>DNA Research</i> , 2013, 20, 567-581.	1.5	109
43	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.	1.2	107
44	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.	1.8	106
45	MAP3K4/CBP-Regulated H2B Acetylation Controls Epithelial-Mesenchymal Transition in Trophoblast Stem Cells. <i>Cell Stem Cell</i> , 2011, 8, 525-537.	5.2	102
46	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, 4245-4269.	3.1	99
47	Chromosome fragility at GAA tracts in yeast depends on repeat orientation and requires mismatch repair. <i>EMBO Journal</i> , 2008, 27, 2896-2906.	3.5	98
48	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, 10854-10859.	3.3	92
49	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.	1.5	90
50	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, 17674-17679.	3.3	88
51	<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.	2.1	85
52	Genome-wide maps of alkylation damage, repair, and mutagenesis in yeast reveal mechanisms of mutational heterogeneity. <i>Genome Research</i> , 2017, 27, 1674-1684.	2.4	83
53	The Impact of Environmental and Endogenous Damage on Somatic Mutation Load in Human Skin Fibroblasts. <i>PLoS Genetics</i> , 2016, 12, e1006385.	1.5	82
54	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.	1.8	81

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55	Specific modulation of the root immune system by a community of commensal bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	81
56	The oncogenic potential of BK polyomavirus is linked to viral integration into the human genome. Journal of Pathology, 2015, 237, 379-389.	2.1	78
57	Intercellular Communication between Airway Epithelial Cells Is Mediated by Exosome-Like Vesicles. American Journal of Respiratory Cell and Molecular Biology, 2019, 60, 209-220.	1.4	78
58	Gene Copy-Number Variation in Haploid and Diploid Strains of the Yeast <i>Saccharomyces cerevisiae</i> . Genetics, 2013, 193, 785-801.	1.2	73
59	Loss of a histone deacetylase dramatically alters the genomic distribution of Spo11p-catalyzed DNA breaks in <i>Saccharomyces cerevisiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3955-3960.	3.3	72
60	High-Resolution Genome-Wide Analysis of Irradiated (UV and β -Rays) Diploid Yeast Cells Reveals a High Frequency of Genomic Loss of Heterozygosity (LOH) Events. Genetics, 2012, 190, 1267-1284.	1.2	71
61	Unisexual Reproduction Drives Meiotic Recombination and Phenotypic and Karyotypic Plasticity in <i>Cryptococcus neoformans</i> . PLoS Genetics, 2014, 10, e1004849.	1.5	71
62	The fidelity of the ligation step determines how ends are resolved during nonhomologous end joining. Nature Communications, 2014, 5, 4286.	5.8	69
63	Dengue type 1 viruses circulating in humans are highly infectious and poorly neutralized by human antibodies. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 227-232.	3.3	69
64	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> . Molecular and Cellular Biology, 2006, 26, 1014-1027.	1.1	64
65	Essential role for polymerase specialization in cellular nonhomologous end joining. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E4537-45.	3.3	61
66	Multiplex amplicon sequencing for microbe identification in community-based culture collections. Scientific Reports, 2016, 6, 29543.	1.6	57
67	Detecting Ultraviolet Damage in Single DNA Molecules by Atomic Force Microscopy. Biophysical Journal, 2007, 93, 1758-1767.	0.2	53
68	<i>Saccharomyces cerevisiae</i> transcriptional reprogramming due to bacterial contamination during industrial scale bioethanol production. Microbial Cell Factories, 2015, 14, 13.	1.9	51
69	Global analysis of genomic instability caused by DNA replication stress in <i>Saccharomyces cerevisiae</i> . Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E8114-E8121.	3.3	50
70	The Compact Chromatin Structure of a Ty Repeated Sequence Suppresses Recombination Hotspot Activity in <i>Saccharomyces cerevisiae</i> . Molecular Cell, 2004, 15, 221-231.	4.5	48
71	Polyglutamine Toxicity Is Controlled by Prion Composition and Gene Dosage in Yeast. PLoS Genetics, 2012, 8, e1002634.	1.5	45
72	The Product of the DNA Damage-Inducible Gene of <i>Saccharomyces cerevisiae</i> , DIN7, Specifically Functions in Mitochondria. Genetics, 2000, 154, 73-81.	1.2	43

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73	Top1 stabilizes promoter nucleosome positioning and occupancy at transcriptionally plastic genes. <i>Nucleic Acids Research</i> , 2011, 39, 8803-8819.	6.5	42
74	fourSig: a method for determining chromosomal interactions in 4C-Seq data. <i>Nucleic Acids Research</i> , 2014, 42, e68-e68.	6.5	42
75	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, 1298-1308.	1.3	41
76	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, 5432-5445.	1.1	41
77	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.	1.1	39
78	Damage-induced localized hypermutability. <i>Cell Cycle</i> , 2011, 10, 1073-1085.	1.3	38
79	Assessing serotonin receptor mRNA editing frequency by a novel ultra high-throughput sequencing method. <i>Nucleic Acids Research</i> , 2010, 38, e118-e118.	6.5	37
80	APOBEC3B cytidine deaminase targets the non-transcribed strand of tRNA genes in yeast. <i>DNA Repair</i> , 2017, 53, 4-14.	1.3	37
81	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.	1.1	36
82	Repair of multiple simultaneous double-strand breaks causes bursts of genome-wide clustered hypermutation. <i>PLoS Biology</i> , 2019, 17, e3000464.	2.6	35
83	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.	0.8	34
84	Chromatin architectures at fission yeast transcriptional promoters and replication origins. <i>Nucleic Acids Research</i> , 2012, 40, 7176-7189.	6.5	34
85	Mutation signatures specific to DNA alkylating agents in yeast and cancers. <i>Nucleic Acids Research</i> , 2020, 48, 3692-3707.	6.5	32
86	Cavitation Enhancing Nanodroplets Mediate Efficient DNA Fragmentation in a Bench Top Ultrasonic Water Bath. <i>PLoS ONE</i> , 2015, 10, e0133014.	1.1	30
87	The mitochondrial genome of <i>Moniliophthora roreri</i> , the frosty pod rot pathogen of cacao. <i>Fungal Biology</i> , 2012, 116, 551-562.	1.1	29
88	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.	2.9	29
89	Long transposon-rich centromeres in an oomycete reveal divergence of centromere features in <i>Stramenopila-Alveolata-Rhizaria</i> lineages. <i>PLoS Genetics</i> , 2020, 16, e1008646.	1.5	29
90	Xylem transcription profiles indicate potential metabolic responses for economically relevant characteristics of <i>Eucalyptus</i> species. <i>BMC Genomics</i> , 2013, 14, 201.	1.2	28

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91	Fragile DNA Motifs Trigger Mutagenesis at Distant Chromosomal Loci in <i>Saccharomyces cerevisiae</i> . <i>PLoS Genetics</i> , 2013, 9, e1003551.	1.5	28
92	Adaptation and selection shape clonal evolution of tumors during residual disease and recurrence. <i>Nature Communications</i> , 2020, 11, 5017.	5.8	28
93	Repair of base damage within break-induced replication intermediates promotes kataegis associated with chromosome rearrangements. <i>Nucleic Acids Research</i> , 2019, 47, 9666-9684.	6.5	27
94	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.	1.5	26
95	Nanoscale Detection of Ionizing Radiation Damage to DNA by Atomic Force Microscopy. <i>Small</i> , 2008, 4, 288-294.	5.2	22
96	Evidence for Local Regulatory Control of Escape from Imprinted X Chromosome Inactivation. <i>Genetics</i> , 2014, 197, 715-723.	1.2	21
97	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.	3.3	20
98	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. <i>Genome Biology</i> , 2021, 22, 109.	3.8	20
99	A Case Study of Genomic Instability in an Industrial Strain of <i>Saccharomyces cerevisiae</i> . <i>G3: Genes, Genomes, Genetics</i> , 2018, 8, 3703-3713.	0.8	19
100	Extreme physiology: Biomass and transcriptional profiling of three abandoned Agave cultivars. <i>Industrial Crops and Products</i> , 2021, 172, 114043.	2.5	16
101	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, 53-59.	0.8	15
102	The two-faced nature of BK polyomavirus: lytic infection or non-cytotoxic large T-antigen-positive carcinoma. <i>Journal of Pathology</i> , 2018, 246, 7-11.	2.1	15
103	A native and an invasive dune grass share similar, patchily distributed, root-associated fungal communities. <i>Fungal Ecology</i> , 2016, 23, 141-155.	0.7	14
104	Atypical UV Photoproducts Induce Non-canonical Mutation Classes Associated with Driver Mutations in Melanoma. <i>Cell Reports</i> , 2020, 33, 108401.	2.9	14
105	Separating DNA with Different Topologies by Atomic Force Microscopy in Comparison with Gel Electrophoresis. <i>Journal of Physical Chemistry B</i> , 2010, 114, 12162-12165.	1.2	12
106	Acetaldehyde makes a distinct mutation signature in single-stranded DNA. <i>Nucleic Acids Research</i> , 2022, 50, 7451-7464.	6.5	10
107	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.	1.6	8
108	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.	4.2	8

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109	Whole Genome Sequence Analysis of Mutations Accumulated in rad27 ^Δ Yeast Strains with Defects in the Processing of Okazaki Fragments Indicates Template-Switching Events. <i>G3: Genes, Genomes, Genetics</i> , 2017, 7, 3775-3787.	0.8	8
110	Unraveling the complex genome of <i>Saccharum spontaneum</i> using Polyploid Gene Assembler. <i>DNA Research</i> , 2019, 26, 205-216.	1.5	8
111	Tn-Seq Analysis Identifies Genes Important for <i>Yersinia pestis</i> Adherence during Primary Pneumonic Plague. <i>MSphere</i> , 2020, 5, .	1.3	8
112	<i>Monilophthora perniciosa</i> , the causal agent of witches' broom disease of cacao, interferes with cytokinin metabolism during infection of <i>Microtom</i> tomato and promotes symptom development. <i>New Phytologist</i> , 2021, 231, 365-381.	3.5	7
113	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.	0.7	6
114	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.	2.9	5
115	Congenital Midline Cervical Cleft: First Report and Genetic Analysis of Two Related Patients. <i>Annals of Otology, Rhinology and Laryngology</i> , 2020, 129, 653-656.	0.6	5
116	The Sisal Virome: Uncovering the Viral Diversity of Agave Varieties Reveals New and Organ-Specific Viruses. <i>Microorganisms</i> , 2021, 9, 1704.	1.6	5
117	The fidelity of DNA replication, particularly on GC-rich templates, is reduced by defects of the Fe ²⁺ cluster in DNA polymerase β . <i>Nucleic Acids Research</i> , 2021, 49, 5623-5636.	6.5	3
118	The Shu complex prevents mutagenesis and cytotoxicity of single-strand specific alkylation lesions. <i>ELife</i> , 2021, 10, .	2.8	3
119	Internode elongation in energy cane shows remarkable clues on lignocellulosic biomass biosynthesis in <i>Saccharum</i> hybrids. <i>Gene</i> , 2022, 828, 146476.	1.0	3
120	Noninvasive prenatal exome sequencing diagnostic utility limited by sequencing depth and fetal fraction. <i>Prenatal Diagnosis</i> , 2021, , .	1.1	2
121	Title is missing!. , 2019, 17, e3000464.		0
122	Title is missing!. , 2019, 17, e3000464.		0
123	Title is missing!. , 2019, 17, e3000464.		0