

Reyka G Jayasinghe

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8314949/publications.pdf>

Version: 2024-02-01

28
papers

2,628
citations

567281

15
h-index

677142

22
g-index

37
all docs

37
docs citations

37
times ranked

6408
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Co-evolution of tumor and immune cells during progression of multiple myeloma. <i>Nature Communications</i> , 2021, 12, 2559.	12.8	68
3	Comprehensive characterization of 536 patient-derived xenograft models prioritizes candidates for targeted treatment. <i>Nature Communications</i> , 2021, 12, 5086.	12.8	58
4	Characterization of T-Cell Exhaustion in Rapid Progressing Multiple Myeloma Using Cross Center Scrna-Seq Study. <i>Blood</i> , 2021, 138, 401-401.	1.4	1
5	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. <i>Blood</i> , 2021, 138, 3816-3816.	1.4	1
6	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. <i>Blood</i> , 2021, 138, 2691-2691.	1.4	0
7	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. <i>Blood</i> , 2021, 138, 2197-2197.	1.4	0
8	Discovery of driver non-coding splice-site-creating mutations in cancer. <i>Nature Communications</i> , 2020, 11, 5573.	12.8	26
9	Evolution and structure of clinically relevant gene fusions in multiple myeloma. <i>Nature Communications</i> , 2020, 11, 2666.	12.8	31
10	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
11	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
12	Myeloma Cell Associated Therapeutic Protein Discovery Using Single Cell RNA-Seq Data. <i>Blood</i> , 2020, 136, 4-5.	1.4	0
13	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
14	Fusion gene detection across a large cohort of multiple myeloma patients. <i>Clinical Lymphoma, Myeloma and Leukemia</i> , 2019, 19, e64-e65.	0.4	0
15	Single-Cell Transcriptomic and Proteomic Diversity in Multiple Myeloma. <i>Blood</i> , 2019, 134, 5531-5531.	1.4	1
16	Single-Cell Pathway Enrichment and Regulatory Profiling of Multiple Myeloma across Disease Stages. <i>Blood</i> , 2019, 134, 364-364.	1.4	0
17	Perspective on Oncogenic Processes at the End of the Beginning of Cancer Genomics. <i>Cell</i> , 2018, 173, 305-320.e10.	28.9	272
18	Pathogenic Germline Variants in 10,389 Adult Cancers. <i>Cell</i> , 2018, 173, 355-370.e14.	28.9	620

#	ARTICLE	IF	CITATIONS
19	Driver Fusions and Their Implications in the Development and Treatment of Human Cancers. Cell Reports, 2018, 23, 227-238.e3.	6.4	407
20	Systematic Analysis of Splice-Site-Creating Mutations in Cancer. Cell Reports, 2018, 23, 270-281.e3.	6.4	177
21	CTCF genetic alterations in endometrial carcinoma are pro-tumorigenic. Oncogene, 2017, 36, 4100-4110.	5.9	50
22	Divergent viral presentation among human tumors and adjacent normal tissues. Scientific Reports, 2016, 6, 28294.	3.3	60
23	Systematic discovery of complex insertions and deletions in human cancers. Nature Medicine, 2016, 22, 97-104.	30.7	93
24	Current theoretical models fail to predict the topological complexity of the human genome. Frontiers in Molecular Biosciences, 2015, 2, 48.	3.5	14
25	Patterns and functional implications of rare germline variants across 12 cancer types. Nature Communications, 2015, 6, 10086.	12.8	243
26	Abstract 1929: Pan-Cancer analysis of the effects of splice-altering variants on mRNA splicing and stability. , 2015, , .		0
27	Abstract 1939: Discovery and proteogenomic investigation of genetic variants in human cancers. , 2015, , .		0
28	Pollock: Fishing for Cell States. Bioinformatics Advances, 0, , .	2.4	0