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	Cell2location maps fine-grained cell types in spatial transcriptomics. Nature Biotechnology, 2022, 40, 661-671.	17.5	335
2	Biallelic mutations in cancer genomes reveal local mutational determinants. Nature Genetics, 2022, 54, 128-133.	21.4	16
3	Somatic mutation rates scale with lifespan across mammals. Nature, 2022, 604, 517-524.	27.8	211
4	The longitudinal dynamics and natural history of clonal haematopoiesis. Nature, 2022, 606, 335-342.	27.8	136
5	Selection of Oncogenic Mutant Clones in Normal Human Skin Varies with Body Site. Cancer Discovery, 2021, 11, 340-361.	9.4	66
6	Somatic mutation landscapes at single-molecule resolution. Nature, 2021, 593, 405-410.	27.8	254
7	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
8	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. Cell, 2021, 184, 2239-2254.e39.	28.9	260
9	Learning mutational signatures and their multidimensional genomic properties with TensorSignatures. Nature Communications, 2021, 12, 3628.	12.8	30
10	Lineage-defined leiomyosarcoma subtypes emerge years before diagnosis and determine patient survival. Nature Communications, 2021, 12, 4496.	12.8	28
11	Patterns of within-host genetic diversity in SARS-CoV-2. ELife, 2021, 10, .	6.0	110
12	Mutant clones in normal epithelium outcompete and eliminate emerging tumours. Nature, 2021, 598, 510-514.	27.8	95
13	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
14	Genomic reconstruction of the SARS-CoV-2 epidemic in England. Nature, 2021, 600, 506-511.	27.8	80
15	Analysis of mutational signatures in C. elegans: Implications for cancer genome analysis. DNA Repair, 2020, 95, 102957.	2.8	8
16	Somatic mutation distributions in cancer genomes vary with three-dimensional chromatin structure. Nature Genetics, 2020, 52, 1178-1188.	21.4	79
17	Pan-cancer computational histopathology reveals mutations, tumor composition and prognosis. Nature Cancer, 2020, 1, 800-810.	13.2	339
18	Genomic copy number predicts esophageal cancer years before transformation. Nature Medicine, 2020, 26, 1726-1732.	30.7	86

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19	Spatial competition shapes the dynamic mutational landscape of normal esophageal epithelium. Nature Genetics, 2020, 52, 604-614.	21.4	107
20	The evolutionary history of 2,658 cancers. Nature, 2020, 578, 122-128.	27.8	690
21	Mutational signatures are jointly shaped by DNA damage and repair. Nature Communications, 2020, 11, 2169.	12.8	137
22	Extensive heterogeneity in somatic mutation and selection in the human bladder. Science, 2020, 370, 75-82.	12.6	195
23	Genomic landscape and chronological reconstruction of driver events in multiple myeloma. Nature Communications, 2019, 10, 3835.	12.8	183
24	Cohesin-dependent regulation of gene expression during differentiation is lost in cohesin-mutated myeloid malignancies. Blood, 2019, 134, 2195-2208.	1.4	39
25	Mutational signatures of DNA mismatch repair deficiency in C. elegans and human cancers. Genome Research, 2018, 28, 666-675.	5.5	112
26	Immuno-oncology from the perspective of somatic evolution. Seminars in Cancer Biology, 2018, 52, 75-85.	9.6	15
27	Identification of Prognostic Phenotypes of Esophageal Adenocarcinoma in 2 Independent Cohorts. Gastroenterology, 2018, 155, 1720-1728.e4.	1.3	67
28	Classification and Personalized Prognosis in Myeloproliferative Neoplasms. New England Journal of Medicine, 2018, 379, 1416-1430.	27.0	442
29	Neutral tumor evolution?. Nature Genetics, 2018, 50, 1630-1633.	21.4	59
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	Prediction of acute myeloid leukaemia risk in healthy individuals. Nature, 2018, 559, 400-404.	27.8	617
32	Precision oncology for acute myeloid leukemia using a knowledge bank approach. Nature Genetics, 2017, 49, 332-340.	21.4	229
33	Somatic mutations reveal asymmetric cellular dynamics in the early human embryo. Nature, 2017, 543, 714-718.	27.8	229
34	Universal Patterns of Selection in Cancer and Somatic Tissues. Cell, 2017, 171, 1029-1041.e21.	28.9	1,085
35	Genomic Evolution of Breast Cancer Metastasis and Relapse. Cancer Cell, 2017, 32, 169-184.e7.	16.8	534
36	Analysis of the genomic landscape of multiple myeloma highlights novel prognostic markers and disease subgroups. Leukemia, 2017, , .	7.2	9

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37	Landscape of somatic mutations in 560 breast cancer whole-genome sequences. Nature, 2016, 534, 47-54.	27.8	1,760
38	RUNX1 mutations in acute myeloid leukemia are associated with distinct clinico-pathologic and genetic features. Leukemia, 2016, 30, 2160-2168.	7.2	197
39	A High-Density Map for Navigating the Human Polycomb Complexome. Cell Reports, 2016, 17, 583-595.	6.4	234
40	Genomic Classification and Prognosis in Acute Myeloid Leukemia. New England Journal of Medicine, 2016, 374, 2209-2221.	27.0	3,067
41	Analysis of Mutational Signatures Suggest That Aid Has an Early and Driver Role in Multiple Myeloma. Blood, 2016, 128, 116-116.	1.4	4
42	High burden and pervasive positive selection of somatic mutations in normal human skin. Science, 2015, 348, 880-886.	12.6	1,431
43	Combining gene mutation with gene expression data improves outcome prediction in myelodysplastic syndromes. Nature Communications, 2015, 6, 5901.	12.8	196
44	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
45	Subclonal diversification of primary breast cancer revealed by multiregion sequencing. Nature Medicine, 2015, 21, 751-759.	30.7	711
46	Frequent somatic transfer of mitochondrial DNA into the nuclear genome of human cancer cells. Genome Research, 2015, 25, 814-824.	5.5	69
47	Cancer Evolution: Mathematical Models and Computational Inference. Systematic Biology, 2015, 64, e1-e25.	5.6	292
48	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
49	Personally Tailored Risk Prediction of AML Based on Comprehensive Genomic and Clinical Data. Blood, 2015, 126, 85-85.	1.4	1
50	Origins and functional consequences of somatic mitochondrial DNA mutations in human cancer. ELife, 2014, 3, .	6.0	318
51	Subclonal variant calling with multiple samples and prior knowledge. Bioinformatics, 2014, 30, 1198-1204.	4.1	122
52	Extensive transduction of nonrepetitive DNA mediated by L1 retrotransposition in cancer genomes. Science, 2014, 345, 1251343.	12.6	348
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	Clinical and biological implications of driver mutations in myelodysplastic syndromes. Blood, 2013, 122, 3616-3627.	1.4	1,562

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55	Kinetic, Energetic, and Mechanical Differences between Dark-State Rhodopsin and Opsin. Structure, 2013, 21, 426-437.	3.3	47
56	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
57	Reliable detection of subclonal single-nucleotide variants in tumour cell populations. Nature Communications, 2012, 3, 811.	12.8	227
58	Genomeâ€wide expression and copy number analysis identifies driver genes in gingivobuccal cancers. Genes Chromosomes and Cancer, 2012, 51, 161-173.	2.8	38
59	Polycomb preferentially targets stalled promoters of coding and noncoding transcripts. Genome Research, 2011, 21, 216-226.	5.5	146
60	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
61	Clinicopathological and prognostic implications of genetic alterations in oral cancers. Oncology Letters, 2011, 2, 445-451.	1.8	24
62	Evolutionary Games with Affine Fitness Functions: Applications to Cancer. Dynamic Games and Applications, 2011, 1, 370-385.	1.9	19
63	The Temporal Order of Genetic and Pathway Alterations in Tumorigenesis. PLoS ONE, 2011, 6, e27136.	2.5	99
64	Waiting Time Models of Cancer Progression. Mathematical Population Studies, 2010, 17, 115-135.	2.2	20
65	Noisy signaling through promoter logic gates. Physical Review E, 2009, 79, 011923.	2.1	13
66	Quantifying cancer progression with conjunctive Bayesian networks. Bioinformatics, 2009, 25, 2809-2815.	4.1	104
67	A Quantitative and Dynamic Model for Plant Stem Cell Regulation. PLoS ONE, 2008, 3, e3553.	2.5	56
68	Control of Plant Organ Size by KLUH/CYP78A5-Dependent Intercellular Signaling. Developmental Cell, 2007, 13, 843-856.	7.0	334