

Marcin Imielinski

List of Publications by Year in descending order

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Version: 2024-02-01

61
papers

30,634
citations

66343

42
h-index

138484

58
g-index

74
all docs

74
docs citations

74
times ranked

50355
citing authors

#	ARTICLE	IF	CITATIONS
1	Signatures of mutational processes in human cancer. <i>Nature</i> , 2013, 500, 415-421.	27.8	8,060
2	Mutational heterogeneity in cancer and the search for new cancer-associated genes. <i>Nature</i> , 2013, 499, 214-218.	27.8	4,761
3	A Landscape of Driver Mutations in Melanoma. <i>Cell</i> , 2012, 150, 251-263.	28.9	2,247
4	Next-generation characterization of the Cancer Cell Line Encyclopedia. <i>Nature</i> , 2019, 569, 503-508.	27.8	2,149
5	Mapping the Hallmarks of Lung Adenocarcinoma with Massively Parallel Sequencing. <i>Cell</i> , 2012, 150, 1107-1120.	28.9	1,591
6	Autism genome-wide copy number variation reveals ubiquitin and neuronal genes. <i>Nature</i> , 2009, 459, 569-573.	27.8	1,270
7	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. <i>Nature Genetics</i> , 2016, 48, 607-616.	21.4	933
8	Common genetic variants on 5p14.1 associate with autism spectrum disorders. <i>Nature</i> , 2009, 459, 528-533.	27.8	912
9	The chromatin accessibility landscape of primary human cancers. <i>Science</i> , 2018, 362, .	12.6	781
10	The evolutionary history of 2,658 cancers. <i>Nature</i> , 2020, 578, 122-128.	27.8	690
11	Patterns of somatic structural variation in human cancer genomes. <i>Nature</i> , 2020, 578, 112-121.	27.8	560
12	Common variants at five new loci associated with early-onset inflammatory bowel disease. <i>Nature Genetics</i> , 2009, 41, 1335-1340.	21.4	459
13	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	27.8	424
14	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.	3.5	374
15	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.	5.5	313
16	Loci on 20q13 and 21q22 are associated with pediatric-onset inflammatory bowel disease. <i>Nature Genetics</i> , 2008, 40, 1211-1215.	21.4	310
17	Variants of <i>DENND1B</i> Associated with Asthma in Children. <i>New England Journal of Medicine</i> , 2010, 362, 36-44.	27.0	306
18	A Genome-Wide Meta-Analysis of Six Type 1 Diabetes Cohorts Identifies Multiple Associated Loci. <i>PLoS Genetics</i> , 2011, 7, e1002293.	3.5	297

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19	SvABA: genome-wide detection of structural variants and indels by local assembly. <i>Genome Research</i> , 2018, 28, 581-591.	5.5	288
20	Identification of focally amplified lineage-specific super-enhancers in human epithelial cancers. <i>Nature Genetics</i> , 2016, 48, 176-182.	21.4	283
21	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021, 184, 2239-2254.e39.	28.9	260
22	Diverse Genome-wide Association Studies Associate the IL12/IL23 Pathway with Crohn Disease. <i>American Journal of Human Genetics</i> , 2009, 84, 399-405.	6.2	246
23	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.	7.1	246
24	Deep Convolutional Neural Networks Enable Discrimination of Heterogeneous Digital Pathology Images. <i>EBioMedicine</i> , 2018, 27, 317-328.	6.1	240
25	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.	7.1	212
26	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.	2.5	176
27	High-throughput Phenotyping of Lung Cancer Somatic Mutations. <i>Cancer Cell</i> , 2016, 30, 214-228.	16.8	171
28	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.	2.5	168
29	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.	2.9	157
30	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. <i>Nature</i> , 2021, 589, 299-305.	27.8	155
31	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. <i>Cell</i> , 2020, 183, 197-210.e32.	28.9	141
32	Follow-Up Analysis of Genome-Wide Association Data Identifies Novel Loci for Type 1 Diabetes. <i>Diabetes</i> , 2009, 58, 290-295.	0.6	136
33	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.	12.8	132
34	Insertions and Deletions Target Lineage-Defining Genes in Human Cancers. <i>Cell</i> , 2017, 168, 460-472.e14.	28.9	106
35	Oncogenic and sorafenib-sensitive ARAF mutations in lung adenocarcinoma. <i>Journal of Clinical Investigation</i> , 2014, 124, 1582-1586.	8.2	101
36	ORMDL3 variants associated with asthma susceptibility in North Americans of European ancestry. <i>Journal of Allergy and Clinical Immunology</i> , 2008, 122, 1225-1227.	2.9	89

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37	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.	4.4	88
38	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.	2.9	68
39	Duplication of the SLIT3 Locus on 5q35.1 Predisposes to Major Depressive Disorder. <i>PLoS ONE</i> , 2010, 5, e15463.	2.5	63
40	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.	9.7	54
41	A Genomic-Pathologic Annotated Risk Model to Predict Recurrence in Early-Stage Lung Adenocarcinoma. <i>JAMA Surgery</i> , 2021, 156, e205601.	4.3	52
42	Integrated mutational landscape analysis of uterine leiomyosarcomas. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	48
43	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.	7.1	46
44	Identifying synergistic high-order 3D chromatin conformations from genome-scale nanopore concatemer sequencing. <i>Nature Biotechnology</i> , 2022, 40, 1488-1499.	17.5	46
45	Systematic Analysis of Conservation Relations in Escherichia coli Genome-Scale Metabolic Network Reveals Novel Growth Media. <i>Biophysical Journal</i> , 2006, 90, 2659-2672.	0.5	43
46	Discovery of Candidate DNA Methylation Cancer Driver Genes. <i>Cancer Discovery</i> , 2021, 11, 2266-2281.	9.4	42
47	System-wide transcriptome damage and tissue identity loss in COVID-19 patients. <i>Cell Reports Medicine</i> , 2022, 3, 100522.	6.5	24
48	Modeling cancer rearrangement landscapes. <i>Current Opinion in Systems Biology</i> , 2017, 1, 54-61.	2.6	17
49	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. <i>Cell Reports</i> , 2021, 34, 108707.	6.4	16
50	Structural variant evolution after telomere crisis. <i>Nature Communications</i> , 2021, 12, 2093.	12.8	16
51	SETD2 Haploinsufficiency Enhances Germinal Center-Associated AICDA Somatic Hypermutation to Drive B-cell Lymphomagenesis. <i>Cancer Discovery</i> , 2022, 12, 1782-1803.	9.4	14
52	Somatic whole genome dynamics of precancer in Barrett's esophagus reveals features associated with disease progression. <i>Nature Communications</i> , 2022, 13, 2300.	12.8	13
53	Recurrent somatic mutations as predictors of immunotherapy response. <i>Nature Communications</i> , 2022, 13, .	12.8	12
54	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.	3.0	8

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55	Breaking new ground in inflammatory bowel disease genetics: genome-wide association studies and beyond. <i>Pharmacogenomics</i> , 2010, 11, 663-665.	1.3	6
56	Fusion oncogenesâ€™ genetic musical chairs. <i>Science</i> , 2018, 361, 848-849.	12.6	4
57	Clinical hallmarks in whole cancer genomes. <i>Nature Reviews Clinical Oncology</i> , 2017, 14, 265-266.	27.6	1
58	Molecular Evolution of Classical Hodgkin Lymphoma Revealed Through Whole Genome Sequencing of Hodgkin and Reed-Sternberg Cells. <i>Blood</i> , 2021, 138, 805-805.	1.4	1
59	Editorial overview: The most difficult of years in cancer research. <i>Current Opinion in Genetics and Development</i> , 2021, 66, iii-iv.	3.3	0
60	Robust Discovery of Candidate DNA Methylation Cancer Drivers. <i>Blood</i> , 2020, 136, 33-34.	1.4	0
61	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.	0.9	0