

# Kent A Riemondy

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7539869/publications.pdf>

Version: 2024-02-01

29  
papers

1,495  
citations

623574

14  
h-index

677027

22  
g-index

40  
all docs

40  
docs citations

40  
times ranked

2553  
citing authors

#	ARTICLE	IF	CITATIONS
1	Venetoclax with azacitidine disrupts energy metabolism and targets leukemia stem cells in patients with acute myeloid leukemia. <i>Nature Medicine</i> , 2018, 24, 1859-1866.	15.2	496
2	Monocytic Subclones Confer Resistance to Venetoclax-Based Therapy in Patients with Acute Myeloid Leukemia. <i>Cancer Discovery</i> , 2020, 10, 536-551.	7.7	252
3	Single-cell RNA sequencing identifies TGF- $\beta$ 2 as a key regenerative cue following LPS-induced lung injury. <i>JCI Insight</i> , 2019, 4, .	2.3	111
4	Ineffectual Type 2 $\alpha$ -to $\alpha$ -Type 1 Alveolar Epithelial Cell Differentiation in Idiopathic Pulmonary Fibrosis: Persistence of the KRT8 <sup>hi</sup> Transitional State. <i>American Journal of Respiratory and Critical Care Medicine</i> , 2020, 201, 1443-1447.	2.5	107
5	TCR signal strength controls thymic differentiation of iNKT cell subsets. <i>Nature Communications</i> , 2018, 9, 2650.	5.8	79
6	clustifyr: an R package for automated single-cell RNA sequencing cluster classification. <i>F1000Research</i> , 2020, 9, 223.	0.8	71
7	Alternative RNA structures formed during transcription depend on elongation rate and modify RNA processing. <i>Molecular Cell</i> , 2021, 81, 1789-1801.e5.	4.5	54
8	Neoplastic and immune single-cell transcriptomics define subgroup-specific intra-tumoral heterogeneity of childhood medulloblastoma. <i>Neuro-Oncology</i> , 2022, 24, 273-286.	0.6	52
9	valr: Reproducible genome interval analysis in R. <i>F1000Research</i> , 2017, 6, 1025.	0.8	50
10	Single-Cell RNA Sequencing of Childhood Ependymoma Reveals Neoplastic Cell Subpopulations That Impact Molecular Classification and Etiology. <i>Cell Reports</i> , 2020, 32, 108023.	2.9	47
11	Dynamic temperature-sensitive A-to-I RNA editing in the brain of a heterothermic mammal during hibernation. <i>Rna</i> , 2018, 24, 1481-1495.	1.6	31
12	clustifyr: an R package for automated single-cell RNA sequencing cluster classification. <i>F1000Research</i> , 2020, 9, 223.	0.8	21
13	ENTPD3 Marks Mature Stem Cell-Derived $\beta$ 2-Cells Formed by Self-Aggregation In Vitro. <i>Diabetes</i> , 2021, 70, 2554-2567.	0.3	20
14	Fatal COVID-19 and Non-COVID-19 Acute Respiratory Distress Syndrome Is Associated with Incomplete Alveolar Type 1 Epithelial Cell Differentiation from the Transitional State without Fibrosis. <i>American Journal of Pathology</i> , 2022, 192, 454-467.	1.9	18
15	Recovery and analysis of transcriptome subsets from pooled single-cell RNA-seq libraries. <i>Nucleic Acids Research</i> , 2019, 47, e20-e20.	6.5	16
16	Redistribution of EC-SOD resolves bleomycin-induced inflammation <i>via</i> increased apoptosis of recruited alveolar macrophages. <i>FASEB Journal</i> , 2019, 33, 13465-13475.	0.2	14
17	Liver Transcriptome Dynamics During Hibernation Are Shaped by a Shifting Balance Between Transcription and RNA Stability. <i>Frontiers in Physiology</i> , 2021, 12, 662132.	1.3	11
18	Dynamic RNA Regulation in the Brain Underlies Physiological Plasticity in a Hibernating Mammal. <i>Frontiers in Physiology</i> , 2020, 11, 624677.	1.3	10

#	ARTICLE	IF	CITATIONS
19	Cell-level metadata are indispensable for documenting single-cell sequencing datasets. <i>PLoS Biology</i> , 2021, 19, e3001077.	2.6	7
20	Single-Cell RNA Sequencing Reveals a Unique Monocyte Population in Bronchoalveolar Lavage Cells of Mice Challenged With Afghanistan Particulate Matter and Allergen. <i>Toxicological Sciences</i> , 2021, 182, 297-309.	1.4	7
21	Simultaneous measurement of biochemical phenotypes and gene expression in single cells. <i>Nucleic Acids Research</i> , 2020, 48, e59-e59.	6.5	6
22	RNA-binding proteins regulate aldosterone homeostasis in human steroidogenic cells. <i>Rna</i> , 2021, 27, 933-945.	1.6	5
23	EPEN-21. SINGLE CELL RNASEQ IDENTIFIES A PUTATIVE CANCER STEM CELL POPULATION IN POSTERIOR FOSSA EPN. <i>Neuro-Oncology</i> , 2018, 20, i77-i77.	0.6	0
24	EMBR-27. NEOPLASTIC AND IMMUNE SINGLE CELL TRANSCRIPTOMICS DEFINE SUBGROUP-SPECIFIC INTRA-TUMORAL HETEROGENEITY OF CHILDHOOD MEDULLOBLASTOMA. <i>Neuro-Oncology</i> , 2021, 23, i11-i12.	0.6	0
25	EPEN-11. TUMOR DIFFERENTIATION IMPACTS THE BIOLOGY OF RECURRENCE IN CHILDHOOD POSTERIOR FOSSA EPENDYMOMA. <i>Neuro-Oncology</i> , 2021, 23, i15-i16.	0.6	0
26	EPEN-07. SINGLE-CELL RNA SEQUENCING IDENTIFIES A UNIQUE MYELOID SUBPOPULATION ASSOCIATED WITH MESENCHYMAL TUMOR SUBPOPULATION IN POOR OUTCOME PEDIATRIC EPENDYMOMA. <i>Neuro-Oncology</i> , 2021, 23, i14-i15.	0.6	0
27	HGG-26. SINGLE-CELL RNA-SEQ OF PEDIATRIC HIGH-GRADE GLIOMAS IDENTIFIES COMMON ONCOGENIC PROCESSES AMONG DISTINCT TUMOR HISTOLOGIES. <i>Neuro-Oncology</i> , 2021, 23, i22-i22.	0.6	0
28	MBRS-46. CHARTING NEOPLASTIC AND IMMUNE CELL HETEROGENEITY IN HUMAN AND GEM MODELS OF MEDULLOBLASTOMA USING scRNAseq. <i>Neuro-Oncology</i> , 2020, 22, iii406-iii406.	0.6	0
29	EPEN-29. Spatial transcriptomic analysis of ependymoma implicates unresolved wound healing as a driver of tumor progression. <i>Neuro-Oncology</i> , 2022, 24, i45-i45.	0.6	0