

Inigo Martincorena

List of Publications by Year in descending order

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Version: 2024-02-01

86
papers

23,830
citations

24978

57
h-index

60497

81
g-index

111
all docs

111
docs citations

111
times ranked

33561
citing authors

#	ARTICLE	IF	CITATIONS
1	Somatic mutation rates scale with lifespan across mammals. <i>Nature</i> , 2022, 604, 517-524.	13.7	211
2	Mutational landscape of normal epithelial cells in Lynch Syndrome patients. <i>Nature Communications</i> , 2022, 13, 2710.	5.8	19
3	The longitudinal dynamics and natural history of clonal haematopoiesis. <i>Nature</i> , 2022, 606, 335-342.	13.7	136
4	Clonal dynamics of haematopoiesis across the human lifespan. <i>Nature</i> , 2022, 606, 343-350.	13.7	160
5	Inherited MUTYH mutations cause elevated somatic mutation rates and distinctive mutational signatures in normal human cells. <i>Nature Communications</i> , 2022, 13, .	5.8	30
6	Reliable detection of somatic mutations in solid tissues by laser-capture microdissection and low-input DNA sequencing. <i>Nature Protocols</i> , 2021, 16, 841-871.	5.5	82
7	Development, maturation, and maintenance of human prostate inferred from somatic mutations. <i>Cell Stem Cell</i> , 2021, 28, 1262-1274.e5.	5.2	29
8	Somatic mutation landscapes at single-molecule resolution. <i>Nature</i> , 2021, 593, 405-410.	13.7	254
9	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021, 184, 2239-2254.e39.	13.5	260
10	Extensive phylogenies of human development inferred from somatic mutations. <i>Nature</i> , 2021, 597, 387-392.	13.7	87
11	Patterns of within-host genetic diversity in SARS-CoV-2. <i>ELife</i> , 2021, 10, .	2.8	110
12	The mutational landscape of human somatic and germline cells. <i>Nature</i> , 2021, 597, 381-386.	13.7	180
13	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. <i>Nature Genetics</i> , 2021, 53, 1434-1442.	9.4	85
14	<i>CDKN2A</i> deletion is a frequent event associated with poor outcome in patients with peripheral T-cell lymphoma not otherwise specified (PTCL-NOS). <i>Haematologica</i> , 2021, 106, 2918-2926.	1.7	18
15	Convergent somatic mutations in metabolism genes in chronic liver disease. <i>Nature</i> , 2021, 598, 473-478.	13.7	87
16	Genomic reconstruction of the SARS-CoV-2 epidemic in England. <i>Nature</i> , 2021, 600, 506-511.	13.7	80
17	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. <i>Science</i> , 2021, 374, eabl9551.	6.0	111
18	Stage-stratified molecular profiling of non-muscle-invasive bladder cancer enhances biological, clinical, and therapeutic insight. <i>Cell Reports Medicine</i> , 2021, 2, 100472.	3.3	13

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19	Genomic evidence supports a clonal diaspora model for metastases of esophageal adenocarcinoma. <i>Nature Genetics</i> , 2020, 52, 74-83.	9.4	53
20	Generating realistic null hypothesis of cancer mutational landscapes using SigProfilerSimulator. <i>BMC Bioinformatics</i> , 2020, 21, 438.	1.2	27
21	Evidence for 28 genetic disorders discovered by combining healthcare and research data. <i>Nature</i> , 2020, 586, 757-762.	13.7	343
22	Whole genome, transcriptome and methylome profiling enhances actionable target discovery in high-risk pediatric cancer. <i>Nature Medicine</i> , 2020, 26, 1742-1753.	15.2	185
23	Somatic Evolution in Non-neoplastic IBD-Affected Colon. <i>Cell</i> , 2020, 182, 672-684.e11.	13.5	122
24	Spatial competition shapes the dynamic mutational landscape of normal esophageal epithelium. <i>Nature Genetics</i> , 2020, 52, 604-614.	9.4	107
25	Tobacco smoking and somatic mutations in human bronchial epithelium. <i>Nature</i> , 2020, 578, 266-272.	13.7	336
26	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. <i>Nature</i> , 2020, 578, 102-111.	13.7	424
27	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. <i>Nature Genetics</i> , 2020, 52, 306-319.	9.4	275
28	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. <i>Nature Genetics</i> , 2020, 52, 331-341.	9.4	431
29	Mutational signatures are jointly shaped by DNA damage and repair. <i>Nature Communications</i> , 2020, 11, 2169.	5.8	137
30	The mutational landscape of normal human endometrial epithelium. <i>Nature</i> , 2020, 580, 640-646.	13.7	338
31	Comprehensive molecular characterization of mitochondrial genomes in human cancers. <i>Nature Genetics</i> , 2020, 52, 342-352.	9.4	256
32	Extensive heterogeneity in somatic mutation and selection in the human bladder. <i>Science</i> , 2020, 370, 75-82.	6.0	195
33	3010 " THE IMPACT OF AGING AND INFLAMMATORY STRESS ON GENOME STABILITY IN HEMATOPOIETIC STEM CELLS. <i>Experimental Hematology</i> , 2020, 88, S40.	0.2	0
34	Seeds of cancer in normal skin. <i>Nature</i> , 2020, 586, 504-506.	13.7	1
35	Somatic evolution and global expansion of an ancient transmissible cancer lineage. <i>Science</i> , 2019, 365, .	6.0	58
36	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. <i>Nature Communications</i> , 2019, 10, 3835.	5.8	183

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37	Somatic mutation and clonal expansions in human tissues. <i>Genome Medicine</i> , 2019, 11, 35.	3.6	100
38	Undifferentiated Sarcomas Develop through Distinct Evolutionary Pathways. <i>Cancer Cell</i> , 2019, 35, 441-456.e8.	7.7	82
39	Embryonal precursors of Wilms tumor. <i>Science</i> , 2019, 366, 1247-1251.	6.0	101
40	Somatic mutations and clonal dynamics in healthy and cirrhotic human liver. <i>Nature</i> , 2019, 574, 538-542.	13.7	251
41	The landscape of somatic mutation in normal colorectal epithelial cells. <i>Nature</i> , 2019, 574, 532-537.	13.7	468
42	Recurrent histone mutations in T-cell acute lymphoblastic leukaemia. <i>British Journal of Haematology</i> , 2019, 184, 676-679.	1.2	7
43	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. <i>Nature Genetics</i> , 2018, 50, 682-692.	9.4	182
44	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. <i>Cell</i> , 2018, 173, 611-623.e17.	13.5	398
45	Somatic mutant clones colonize the human esophagus with age. <i>Science</i> , 2018, 362, 911-917.	6.0	805
46	Neutral tumor evolution?. <i>Nature Genetics</i> , 2018, 50, 1630-1633.	9.4	59
47	Population dynamics of normal human blood inferred from somatic mutations. <i>Nature</i> , 2018, 561, 473-478.	13.7	427
48	An integrated genomic analysis of anaplastic meningioma identifies prognostic molecular signatures. <i>Scientific Reports</i> , 2018, 8, 13537.	1.6	49
49	Prediction of acute myeloid leukaemia risk in healthy individuals. <i>Nature</i> , 2018, 559, 400-404.	13.7	617
50	Cancer-mutation network and the number and specificity of driver mutations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E6010-E6019.	3.3	91
51	Whole Genome Sequencing Reveals Recurrent Structural Driver Events in Peripheral T-Cell Lymphomas Not Otherwise Specified. <i>Blood</i> , 2018, 132, 4115-4115.	0.6	0
52	Precision oncology for acute myeloid leukemia using a knowledge bank approach. <i>Nature Genetics</i> , 2017, 49, 332-340.	9.4	229
53	Genome-wide chemical mutagenesis screens allow unbiased saturation of the cancer genome and identification of drug resistance mutations. <i>Genome Research</i> , 2017, 27, 613-625.	2.4	20
54	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. <i>Nature Communications</i> , 2017, 8, 15936.	5.8	179

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55	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. <i>Nature</i> , 2017, 543, 714-718.	13.7	229
56	Universal Patterns of Selection in Cancer and Somatic Tissues. <i>Cell</i> , 2017, 171, 1029-1041.e21.	13.5	1,085
57	GOTHIC, a probabilistic model to resolve complex biases and to identify real interactions in Hi-C data. <i>PLoS ONE</i> , 2017, 12, e0174744.	1.1	58
58	Mitochondrial genetic diversity, selection and recombination in a canine transmissible cancer. <i>ELife</i> , 2016, 5, .	2.8	49
59	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. <i>Nature</i> , 2016, 534, 47-54.	13.7	1,760
60	Tissue-specific mutation accumulation in human adult stem cells during life. <i>Nature</i> , 2016, 538, 260-264.	13.7	759
61	Mutational signatures associated with tobacco smoking in human cancer. <i>Science</i> , 2016, 354, 618-622.	6.0	842
62	Genomic Classification and Prognosis in Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2016, 374, 2209-2221.	13.9	3,067
63	Constrained positive selection on cancer mutations in normal skin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E1128-9.	3.3	23
64	Analysis of Mutational Signatures Suggest That AID Has an Early and Driver Role in Multiple Myeloma. <i>Blood</i> , 2016, 128, 116-116.	0.6	4
65	Whole Genome Sequencing of Unique Paired SMM/MGUS Progressing to MM Samples Reveals a Genomic Landscape with Diverse Evolutionary Pattern. <i>Blood</i> , 2016, 128, 2088-2088.	0.6	1
66	The Complex Landscape of Rearrangements in Smoldering and Symptomatic Multiple Myeloma Revealed By Whole-Genome Sequencing. <i>Blood</i> , 2016, 128, 236-236.	0.6	0
67	High burden and pervasive positive selection of somatic mutations in normal human skin. <i>Science</i> , 2015, 348, 880-886.	6.0	1,431
68	Somatic mutation in cancer and normal cells. <i>Science</i> , 2015, 349, 1483-1489.	6.0	996
69	Personally Tailored Risk Prediction of AML Based on Comprehensive Genomic and Clinical Data. <i>Blood</i> , 2015, 126, 85-85.	0.6	1
70	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. <i>ELife</i> , 2014, 3, .	2.8	318
71	Recurrent PTPRB and PLCG1 mutations in angiosarcoma. <i>Nature Genetics</i> , 2014, 46, 376-379.	9.4	269
72	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. <i>Nature Communications</i> , 2014, 5, 2997.	5.8	741

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73	Transmissible Dog Cancer Genome Reveals the Origin and History of an Ancient Cell Lineage. <i>Science</i> , 2014, 343, 437-440.	6.0	144
74	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. <i>Nature Genetics</i> , 2014, 46, 116-125.	9.4	313
75	Inactivating CUX1 mutations promote tumorigenesis. <i>Nature Genetics</i> , 2014, 46, 33-38.	9.4	111
76	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. <i>Science</i> , 2014, 345, 1251343.	6.0	348
77	Genome sequencing of normal cells reveals developmental lineages and mutational processes. <i>Nature</i> , 2014, 513, 422-425.	13.7	315
78	Non-random mutation: The evolution of targeted hypermutation and hypomutation. <i>BioEssays</i> , 2013, 35, 123-130.	1.2	70
79	Direct Competition between hnRNP C and U2AF65 Protects the Transcriptome from the Exonization of Alu Elements. <i>Cell</i> , 2013, 152, 453-466.	13.5	398
80	Whole Exome Sequencing Of Multiple Myeloma Reveals An Heterogeneous Clonal Architecture and Genomic Evolution. <i>Blood</i> , 2013, 122, 399-399.	0.6	0
81	Evidence of non-random mutation rates suggests an evolutionary risk management strategy. <i>Nature</i> , 2012, 485, 95-98.	13.7	183
82	Lexical access changes in patients with multiple sclerosis: A two-year follow-up study. <i>Journal of Clinical and Experimental Neuropsychology</i> , 2011, 33, 169-175.	0.8	40
83	The semantic organization of the animal category: evidence from semantic verbal fluency and network theory. <i>Cognitive Processing</i> , 2011, 12, 183-196.	0.7	87
84	SWITCHER-RANDOM-WALKS: A COGNITIVE-INSPIRED MECHANISM FOR NETWORK EXPLORATION. <i>International Journal of Bifurcation and Chaos in Applied Sciences and Engineering</i> , 2010, 20, 913-922.	0.7	23
85	The Organization of Local and Distant Functional Connectivity in the Human Brain. <i>PLoS Computational Biology</i> , 2010, 6, e1000808.	1.5	362
86	Undifferentiated Sarcomas Develop Through Distinct Evolutionary Pathways. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0