Marcin Imielinski

List of Publications by Year
in descending order

Source: https://exaly.com/author-pdf/3454272/publications.pdf

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61	30,634	66234	138251
papers	citations	42 h-index	58 g-index

74	74	74	50355
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Signatures of mutational processes in human cancer. Nature, 2013, 500, 415-421.	13.7	8,060
2	Mutational heterogeneity in cancer and the search for new cancer-associated genes. Nature, 2013, 499, 214-218.	13.7	4,761
3	A Landscape of Driver Mutations in Melanoma. Cell, 2012, 150, 251-263.	13.5	2,247
4	Next-generation characterization of the Cancer Cell Line Encyclopedia. Nature, 2019, 569, 503-508.	13.7	2,149
5	Mapping the Hallmarks of Lung Adenocarcinoma with Massively Parallel Sequencing. Cell, 2012, 150, 1107-1120.	13.5	1,591
6	Autism genome-wide copy number variation reveals ubiquitin and neuronal genes. Nature, 2009, 459, 569-573.	13.7	1,270
7	Distinct patterns of somatic genome alterations in lung adenocarcinomas and squamous cell carcinomas. Nature Genetics, 2016, 48, 607-616.	9.4	933
8	Common genetic variants on 5p14.1 associate with autism spectrum disorders. Nature, 2009, 459, 528-533.	13.7	912
9	The chromatin accessibility landscape of primary human cancers. Science, 2018, 362, .	6.0	781
10	The evolutionary history of 2,658 cancers. Nature, 2020, 578, 122-128.	13.7	690
11	Patterns of somatic structural variation in human cancer genomes. Nature, 2020, 578, 112-121.	13.7	560
12	Common variants at five new loci associated with early-onset inflammatory bowel disease. Nature Genetics, 2009, 41, 1335-1340.	9.4	459
13	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
14	Genome-Wide Analyses of Exonic Copy Number Variants in a Family-Based Study Point to Novel Autism Susceptibility Genes. PLoS Genetics, 2009, 5, e1000536.	1.5	374
15	High-resolution mapping and analysis of copy number variations in the human genome: A data resource for clinical and research applications. Genome Research, 2009, 19, 1682-1690.	2.4	313
16	Loci on 20q13 and 21q22 are associated with pediatric-onset inflammatory bowel disease. Nature Genetics, 2008, 40, 1211-1215.	9.4	310
17	Variants ofDENND1BAssociated with Asthma in Children. New England Journal of Medicine, 2010, 362, 36-44.	13.9	306
18	A Genome-Wide Meta-Analysis of Six Type 1 Diabetes Cohorts Identifies Multiple Associated Loci. PLoS Genetics, 2011, 7, e1002293.	1.5	297

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19	SvABA: genome-wide detection of structural variants and indels by local assembly. Genome Research, 2018, 28, 581-591.	2.4	288
20	Identification of focally amplified lineage-specific super-enhancers in human epithelial cancers. Nature Genetics, 2016, 48, 176-182.	9.4	283
21	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	13.5	260
22	Diverse Genome-wide Association Studies Associate the IL12/IL23 Pathway with Crohn Disease. American Journal of Human Genetics, 2009, 84, 399-405.	2.6	246
23	Functional analysis of receptor tyrosine kinase mutations in lung cancer identifies oncogenic extracellular domain mutations of ERBB2. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 14476-14481.	3.3	246
24	Deep Convolutional Neural Networks Enable Discrimination of Heterogeneous Digital Pathology Images. EBioMedicine, 2018, 27, 317-328.	2.7	240
25	Strong synaptic transmission impact by copy number variations in schizophrenia. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 10584-10589.	3.3	212
26	Association Analysis of the FTO Gene with Obesity in Children of Caucasian and African Ancestry Reveals a Common Tagging SNP. PLoS ONE, 2008, 3, e1746.	1.1	176
27	High-throughput Phenotyping of Lung Cancer Somatic Mutations. Cancer Cell, 2016, 30, 214-228.	7.7	171
28	A Pan-Cancer Analysis of Transcriptome Changes Associated with Somatic Mutations in U2AF1 Reveals Commonly Altered Splicing Events. PLoS ONE, 2014, 9, e87361.	1.1	168
29	Comparative genetic analysis of inflammatory bowel disease and type 1 diabetes implicates multiple loci with opposite effects. Human Molecular Genetics, 2010, 19, 2059-2067.	1.4	157
30	Histone H1 loss drives lymphoma by disrupting 3D chromatin architecture. Nature, 2021, 589, 299-305.	13.7	155
31	Distinct Classes of Complex Structural Variation Uncovered across Thousands of Cancer Genome Graphs. Cell, 2020, 183, 197-210.e32.	13.5	141
32	Follow-Up Analysis of Genome-Wide Association Data Identifies Novel Loci for Type 1 Diabetes. Diabetes, 2009, 58, 290-295.	0.3	136
33	Shotgun transcriptome, spatial omics, and isothermal profiling of SARS-CoV-2 infection reveals unique host responses, viral diversification, and drug interactions. Nature Communications, 2021, 12, 1660.	5.8	132
34	Insertions and Deletions Target Lineage-Defining Genes in Human Cancers. Cell, 2017, 168, 460-472.e14.	13.5	106
35	Oncogenic and sorafenib-sensitive ARAF mutations in lung adenocarcinoma. Journal of Clinical Investigation, 2014, 124, 1582-1586.	3.9	101
36	ORMDL3 variants associated with asthma susceptibility in North Americans of European ancestry. Journal of Allergy and Clinical Immunology, 2008, 122, 1225-1227.	1.5	89

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37	The cancer precision medicine knowledge base for structured clinical-grade mutations and interpretations. Journal of the American Medical Informatics Association: JAMIA, 2017, 24, 513-519.	2.2	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. Journal of Allergy and Clinical Immunology, 2009, 124, 605-607.	1.5	68
39	Duplication of the SLIT3 Locus on 5q35.1 Predisposes to Major Depressive Disorder. PLoS ONE, 2010, 5, e15463.	1.1	63
40	Impact of Lineage Plasticity to and from a Neuroendocrine Phenotype on Progression and Response in Prostate and Lung Cancers. Molecular Cell, 2020, 80, 562-577.	4.5	54
41	A Genomic-Pathologic Annotated Risk Model to Predict Recurrence in Early-Stage Lung Adenocarcinoma. JAMA Surgery, 2021, 156, e205601.	2.2	52
42	Integrated mutational landscape analysis of uterine leiomyosarcomas. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	48
43	Genetic modifiers of EGFR dependence in non-small cell lung cancer. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 18661-18666.	3.3	46
44	Identifying synergistic high-order 3D chromatin conformations from genome-scale nanopore concatemer sequencing. Nature Biotechnology, 2022, 40, 1488-1499.	9.4	46
45	Systematic Analysis of Conservation Relations in Escherichia coli Genome-Scale Metabolic Network Reveals Novel Growth Media. Biophysical Journal, 2006, 90, 2659-2672.	0.2	43
46	Discovery of Candidate DNA Methylation Cancer Driver Genes. Cancer Discovery, 2021, 11, 2266-2281.	7.7	42
47	System-wide transcriptome damage and tissue identity loss in COVID-19 patients. Cell Reports Medicine, 2022, 3, 100522.	3.3	24
48	Modeling cancer rearrangement landscapes. Current Opinion in Systems Biology, 2017, 1, 54-61.	1.3	17
49	Whole-genome characterization of lung adenocarcinomas lacking alterations in the RTK/RAS/RAF pathway. Cell Reports, 2021, 34, 108707.	2.9	16
50	Structural variant evolution after telomere crisis. Nature Communications, 2021, 12, 2093.	5.8	16
51	SETD2 Haploinsufficiency Enhances Germinal Centerâ€“Associated AICDA Somatic Hypermutation to Drive B-cell Lymphomagenesis. Cancer Discovery, 2022, 12, 1782-1803.	7.7	14
52	Somatic whole genome dynamics of precancer in Barrettâ€™s esophagus reveals features associated with disease progression. Nature Communications, 2022, 13, 2300.	5.8	13
53	Recurrent somatic mutations as predictors of immunotherapy response. Nature Communications, 2022, 13, .	5.8	12
54	Association of the BANK1 R61H variant with systemic lupus erythematosus in Americans of European and African ancestry. The Application of Clinical Genetics, 2008, Volume 2, 1-5.	1.4	8

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55	Breaking new ground in inflammatory bowel disease genetics: genome-wide association studies and beyond. Pharmacogenomics, 2010, 11, 663-665.	0.6	6
56	Fusion oncogenesâ€”genetic musical chairs. Science, 2018, 361, 848-849.	6.0	4
57	Clinical hallmarks in whole cancer genomes. Nature Reviews Clinical Oncology, 2017, 14, 265-266.	12.5	1
58	Molecular Evolution of Classical Hodgkin Lymphoma Revealed Though Whole Genome Sequencing of Hodgkin and Reed-Sternberg Cells. Blood, 2021, 138, 805-805.	0.6	1
59	Editorial overview: The most difficult of years in cancer research. Current Opinion in Genetics and Development, 2021, 66, iii-iv.	1.5	0
60	Robust Discovery of Candidate DNA Methylation Cancer Drivers. Blood, 2020, 136, 33-34.	0.6	0
61	Abstract P2-06-04: Pathognomonic long molecule footprints of backup repair pathways in homologous recombination deficient cancers. Cancer Research, 2022, 82, P2-06-04-P2-06-04.	0.4	0