Matan Hofree

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/1613642/publications.pdf

Version: 2024-02-01

33 papers 8,725 citations

236925 25 h-index 32 g-index

40 all docs

40 docs citations

40 times ranked

19186 citing authors

#	Article	IF	CITATIONS
1	Integrated Genomic Characterization of Papillary Thyroid Carcinoma. Cell, 2014, 159, 676-690.	28.9	2,318
2	Massively parallel single-nucleus RNA-seq with DroNc-seq. Nature Methods, 2017, 14, 955-958.	19.0	859
3	Intra- and Inter-cellular Rewiring of the Human Colon during Ulcerative Colitis. Cell, 2019, 178, 714-730.e22.	28.9	806
4	Network-based stratification of tumor mutations. Nature Methods, 2013, 10, 1108-1115.	19.0	698
5	A Cellular Taxonomy of the Bone Marrow Stroma in Homeostasis and Leukemia. Cell, 2019, 177, 1915-1932.e16.	28.9	640
6	Exome Sequencing Links Corticospinal Motor Neuron Disease to Common Neurodegenerative Disorders. Science, 2014, 343, 506-511.	12.6	466
7	The neuropeptide NMU amplifies ILC2-driven allergic lung inflammation. Nature, 2017, 549, 351-356.	27.8	460
8	A single-cell and single-nucleus RNA-Seq toolbox for fresh and frozen human tumors. Nature Medicine, 2020, 26, 792-802.	30.7	381
9	Anatomically and Functionally Distinct Lung Mesenchymal Populations Marked by Lgr5 and Lgr6. Cell, 2017, 170, 1149-1163.e12.	28.9	304
10	A Decade of Systems Biology. Annual Review of Cell and Developmental Biology, 2010, 26, 721-744.	9.4	277
11	Spatially organized multicellular immune hubs in human colorectal cancer. Cell, 2021, 184, 4734-4752.e20.	28.9	256
12	Regenerative potential of prostate luminal cells revealed by single-cell analysis. Science, 2020, 368, 497-505.	12.6	165
13	Inactivation of Capicua drives cancer metastasis. Nature Genetics, 2017, 49, 87-96.	21.4	130
14	Genotype to phenotype via network analysis. Current Opinion in Genetics and Development, 2013, 23, 611-621.	3.3	126
15	Multi-tiered genomic analysis of head and neck cancer ties TP53 mutation to 3p loss. Nature Genetics, 2014, 46, 939-943.	21.4	126
16	Interaction Landscape of Inherited Polymorphisms with Somatic Events in Cancer. Cancer Discovery, 2017, 7, 410-423.	9.4	121
17	Exome Sequencing of African-American Prostate Cancer Reveals Loss-of-Function <i>ERF</i> Mutations. Cancer Discovery, 2017, 7, 973-983.	9.4	94
18	Using Functional Signature Ontology (FUSION) to Identify Mechanisms of Action for Natural Products. Science Signaling, 2013, 6, ra90.	3.6	66

#	Article	IF	CITATIONS
19	Functional genome-wide siRNA screen identifies KIAA0586 as mutated in Joubert syndrome. ELife, 2015, 4, e06602.	6.0	64
20	Intrinsic Resistance to Immune Checkpoint Blockade in a Mismatch Repair–Deficient Colorectal Cancer. Cancer Immunology Research, 2019, 7, 1230-1236.	3.4	59
21	A Distinct Transcriptional Program in Human CAR T Cells Bearing the 4-1BB Signaling Domain Revealed by scRNA-Seq. Molecular Therapy, 2020, 28, 2577-2592.	8.2	58
22	RepTar: a database of predicted cellular targets of host and viral miRNAs. Nucleic Acids Research, 2011, 39, D188-D194.	14.5	45
23	Genome Wide Proteomics of ERBB2 and EGFR and Other Oncogenic Pathways in Inflammatory Breast Cancer. Journal of Proteome Research, 2013, 12, 2805-2817.	3.7	38
24	Network-driven plasma proteomics expose molecular changes in the Alzheimer's brain. Molecular Neurodegeneration, 2016, 11, 31.	10.8	34
25	Challenges in identifying cancer genes by analysis of exome sequencing data. Nature Communications, 2016, 7, 12096.	12.8	34
26	Rapid CLIP dissociation from MHC II promotes an unusual antigen presentation pathway in autoimmunity. Journal of Experimental Medicine, 2018, 215, 2617-2635.	8.5	20
27	Implications of Intratumor Heterogeneity on Consensus Molecular Subtype (CMS) in Colorectal Cancer. Cancers, 2021, 13, 4923.	3.7	19
28	Synthetic Essentiality of Metabolic Regulator PDHK1 in PTEN-Deficient Cells and Cancers. Cell Reports, 2019, 28, 2317-2330.e8.	6.4	12
29	Integrated Proteomic and Genomic Analysis of Gastric Cancer Patient Tissues. Journal of Proteome Research, 2015, 14, 4995-5006.	3.7	7
30	Identifying mutation specific cancer pathways using a structurally resolved protein interaction network. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 84-95.	0.7	7
31	IDENTIFYING MUTATION SPECIFIC CANCER PATHWAYS USING A STRUCTURALLY RESOLVED PROTEIN INTERACTION NETWORK. , 2014, , .		3
32	DroNc-seq step-by-step. Protocol Exchange, 0, , .	0.3	1
33	A platinum-resistant subtype of high-grade serous ovarian cancer identified by a network of somatic mutations Journal of Clinical Oncology, 2017, 35, 5561-5561.	1.6	0