

Marcin Imielinski

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

30,634
citations

66234

42
h-index

138251

58
g-index

74
all docs

74
docs citations

74
times ranked

50355
citing authors

#	ARTICLE	IF	CITATIONS
1	System-wide transcriptome damage and tissue identity loss in COVID-19 patients. <i>Cell Reports Medicine</i> , 2022, 3, 100522.	3.3	24
2	Abstract P2-06-04: Pathognomonic long molecule footprints of backup repair pathways in homologous recombination deficient cancers. <i>Cancer Research</i> , 2022, 82, P2-06-04-P2-06-04.	0.4	0
3	SETD2 Haploinsufficiency Enhances Germinal Center-Associated AICDA Somatic Hypermutation to Drive B-cell Lymphomagenesis. <i>Cancer Discovery</i> , 2022, 12, 1782-1803.	7.7	14
4	Somatic whole genome dynamics of precancer in Barrett's esophagus reveals features associated with disease progression. <i>Nature Communications</i> , 2022, 13, 2300.	5.8	13
5	Identifying synergistic high-order 3D chromatin conformations from genome-scale nanopore concatemer sequencing. <i>Nature Biotechnology</i> , 2022, 40, 1488-1499.	9.4	46
6	Recurrent somatic mutations as predictors of immunotherapy response. <i>Nature Communications</i> , 2022, 13, .	5.8	12
7	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. <i>Nature</i> , 2021, 589, 299-305.	13.7	155
8	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021, 34, 108707.	2.9	16
9	Editorial overview: The most difficult of years in cancer research. <i>Current Opinion in Genetics and Development</i> , 2021, 66, iii-iv.	1.5	0
10	A Genomic-Pathologic Annotated Risk Model to Predict Recurrence in Early-Stage Lung Adenocarcinoma. <i>JAMA Surgery</i> , 2021, 156, e205601.	2.2	52
11	Shotgun transcriptome, spatial omics, and isothermal profiling of SARS-CoV-2 infection reveals unique host responses, viral diversification, and drug interactions. <i>Nature Communications</i> , 2021, 12, 1660.	5.8	132
12	Integrated mutational landscape analysis of uterine leiomyosarcomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	48
13	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021, 184, 2239-2254.e39.	13.5	260
14	Structural variant evolution after telomere crisis. <i>Nature Communications</i> , 2021, 12, 2093.	5.8	16
15	Discovery of Candidate DNA Methylation Cancer Driver Genes. <i>Cancer Discovery</i> , 2021, 11, 2266-2281.	7.7	42
16	Molecular Evolution of Classical Hodgkin Lymphoma Revealed Through Whole Genome Sequencing of Hodgkin and Reed-Sternberg Cells. <i>Blood</i> , 2021, 138, 805-805.	0.6	1
17	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. <i>Cell</i> , 2020, 183, 197-210.e32.	13.5	141
18	Impact of Lineage Plasticity to and from a Neuroendocrine Phenotype on Progression and Response in Prostate and Lung Cancers. <i>Molecular Cell</i> , 2020, 80, 562-577.	4.5	54

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19	The evolutionary history of 2,658 cancers. <i>Nature</i> , 2020, 578, 122-128.	13.7	690
20	Patterns of somatic structural variation in human cancer genomes. <i>Nature</i> , 2020, 578, 112-121.	13.7	560
21	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	13.7	424
22	Robust Discovery of Candidate DNA Methylation Cancer Drivers. <i>Blood</i> , 2020, 136, 33-34.	0.6	0
23	Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , 2019, 569, 503-508.	13.7	2,149
24	Deep Convolutional Neural Networks Enable Discrimination of Heterogeneous Digital Pathology Images. <i>EBioMedicine</i> , 2018, 27, 317-328.	2.7	240
25	SvABA: genome-wide detection of structural variants and indels by local assembly. <i>Genome Research</i> , 2018, 28, 581-591.	2.4	288
26	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	6.0	781
27	Fusion oncogenes as "genetic musical chairs". <i>Science</i> , 2018, 361, 848-849.	6.0	4
28	Insertions and Deletions Target Lineage-Defining Genes in Human Cancers. <i>Cell</i> , 2017, 168, 460-472.e14.	13.5	106
29	Clinical hallmarks in whole cancer genomes. <i>Nature Reviews Clinical Oncology</i> , 2017, 14, 265-266.	12.5	1
30	Modeling cancer rearrangement landscapes. <i>Current Opinion in Systems Biology</i> , 2017, 1, 54-61.	1.3	17
31	The cancer precision medicine knowledge base for structured clinical-grade mutations and interpretations. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2017, 24, 513-519.	2.2	88
32	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016, 48, 607-616.	9.4	933
33	High-throughput Phenotyping of Lung Cancer Somatic Mutations. <i>Cancer Cell</i> , 2016, 30, 214-228.	7.7	171
34	Identification of focally amplified lineage-specific super-enhancers in human epithelial cancers. <i>Nature Genetics</i> , 2016, 48, 176-182.	9.4	283
35	A Pan-Cancer Analysis of Transcriptome Changes Associated with Somatic Mutations in U2AF1 Reveals Commonly Altered Splicing Events. <i>PLoS ONE</i> , 2014, 9, e87361.	1.1	168
36	Genetic modifiers of EGFR dependence in non-small cell lung cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 18661-18666.	3.3	46

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37	Oncogenic and sorafenib-sensitive ARAF mutations in lung adenocarcinoma. <i>Journal of Clinical Investigation</i> , 2014, 124, 1582-1586.	3.9	101
38	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013, 500, 415-421.	13.7	8,060
39	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , 2013, 499, 214-218.	13.7	4,761
40	Functional analysis of receptor tyrosine kinase mutations in lung cancer identifies oncogenic extracellular domain mutations of <i>ERBB2</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 14476-14481.	3.3	246
41	Mapping the Hallmarks of Lung Adenocarcinoma with Massively Parallel Sequencing. <i>Cell</i> , 2012, 150, 1107-1120.	13.5	1,591
42	A Landscape of Driver Mutations in Melanoma. <i>Cell</i> , 2012, 150, 251-263.	13.5	2,247
43	A Genome-Wide Meta-Analysis of Six Type 1 Diabetes Cohorts Identifies Multiple Associated Loci. <i>PLoS Genetics</i> , 2011, 7, e1002293.	1.5	297
44	Duplication of the <i>SLIT3</i> Locus on 5q35.1 Predisposes to Major Depressive Disorder. <i>PLoS ONE</i> , 2010, 5, e15463.	1.1	63
45	Comparative genetic analysis of inflammatory bowel disease and type 1 diabetes implicates multiple loci with opposite effects. <i>Human Molecular Genetics</i> , 2010, 19, 2059-2067.	1.4	157
46	Strong synaptic transmission impact by copy number variations in schizophrenia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 10584-10589.	3.3	212
47	Breaking new ground in inflammatory bowel disease genetics: genome-wide association studies and beyond. <i>Pharmacogenomics</i> , 2010, 11, 663-665.	0.6	6
48	Variants of <i>DENND1B</i> Associated with Asthma in Children. <i>New England Journal of Medicine</i> , 2010, 362, 36-44.	13.9	306
49	Follow-Up Analysis of Genome-Wide Association Data Identifies Novel Loci for Type 1 Diabetes. <i>Diabetes</i> , 2009, 58, 290-295.	0.3	136
50	High-resolution mapping and analysis of copy number variations in the human genome: A data resource for clinical and research applications. <i>Genome Research</i> , 2009, 19, 1682-1690.	2.4	313
51	Genome-Wide Analyses of Exonic Copy Number Variants in a Family-Based Study Point to Novel Autism Susceptibility Genes. <i>PLoS Genetics</i> , 2009, 5, e1000536.	1.5	374
52	Autism genome-wide copy number variation reveals ubiquitin and neuronal genes. <i>Nature</i> , 2009, 459, 569-573.	13.7	1,270
53	Common genetic variants on 5p14.1 associate with autism spectrum disorders. <i>Nature</i> , 2009, 459, 528-533.	13.7	912
54	Common variants at five new loci associated with early-onset inflammatory bowel disease. <i>Nature Genetics</i> , 2009, 41, 1335-1340.	9.4	459

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55	Diverse Genome-wide Association Studies Associate the IL12/IL23 Pathway with Crohn Disease. <i>American Journal of Human Genetics</i> , 2009, 84, 399-405.	2.6	246
56	17q12-21 variants interact with smoke exposure as a risk factor for pediatric asthma but are equally associated with early-onset versus late-onset asthma in North Americans of European ancestry. <i>Journal of Allergy and Clinical Immunology</i> , 2009, 124, 605-607.	1.5	68
57	Loci on 20q13 and 21q22 are associated with pediatric-onset inflammatory bowel disease. <i>Nature Genetics</i> , 2008, 40, 1211-1215.	9.4	310
58	ORMDL3 variants associated with asthma susceptibility in North Americans of European ancestry. <i>Journal of Allergy and Clinical Immunology</i> , 2008, 122, 1225-1227.	1.5	89
59	Association Analysis of the FTO Gene with Obesity in Children of Caucasian and African Ancestry Reveals a Common Tagging SNP. <i>PLoS ONE</i> , 2008, 3, e1746.	1.1	176
60	Association of the BANK1 R61H variant with systemic lupus erythematosus in Americans of European and African ancestry. <i>The Application of Clinical Genetics</i> , 2008, Volume 2, 1-5.	1.4	8
61	Systematic Analysis of Conservation Relations in Escherichia coli Genome-Scale Metabolic Network Reveals Novel Growth Media. <i>Biophysical Journal</i> , 2006, 90, 2659-2672.	0.2	43