

Lijun Yao

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11884689/publications.pdf>

Version: 2024-02-01

13
papers

1,247
citations

1684188

5
h-index

1588992

8
g-index

13
all docs

13
docs citations

13
times ranked

2590
citing authors

#	ARTICLE	IF	CITATIONS
1	Proteogenomic Characterization Reveals Therapeutic Vulnerabilities in Lung Adenocarcinoma. <i>Cell</i> , 2020, 182, 200-225.e35.	28.9	410
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	Proteogenomic and metabolomic characterization of human glioblastoma. <i>Cancer Cell</i> , 2021, 39, 509-528.e20.	16.8	327
4	Co-evolution of tumor and immune cells during progression of multiple myeloma. <i>Nature Communications</i> , 2021, 12, 2559.	12.8	68
5	Evolution and structure of clinically relevant gene fusions in multiple myeloma. <i>Nature Communications</i> , 2020, 11, 2666.	12.8	31
6	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
7	Single-Cell Transcriptomic and Proteomic Diversity in Multiple Myeloma. <i>Blood</i> , 2019, 134, 5531-5531.	1.4	1
8	Architecture of Sample Preparation and Data Governance of Immuno-Genomic Data Collected from Bone Marrow and Peripheral Blood Samples Obtained from Multiple Myeloma Patients. <i>Blood</i> , 2020, 136, 17-18.	1.4	1
9	Single-Cell Pathway Enrichment and Regulatory Profiling of Multiple Myeloma across Disease Stages. <i>Blood</i> , 2019, 134, 364-364.	1.4	0
10	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
11	Myeloma Cell Associated Therapeutic Protein Discovery Using Single Cell RNA-Seq Data. <i>Blood</i> , 2020, 136, 4-5.	1.4	0
12	Identification and Validation of CD138- Multiple Myeloma Immune and Tumor Subpopulations Using Cross Center Scrna-Seq Data. <i>Blood</i> , 2020, 136, 15-15.	1.4	0
13	Pollock: Fishing for Cell States. <i>Bioinformatics Advances</i> , 0, , .	2.4	0