

Charles Gawad

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

6,025
citations

471371

17
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580701

25
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all docs

36
docs citations

36
times ranked

12052
citing authors

#	ARTICLE	IF	CITATIONS
1	Circular RNAs Are the Predominant Transcript Isoform from Hundreds of Human Genes in Diverse Cell Types. PLoS ONE, 2012, 7, e30733.	1.1	2,088
2	Single-cell genome sequencing: current state of the science. Nature Reviews Genetics, 2016, 17, 175-188.	7.7	1,134
3	Pan-cancer genome and transcriptome analyses of 1,699 paediatric leukaemias and solid tumours. Nature, 2018, 555, 371-376.	13.7	649
4	Noninvasive in vivo monitoring of tissue-specific global gene expression in humans. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 7361-7366.	3.3	275
5	Dissecting the clonal origins of childhood acute lymphoblastic leukemia by single-cell genomics. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 17947-17952.	3.3	273
6	Resolving medulloblastoma cellular architecture by single-cell genomics. Nature, 2019, 572, 74-79.	13.7	273
7	A Quantitative Comparison of Single-Cell Whole Genome Amplification Methods. PLoS ONE, 2014, 9, e105585.	1.1	259
8	LC3-Associated Phagocytosis in Myeloid Cells Promotes Tumor Immune Tolerance. Cell, 2018, 175, 429-441.e16.	13.5	242
9	Measurable residual disease detection by high-throughput sequencing improves risk stratification for pediatric B-ALL. Blood, 2018, 131, 1350-1359.	0.6	158
10	A Single-Cell Transcriptional Atlas of the Developing Murine Cerebellum. Current Biology, 2018, 28, 2910-2920.e2.	1.8	158
11	Massive evolution of the immunoglobulin heavy chain locus in children with B precursor acute lymphoblastic leukemia. Blood, 2012, 120, 4407-4417.	0.6	118
12	Evaluation of Plasma Microbial Cell-Free DNA Sequencing to Predict Bloodstream Infection in Pediatric Patients With Relapsed or Refractory Cancer. JAMA Oncology, 2020, 6, 552.	3.4	77
13	Accurate genomic variant detection in single cells with primary template-directed amplification. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	3.3	69
14	High-resolution transcriptional dissection of in vivo Atoh1-mediated hair cell conversion in mature cochleae identifies Isl1 as a co-reprogramming factor. PLoS Genetics, 2018, 14, e1007552.	1.5	68
15	Integrative genomic analyses reveal mechanisms of glucocorticoid resistance in acute lymphoblastic leukemia. Nature Cancer, 2020, 1, 329-344.	5.7	44
16	Early somatic mosaicism is a rare cause of long-QT syndrome. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 11555-11560.	3.3	39
17	Single-cell RNA sequencing reveals the impact of chromosomal instability on glioblastoma cancer stem cells. BMC Medical Genomics, 2019, 12, 79.	0.7	30
18	Murine hematopoietic stem cell activity is derived from pre-circulation embryos but not yolk sacs. Nature Communications, 2018, 9, 5405.	5.8	19

#	ARTICLE	IF	CITATIONS
19	Dynamic ASXL1 Exon Skipping and Alternative Circular Splicing in Single Human Cells. PLoS ONE, 2016, 11, e0164085.	1.1	15
20	Towards Molecular Medicine. Molecular Diagnosis and Therapy, 2005, 5, 207-211.	3.3	4
21	Genome-wide segregation of single nucleotide and structural variants into single cancer cells. BMC Genomics, 2017, 18, 906.	1.2	4
22	Sequencing the Genomes of Single Cells. Methods in Molecular Biology, 2019, 1979, 227-234.	0.4	3
23	Residual Disease Monitoring By High Throughput Sequencing Provides Risk Stratification in Childhood B-ALL and Identifies a Novel Subset of Patients Having Poor Outcome. Blood, 2016, 128, 1086-1086.	0.6	2
24	Simultaneous monitoring of disease and microbe dynamics through plasma DNA sequencing in pediatric patients with acute lymphoblastic leukemia. Science Advances, 2022, 8, eabj1360.	4.7	2
25	Bringing precision oncology to cellular resolution with single-cell genomics. Clinical and Experimental Metastasis, 2021, , 1.	1.7	1
26	Robust Autonomous Generation of Definitive Hematopoietic Stem Cells From Pre-Circulation Murine Embryos. Experimental Hematology, 2018, 64, S66.	0.2	0
27	Gene Expression Arrays in Pancreatic Cancer Drug Discovery Research. , 2010, , 113-134.		0
28	Next-Generation Sequencing of Immunoglobulin Heavy Chain Variable Region in Diagnostic Samples of Pediatric Acute Lymphoblastic Leukemia Identifies Hundreds of Clonal Subpopulations with Multiple Immunophenotypes. Blood, 2011, 118, 1436-1436.	0.6	0
29	Comparison of High-Throughput Sequencing and Flow Cytometry for Measuring Minimal Residual Disease in Pediatric Acute Lymphoblastic Leukemia: A Children's Oncology Group Cohort. Blood, 2012, 120, 1440-1440.	0.6	0
30	Use Of Rearranged Immune Receptor Sequencing To Measure Minimal Residual Disease (MRD) In Bone Marrow, Cerebrospinal Fluid and Testes In Relapsed Childhood Acute Lymphoblastic Leukemia. Blood, 2013, 122, 4984-4984.	0.6	0