

Reyka G Jayasinghe

List of Publications by Year in descending order

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Version: 2024-02-01

28
papers

2,628
citations

567281

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37
all docs

37
docs citations

37
times ranked

6408
citing authors

#	ARTICLE	IF	CITATIONS
1	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	28.9	620
2	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. <i>Cell Reports</i> , 2018, 23, 227-238.e3.	6.4	407
3	The Human Tumor Atlas Network: Charting Tumor Transitions across Space and Time at Single-Cell Resolution. <i>Cell</i> , 2020, 181, 236-249.	28.9	334
4	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	28.9	272
5	Patterns and functional implications of rare germline variants across 12 cancer types. <i>Nature Communications</i> , 2015, 6, 10086.	12.8	243
6	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. <i>Cell Reports</i> , 2018, 23, 270-281.e3.	6.4	177
7	Before and After: Comparison of Legacy and Harmonized TCGA Genomic Data Commons™ Data. <i>Cell Systems</i> , 2019, 9, 24-34.e10.	6.2	103
8	Systematic discovery of complex insertions and deletions in human cancers. <i>Nature Medicine</i> , 2016, 22, 97-104.	30.7	93
9	Co-evolution of tumor and immune cells during progression of multiple myeloma. <i>Nature Communications</i> , 2021, 12, 2559.	12.8	68
10	Divergent viral presentation among human tumors and adjacent normal tissues. <i>Scientific Reports</i> , 2016, 6, 28294.	3.3	60
11	Comprehensive characterization of 536 patient-derived xenograft models prioritizes candidates for targeted treatment. <i>Nature Communications</i> , 2021, 12, 5086.	12.8	58
12	CTCF genetic alterations in endometrial carcinoma are pro-tumorigenic. <i>Oncogene</i> , 2017, 36, 4100-4110.	5.9	50
13	Evolution and structure of clinically relevant gene fusions in multiple myeloma. <i>Nature Communications</i> , 2020, 11, 2666.	12.8	31
14	Discovery of driver non-coding splice-site-creating mutations in cancer. <i>Nature Communications</i> , 2020, 11, 5573.	12.8	26
15	CS1 CAR-T targeting the distal domain of CS1 (SLAMF7) shows efficacy in high tumor burden myeloma model despite fratricide of CD8+CS1 expressing CAR-T cells. <i>Leukemia</i> , 2022, 36, 1625-1634.	7.2	15
16	Current theoretical models fail to predict the topological complexity of the human genome. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 48.	3.5	14
17	Integrated Cytof, Scrna-Seq and Cite-Seq Analysis of Bone Marrow Immune Microenvironment in the Mmrf Compass Study. <i>Blood</i> , 2020, 136, 28-29.	1.4	2
18	Single-Cell Transcriptomic and Proteomic Diversity in Multiple Myeloma. <i>Blood</i> , 2019, 134, 5531-5531.	1.4	1

#	ARTICLE	IF	CITATIONS
19	Characterization of T-Cell Exhaustion in Rapid Progressing Multiple Myeloma Using Cross Center Scrna-Seq Study. Blood, 2021, 138, 401-401.	1.4	1
20	Immunophenotypic and Single-Cell Transcriptional Profiling of CD34+ Hematopoietic Stem and Progenitor Cells Mobilized with Motixafortide (BL-8040) and G-CSF Versus Plerixafor and G-CSF Versus Placebo and G-CSF: A Correlative Study of the Genesis Trial. Blood, 2021, 138, 3816-3816.	1.4	1
21	Fusion gene detection across a large cohort of multiple myeloma patients. Clinical Lymphoma, Myeloma and Leukemia, 2019, 19, e64-e65.	0.4	0
22	Abstract 1929: Pan-Cancer analysis of the effects of splice-altering variants on mRNA splicing and stability. , 2015, , .		0
23	Abstract 1939: Discovery and proteogenomic investigation of genetic variants in human cancers. , 2015, , .		0
24	Single-Cell Pathway Enrichment and Regulatory Profiling of Multiple Myeloma across Disease Stages. Blood, 2019, 134, 364-364.	1.4	0
25	Single-Cell RNA-Seq Analysis of CD138-Depleted Bone Marrow Samples Reveals Genetic Alterations and Disease Progression Correlate with Tumor and Bone Marrow Immune Microenvironment in the Mmrf Compass Study. Blood, 2021, 138, 2691-2691.	1.4	0
26	Interim Analysis of Mmrf Curecloud Research Initiative Identifies High Prevalence and Patterns of Clonal Hematopoiesis of Indeterminate Potential (CHIP) Mutations in a Real World Myeloma Cohort. Blood, 2021, 138, 2197-2197.	1.4	0
27	Myeloma Cell Associated Therapeutic Protein Discovery Using Single Cell RNA-Seq Data. Blood, 2020, 136, 4-5.	1.4	0
28	Pollock: Fishing for Cell States. Bioinformatics Advances, 0, , .	2.4	0