Moritz Gerstung

List of Publications by Year
in descending order

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68	19,135	53794 45	95266 68
papers	citations	h-index	g-index

95	95	95	28205
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Genomic Classification and Prognosis in Acute Myeloid Leukemia. New England Journal of Medicine, 2016, 374, 2209-2221.	27.0	3,067
2	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	27.8	1,760
3	Clinical and biological implications of driver mutations in myelodysplastic syndromes. Blood, 2013, 122, 3616-3627.	1.4	1,562
4	High burden and pervasive positive selection of somatic mutations in normal human skin. Science, 2015, 348, 880-886.	12.6	1,431
5	Universal Patterns of Selection in Cancer and Somatic Tissues. Cell, 2017, 171, 1029-1041.e21.	28.9	1,085
6	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. Nature Medicine, 2015, 21, 751-759.	30.7	711
7	The evolutionary history of 2,658 cancers. Nature, 2020, 578, 122-128.	27.8	690
8	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	27.8	617
9	Genomic Evolution of Breast Cancer Metastasis and Relapse. Cancer Cell, 2017, 32, 169-184.e7.	16.8	534
10	Classification and Personalized Prognosis in Myeloproliferative Neoplasms. New England Journal of Medicine, 2018, 379, 1416-1430.	27.0	442
11	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	12.6	348
12	Pan-cancer computational histopathology reveals mutations, tumor composition and prognosis. Nature Cancer, 2020, 1, 800-810.	13.2	339
13	Cell2location maps fine-grained cell types in spatial transcriptomics. Nature Biotechnology, 2022, 40, 661-671.	17.5	335
14	Control of Plant Organ Size by KLUH/CYP78A5-Dependent Intercellular Signaling. Developmental Cell, 2007, 13, 843-856.	7.0	334
15	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	6.0	318
16	Combined hereditary and somatic mutations of replication error repair genes result in rapid onset of ultra-hypermutated cancers. Nature Genetics, 2015, 47, 257-262.	21.4	306
17	Cancer Evolution: Mathematical Models and Computational Inference. Systematic Biology, 2015, 64, e1-e25.	5.6	292
18	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	28.9	260

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19	Somatic mutation landscapes at single-molecule resolution. Nature, 2021, 593, 405-410.	27.8	254
20	A High-Density Map for Navigating the Human Polycomb Complexome. Cell Reports, 2016, 17, 583-595.	6.4	234
21	Precision oncology for acute myeloid leukemia using a knowledge bank approach. Nature Genetics, 2017, 49, 332-340.	21.4	229
22	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	27.8	229
23	Reliable detection of subclonal single-nucleotide variants in tumour cell populations. Nature Communications, 2012, 3, 811.	12.8	227
24	Somatic mutation rates scale with lifespan across mammals. Nature, 2022, 604, 517-524.	27.8	211
25	RUNX1 mutations in acute myeloid leukemia are associated with distinct clinico-pathologic and genetic features. Leukemia, 2016, 30, 2160-2168.	7.2	197
26	Combining gene mutation with gene expression data improves outcome prediction in myelodysplastic syndromes. Nature Communications, 2015, 6, 5901.	12.8	196
27	Extensive heterogeneity in somatic mutation and selection in the human bladder. Science, 2020, 370, 75-82.	12.6	195
28	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. Nature Communications, 2019, 10, 3835.	12.8	183
29	Polycomb preferentially targets stalled promoters of coding and noncoding transcripts. Genome Research, 2011, 21, 216-226.	5.5	146
30	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. Leukemia, 2018, 32, 2604-2616.	7.2	137
31	Mutational signatures are jointly shaped by DNA damage and repair. Nature Communications, 2020, 11, 2169.	12.8	137
32	The longitudinal dynamics and natural history of clonal haematopoiesis. Nature, 2022, 606, 335-342.	27.8	136
33	Subclonal variant calling with multiple samples and prior knowledge. Bioinformatics, 2014, 30, 1198-1204.	4.1	122
34	Mutational signatures of DNA mismatch repair deficiency in C. elegans and human cancers. Genome Research, 2018, 28, 666-675.	5.5	112
35	Patterns of within-host genetic diversity in SARS-CoV-2. ELife, 2021, 10, .	6.0	110
36	Spatial competition shapes the dynamic mutational landscape of normal esophageal epithelium. Nature Genetics, 2020, 52, 604-614.	21.4	107

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37	Quantifying cancer progression with conjunctive Bayesian networks. Bioinformatics, 2009, 25, 2809-2815.	4.1	104
38	The Temporal Order of Genetic and Pathway Alterations in Tumorigenesis. PLoS ONE, 2011, 6, e27136.	2.5	99
39	Mutant clones in normal epithelium outcompete and eliminate emerging tumours. Nature, 2021, 598, 510-514.	27.8	95
40	Genomic copy number predicts esophageal cancer years before transformation. Nature Medicine, 2020, 26, 1726-1732.	30.7	86
41	Genomic reconstruction of the SARS-CoV-2 epidemic in England. Nature, 2021, 600, 506-511.	27.8	80
42	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. Nature Genetics, 2020, 52, 1178-1188.	21.4	79
43	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	5.5	69
44	Identification of Prognostic Phenotypes of Esophageal Adenocarcinoma in 2 Independent Cohorts. Gastroenterology, 2018, 155, 1720-1728.e4.	1.3	67
45	Selection of Oncogenic Mutant Clones in Normal Human Skin Varies with Body Site. Cancer Discovery, 2021, 11, 340-361.	9.4	66
46	Neutral tumor evolution?. Nature Genetics, 2018, 50, 1630-1633.	21.4	59
47	A Quantitative and Dynamic Model for Plant Stem Cell Regulation. PLoS ONE, 2008, 3, e3553.	2.5	56
48	Genomic Profiling of Advanced-Stage Oral Cancers Reveals Chromosome 11q Alterations as Markers of Poor Clinical Outcome. PLoS ONE, 2011, 6, e17250.	2.5	47
49	Kinetic, Energetic, and Mechanical Differences between Dark-State Rhodopsin and Opsin. Structure, 2013, 21, 426-437.	3.3	47
50	Cohesin-dependent regulation of gene expression during differentiation is lost in cohesin-mutated myeloid malignancies. Blood, 2019, 134, 2195-2208.	1.4	39
51	Genomeâ€wide expression and copy number analysis identifies driver genes in gingivobuccal cancers. Genes Chromosomes and Cancer, 2012, 51, 161-173.	2.8	38
52	Learning mutational signatures and their multidimensional genomic properties with TensorSignatures. Nature Communications, 2021, 12, 3628.	12.8	30
53	The BET protein FSH functionally interacts with ASH1 to orchestrate global gene activity in Drosophila. Genome Biology, 2013, 14, R18.	9.6	29
54	Lineage-defined leiomyosarcoma subtypes emerge years before diagnosis and determine patient survival. Nature Communications, 2021, 12, 4496.	12.8	28

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55	Clinicopathological and prognostic implications of genetic alterations in oral cancers. Oncology Letters, 2011, 2, 445-451.	1.8	24
56	Waiting Time Models of Cancer Progression. Mathematical Population Studies, 2010, 17, 115-135.	2.2	20
57	Evolutionary Games with Affine Fitness Functions: Applications to Cancer. Dynamic Games and Applications, 2011, 1, 370-385.	1.9	19
58	Protection of the C. elegans germ cell genome depends on diverse DNA repair pathways during normal proliferation. PLoS ONE, 2021, 16, e0250291.	2.5	18
59	Biallelic mutations in cancer genomes reveal local mutational determinants. Nature Genetics, 2022, 54, 128-133.	21.4	16
60	Immuno-oncology from the perspective of somatic evolution. Seminars in Cancer Biology, 2018, 52, 75-85.	9.6	15
61	Noisy signaling through promoter logic gates. Physical Review E, 2009, 79, 011923.	2.1	13
62	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. Leukemia, 2017, , .	7.2	9
63	Analysis of mutational signatures in C. elegans: Implications for cancer genome analysis. DNA Repair, 2020, 95, 102957.	2.8	8
64	Analysis of Mutational Signatures Suggest That Aid Has an Early and Driver Role in Multiple Myeloma. Blood, 2016, 128, 116-116.	1.4	4
65	Dissecting Genetic and Phenotypic Heterogeneity to Map Molecular Phylogenies and Deliver Personalized Outcome and Treatment Predictions in AML. Blood, 2015, 126, 803-803.	1.4	2
66	Association Between Gene Expression Profiles and Commonly Mutated Genes In The Hematopoietic Stem Cells Of Patients With Myelodysplastic Syndromes. Blood, 2013, 122, 2779-2779.	1.4	1
67	Personally Tailored Risk Prediction of AML Based on Comprehensive Genomic and Clinical Data. Blood, 2015, 126, 85-85.	1.4	1
68	C. elegans genome-wide analysis reveals DNA repair pathways that act cooperatively to preserve genome integrity upon ionizing radiation. PLoS ONE, 2021, 16, e0258269.	2.5	0