

Tom S Smith

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2728993/publications.pdf>

Version: 2024-02-01

12
papers

2,133
citations

1040018

9
h-index

1372553

10
g-index

17
all docs

17
docs citations

17
times ranked

4463
citing authors

#	ARTICLE	IF	CITATIONS
1	UMI-tools: modeling sequencing errors in Unique Molecular Identifiers to improve quantification accuracy. <i>Genome Research</i> , 2017, 27, 491-499.	5.5	1,316
2	Comprehensive identification of RNA-protein interactions in any organism using orthogonal organic phase separation (OOPS). <i>Nature Biotechnology</i> , 2019, 37, 169-178.	17.5	247
3	Alevin efficiently estimates accurate gene abundances from dscRNA-seq data. <i>Genome Biology</i> , 2019, 20, 65.	8.8	195
4	Combining LOPIT with differential ultracentrifugation for high-resolution spatial proteomics. <i>Nature Communications</i> , 2019, 10, 331.	12.8	146
5	Transacting translational regulatory RNA binding proteins. <i>Wiley Interdisciplinary Reviews RNA</i> , 2018, 9, e1465.	6.4	79
6	The Light Chain IgLV3-21 Defines a New Poor Prognostic Subgroup in Chronic Lymphocytic Leukemia: Results of a Multicenter Study. <i>Clinical Cancer Research</i> , 2018, 24, 5048-5057.	7.0	38
7	Organic phase separation opens up new opportunities to interrogate the RNA-binding proteome. <i>Current Opinion in Chemical Biology</i> , 2020, 54, 70-75.	6.1	35
8	CGAT-core: a python framework for building scalable, reproducible computational biology workflows. <i>F1000Research</i> , 0, 8, 377.	1.6	20
9	Moving Profiling Spatial Proteomics Beyond Discrete Classification. <i>Proteomics</i> , 2020, 20, e1900392.	2.2	19
10	Efficient recovery of the RNA-bound proteome and protein-bound transcriptome using phase separation (OOPS). <i>Nature Protocols</i> , 2020, 15, 2568-2588.	12.0	15
11	CGAT-core: a python framework for building scalable, reproducible computational biology workflows. <i>F1000Research</i> , 0, 8, 377.	1.6	11
12	Prior Signal Acquisition Software Versions for Orbitrap Underestimate Low Isobaric Mass Tag Intensities, Without Detriment to Differential Abundance Experiments. <i>ACS Measurement Science Au</i> , 2022, 2, 233-240.	4.4	0