Inigo Martincorena

List of Publications by Year
in descending order

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Version: 2024-02-01

86 papers	23,830 citations	25014 57 h-index	60583 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. Nature, 2022, 604, 517-524.	13.7	211
2	Mutational landscape of normal epithelial cells in Lynch Syndrome patients. Nature Communications, 2022, 13, 2710.	5.8	19
3	The longitudinal dynamics and natural history of clonal haematopoiesis. Nature, 2022, 606, 335-342.	13.7	136
4	Clonal dynamics of haematopoiesis across the human lifespan. Nature, 2022, 606, 343-350.	13.7	160
5	Inherited MUTYH mutations cause elevated somatic mutation rates and distinctive mutational signatures in normal human cells. Nature Communications, 2022, 13, .	5.8	30
6	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
7	Development, maturation, and maintenance of human prostate inferred from somatic mutations. Cell Stem Cell, 2021, 28, 1262-1274.e5.	5.2	29
8	Somatic mutation landscapes at single-molecule resolution. Nature, 2021, 593, 405-410.	13.7	254
9	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	13.5	260
10	Extensive phylogenies of human development inferred from somatic mutations. Nature, 2021, 597, 387-392.	13.7	87
11	Patterns of within-host genetic diversity in SARS-CoV-2. ELife, 2021, 10, .	2.8	110
12	The mutational landscape of human somatic and germline cells. Nature, 2021, 597, 381-386.	13.7	180
13	Increased somatic mutation burdens in normal human cells due to defective DNA polymerases. Nature Genetics, 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). Haematologica, 2021, 106, 2918-2926.	1.7	18
15	Convergent somatic mutations in metabolism genes in chronic liver disease. Nature, 2021, 598, 473-478.	13.7	87
16	Genomic reconstruction of the SARS-CoV-2 epidemic in England. Nature, 2021, 600, 506-511.	13.7	80
17	Exponential growth, high prevalence of SARS-CoV-2, and vaccine effectiveness associated with the Delta variant. Science, 2021, 374, eabl9551.	6.0	111
18	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

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

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

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55	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	13.7	229
56	Universal Patterns of Selection in Cancer and Somatic Tissues. Cell, 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. PLoS ONE, 2017, 12, e0174744.	1.1	58
58	Mitochondrial genetic diversity, selection and recombination in a canine transmissible cancer. ELife, 2016, 5, .	2.8	49
59	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	13.7	1,760
60	Tissue-specific mutation accumulation in human adult stem cells during life. Nature, 2016, 538, 260-264.	13.7	759
61	Mutational signatures associated with tobacco smoking in human cancer. Science, 2016, 354, 618-622.	6.0	842
62	Genomic Classification and Prognosis in Acute Myeloid Leukemia. New England Journal of Medicine, 2016, 374, 2209-2221.	13.9	3,067
63	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
64	Analysis of Mutational Signatures Suggest That Aid Has an Early and Driver Role in Multiple Myeloma. Blood, 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. Blood, 2016, 128, 2088-2088.	0.6	1
66	The Complex Landscape of Rearrangements in Smoldering and Symptomatic Multiple Myeloma Revealed By Whole-Genome Sequencing. Blood, 2016, 128, 236-236.	0.6	0
67	High burden and pervasive positive selection of somatic mutations in normal human skin. Science, 2015, 348, 880-886.	6.0	1,431
68	Somatic mutation in cancer and normal cells. Science, 2015, 349, 1483-1489.	6.0	996
69	Personally Tailored Risk Prediction of AML Based on Comprehensive Genomic and Clinical Data. Blood, 2015, 126, 85-85.	0.6	1
70	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	2.8	318
71	Recurrent PTPRB and PLCG1 mutations in angiosarcoma. Nature Genetics, 2014, 46, 376-379.	9.4	269
72	Heterogeneity of genomic evolution and mutational profiles in multiple myeloma. Nature Communications, 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. Science, 2014, 343, 437-440.	6.0	144
74	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
75	Inactivating CUX1 mutations promote tumorigenesis. Nature Genetics, 2014, 46, 33-38.	9.4	111
76	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	6.0	348
77	Genome sequencing of normal cells reveals developmental lineages and mutational processes. Nature, 2014, 513, 422-425.	13.7	315
78	Nonâ€random mutation: The evolution of targeted hypermutation and hypomutation. BioEssays, 2013, 35, 123-130.	1.2	70
79	Direct Competition between hnRNP C and U2AF65 Protects the Transcriptome from the Exonization of Alu Elements. Cell, 2013, 152, 453-466.	13.5	398
80	Whole Exome Sequencing Of Multiple Myeloma Reveals An Heterogeneous Clonal Architecture and Genomic Evolution. Blood, 2013, 122, 399-399.	0.6	0
81	Evidence of non-random mutation rates suggests an evolutionary risk management strategy. Nature, 2012, 485, 95-98.	13.7	183
82	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
83	The semantic organization of the animal category: evidence from semantic verbal fluency and network theory. Cognitive Processing, 2011, 12, 183-196.	0.7	87
84	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
85	The Organization of Local and Distant Functional Connectivity in the Human Brain. PLoS Computational Biology, 2010, 6, e1000808.	1.5	362
86	Undifferentiated Sarcomas Develop Through Distinct Evolutionary Pathways. SSRN Electronic Journal, 0, , .	0.4	0