Inigo Martincorena

List of Publications by Year
in descending order

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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	Genomic Classification and Prognosis in Acute Myeloid Leukemia. New England Journal of Medicine, 2016, 374, 2209-2221.	13.9	3,067
2	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	13.7	1,760
3	High burden and pervasive positive selection of somatic mutations in normal human skin. Science, 2015, 348, 880-886.	6.0	1,431
4	Universal Patterns of Selection in Cancer and Somatic Tissues. Cell, 2017, 171, 1029-1041.e21.	13.5	1,085
5	Somatic mutation in cancer and normal cells. Science, 2015, 349, 1483-1489.	6.0	996
6	Mutational signatures associated with tobacco smoking in human cancer. Science, 2016, 354, 618-622.	6.0	842
7	Somatic mutant clones colonize the human esophagus with age. Science, 2018, 362, 911-917.	6.0	805
8	Tissue-specific mutation accumulation in human adult stem cells during life. Nature, 2016, 538, 260-264.	13.7	759
9	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. Nature Communications, 2014, 5, 2997.	5.8	741
10	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	13.7	617
11	The landscape of somatic mutation in normal colorectal epithelial cells. Nature, 2019, 574, 532-537.	13.7	468
12	Comprehensive analysis of chromothripsis in 2,658 human cancers using whole-genome sequencing. Nature Genetics, 2020, 52, 331-341.	9.4	431
13	Population dynamics of normal human blood inferred from somatic mutations. Nature, 2018, 561, 473-478.	13.7	427
14	Analyses of non-coding somatic drivers in 2,658Âcancer whole genomes. Nature, 2020, 578, 102-111.	13.7	424
15	Direct Competition between hnRNP C and U2AF65 Protects the Transcriptome from the Exonization of Alu Elements. Cell, 2013, 152, 453-466.	13.5	398
16	Timing the Landmark Events in the Evolution of Clear Cell Renal Cell Cancer: TRACERx Renal. Cell, 2018, 173, 611-623.e17.	13.5	398
17	The Organization of Local and Distant Functional Connectivity in the Human Brain. PLoS Computational Biology, 2010, 6, e1000808.	1.5	362
18	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	6.0	348

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19	Evidence for 28 genetic disorders discovered by combining healthcare and research data. Nature, 2020, 586, 757-762.	13.7	343
20	The mutational landscape of normal human endometrial epithelium. Nature, 2020, 580, 640-646.	13.7	338
21	Tobacco smoking and somatic mutations in human bronchial epithelium. Nature, 2020, 578, 266-272.	13.7	336
22	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	2.8	318
23	Genome sequencing of normal cells reveals developmental lineages and mutational processes. Nature, 2014, 513, 422-425.	13.7	315
24	RAG-mediated recombination is the predominant driver of oncogenic rearrangement in ETV6-RUNX1 acute lymphoblastic leukemia. Nature Genetics, 2014, 46, 116-125.	9.4	313
25	Pan-cancer analysis of whole genomes identifies driver rearrangements promoted by LINE-1 retrotransposition. Nature Genetics, 2020, 52, 306-319.	9.4	275
26	Recurrent PTPRB and PLCG1 mutations in angiosarcoma. Nature Genetics, 2014, 46, 376-379.	9.4	269
27	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	13.5	260
28	Comprehensive molecular characterization of mitochondrial genomes in human cancers. Nature Genetics, 2020, 52, 342-352.	9.4	256
29	Somatic mutation landscapes at single-molecule resolution. Nature, 2021, 593, 405-410.	13.7	254
30	Somatic mutations and clonal dynamics in healthy and cirrhotic human liver. Nature, 2019, 574, 538-542.	13.7	251
31	Precision oncology for acute myeloid leukemia using a knowledge bank approach. Nature Genetics, 2017, 49, 332-340.	9.4	229
32	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	13.7	229
33	Somatic mutation rates scale with lifespan across mammals. Nature, 2022, 604, 517-524.	13.7	211
34	Extensive heterogeneity in somatic mutation and selection in the human bladder. Science, 2020, 370, 75-82.	6.0	195
35	Whole genome, transcriptome and methylome profiling enhances actionable target discovery in high-risk pediatric cancer. Nature Medicine, 2020, 26, 1742-1753.	15.2	185
36	Evidence of non-random mutation rates suggests an evolutionary risk management strategy. Nature, 2012, 485, 95-98.	13.7	183

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37	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. Nature Communications, 2019, 10, 3835.	5.8	183
38	Sequencing of prostate cancers identifies new cancer genes, routes of progression and drug targets. Nature Genetics, 2018, 50, 682-692.	9.4	182
39	The mutational landscape of human somatic and germline cells. Nature, 2021, 597, 381-386.	13.7	180
40	Recurrent mutation of IGF signalling genes and distinct patterns of genomic rearrangement in osteosarcoma. Nature Communications, 2017, 8, 15936.	5.8	179
41	Clonal dynamics of haematopoiesis across the human lifespan. Nature, 2022, 606, 343-350.	13.7	160
42	Transmissible Dog Cancer Genome Reveals the Origin and History of an Ancient Cell Lineage. Science, 2014, 343, 437-440.	6.0	144
43	Mutational signatures are jointly shaped by DNA damage and repair. Nature Communications, 2020, 11, 2169.	5.8	137
44	The longitudinal dynamics and natural history of clonal haematopoiesis. Nature, 2022, 606, 335-342.	13.7	136
45	Somatic Evolution in Non-neoplastic IBD-Affected Colon. Cell, 2020, 182, 672-684.e11.	13.5	122
46	Inactivating CUX1 mutations promote tumorigenesis. Nature Genetics, 2014, 46, 33-38.	9.4	111
47	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. Science, 2021, 374, eabl9551.	6.0	111
48	Patterns of within-host genetic diversity in SARS-CoV-2. ELife, 2021, 10, .	2.8	110
49	Spatial competition shapes the dynamic mutational landscape of normal esophageal epithelium. Nature Genetics, 2020, 52, 604-614.	9.4	107
50	Embryonal precursors of Wilms tumor. Science, 2019, 366, 1247-1251.	6.0	101
51	Somatic mutation and clonal expansions in human tissues. Genome Medicine, 2019, 11, 35.	3.6	100
52	Cancer-mutation network and the number and specificity of driver mutations. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6010-E6019.	3.3	91
53	The semantic organization of the animal category: evidence from semantic verbal fluency and network theory. Cognitive Processing, 2011, 12, 183-196.	0.7	87
54	Extensive phylogenies of human development inferred from somatic mutations. Nature, 2021, 597, 387-392.	13.7	87

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55	Convergent somatic mutations in metabolism genes in chronic liver disease. Nature, 2021, 598, 473-478.	13.7	87
56	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. Nature Genetics, 2021, 53, 1434-1442.	9.4	85
57	Undifferentiated Sarcomas Develop through Distinct Evolutionary Pathways. Cancer Cell, 2019, 35, 441-456.e8.	7.7	82
58	Reliable detection of somatic mutations in solid tissues by laser-capture microdissection and low-input DNA sequencing. Nature Protocols, 2021, 16, 841-871.	5.5	82
59	Genomic reconstruction of the SARS-CoV-2 epidemic in England. Nature, 2021, 600, 506-511.	13.7	80
60	Nonâ€random mutation: The evolution of targeted hypermutation and hypomutation. BioEssays, 2013, 35, 123-130.	1.2	70
61	Neutral tumor evolution?. Nature Genetics, 2018, 50, 1630-1633.	9.4	59
62	GOTHiC, a probabilistic model to resolve complex biases and to identify real interactions in Hi-C data. PLoS ONE, 2017, 12, e0174744.	1.1	58
63	Somatic evolution and global expansion of an ancient transmissible cancer lineage. Science, 2019, 365, .	6.0	58
64	Genomic evidence supports a clonal diaspora model for metastases of esophageal adenocarcinoma. Nature Genetics, 2020, 52, 74-83.	9.4	53
65	Mitochondrial genetic diversity, selection and recombination in a canine transmissible cancer. ELife, 2016, 5, .	2.8	49
66	An integrated genomic analysis of anaplastic meningioma identifies prognostic molecular signatures. Scientific Reports, 2018, 8, 13537.	1.6	49
67	Lexical access changes in patients with multiple sclerosis: A two-year follow-up study. Journal of Clinical and Experimental Neuropsychology, 2011, 33, 169-175.	0.8	40
68	Inherited MUTYH mutations cause elevated somatic mutation rates and distinctive mutational signatures in normal human cells. Nature Communications, 2022, 13, .	5.8	30
69	Development, maturation, and maintenance of human prostate inferred from somatic mutations. Cell Stem Cell, 2021, 28, 1262-1274.e5.	5.2	29
70	Generating realistic null hypothesis of cancer mutational landscapes using SigProfilerSimulator. BMC Bioinformatics, 2020, 21, 438.	1.2	27
71	SWITCHER-RANDOM-WALKS: A COGNITIVE-INSPIRED MECHANISM FOR NETWORK EXPLORATION. International Journal of Bifurcation and Chaos in Applied Sciences and Engineering, 2010, 20, 913-922.	0.7	23
72	Constrained positive selection on cancer mutations in normal skin. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E1128-9.	3.3	23

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73	Genome-wide chemical mutagenesis screens allow unbiased saturation of the cancer genome and identification of drug resistance mutations. Genome Research, 2017, 27, 613-625.	2.4	20
74	Mutational landscape of normal epithelial cells in Lynch Syndrome patients. Nature Communications, 2022, 13, 2710.	5.8	19
75	<i>CDKN2A</i> deletion is a frequent event associated with poor outcome in patients with peripheral T-cell lymphoma not otherwise specified (PTCL-NOS). Haematologica, 2021, 106, 2918-2926.	1.7	18
76	Stage-stratified molecular profiling of non-muscle-invasive bladder cancer enhances biological, clinical, and therapeutic insight. Cell Reports Medicine, 2021, 2, 100472.	3.3	13
77	Recurrent histone mutations in Tâ€cell acute lymphoblastic leukaemia. British Journal of Haematology, 2019, 184, 676-679.	1.2	7
78	Analysis of Mutational Signatures Suggest That Aid Has an Early and Driver Role in Multiple Myeloma. Blood, 2016, 128, 116-116.	0.6	4
79	Personally Tailored Risk Prediction of AML Based on Comprehensive Genomic and Clinical Data. Blood, 2015, 126, 85-85.	0.6	1
80	Whole Genome Sequencing of Unique Paired SMM/MGUS Progressing to MM Samples Reveals a Genomic Landscape with Diverse Evolutionary Pattern. Blood, 2016, 128, 2088-2088.	0.6	1
81	Seeds of cancer in normal skin. Nature, 2020, 586, 504-506.	13.7	1
82	Whole Exome Sequencing Of Multiple Myeloma Reveals An Heterogeneous Clonal Architecture and Genomic Evolution. Blood, 2013, 122, 399-399.	0.6	0
83	The Complex Landscape of Rearrangements in Smoldering and Symptomatic Multiple Myeloma Revealed By Whole-Genome Sequencing. Blood, 2016, 128, 236-236.	0.6	0
84	Undifferentiated Sarcomas Develop Through Distinct Evolutionary Pathways. SSRN Electronic Journal, 0, , .	0.4	0
85	Whole Genome Sequencing Reveals Recurrent Structural Driver Events in Peripheral T-Cell Lymphomas Not Otherwise Specified. Blood, 2018, 132, 4115-4115.	0.6	0
86	3010 â€“ THE IMPACT OF AGING AND INFLAMMATORY STRESS ON GENOME STABILITY IN HEMATOPOIETIC STEM CELLS. Experimental Hematology, 2020, 88, S40.	0.2	0