

Britt Adamson

List of Publications by Citations

Source: <https://exaly.com/author-pdf/6917941/britt-adamson-publications-by-citations.pdf>

Version: 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

20
papers

4,942
citations

16
h-index

20
g-index

20
ext. papers

6,608
ext. citations

34.3
avg, IF

5.22
L-index

#	Paper	IF	Citations
20	Genome-Scale CRISPR-Mediated Control of Gene Repression and Activation. <i>Cell</i> , 2014 , 159, 647-61	56.2	1556
19	Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens. <i>Cell</i> , 2016 , 167, 1853-1866.e17	56.2	675
18	A Multiplexed Single-Cell CRISPR Screening Platform Enables Systematic Dissection of the Unfolded Protein Response. <i>Cell</i> , 2016 , 167, 1867-1882.e21	56.2	518
17	A chromatin localization screen reveals poly (ADP ribose)-regulated recruitment of the repressive polycomb and NuRD complexes to sites of DNA damage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 18475-80	11.5	408
16	Compact and highly active next-generation libraries for CRISPR-mediated gene repression and activation. <i>ELife</i> , 2016 , 5,	8.9	343
15	A genome-wide homologous recombination screen identifies the RNA-binding protein RBMX as a component of the DNA-damage response. <i>Nature Cell Biology</i> , 2012 , 14, 318-28	23.4	300
14	Polyubiquitinated PCNA recruits the ZRANB3 translocase to maintain genomic integrity after replication stress. <i>Molecular Cell</i> , 2012 , 47, 396-409	17.6	194
13	Pervasive functional translation of noncanonical human open reading frames. <i>Science</i> , 2020 , 367, 1140-1146	33.6	168
12	Molecular recording of mammalian embryogenesis. <i>Nature</i> , 2019 , 570, 77-82	50.4	140
11	Mapping the Genetic Landscape of Human Cells. <i>Cell</i> , 2018 , 174, 953-967.e22	56.2	136
10	A bioinformatics method identifies prominent off-targeted transcripts in RNAi screens. <i>Nature Methods</i> , 2012 , 9, 363-6	21.6	119
9	A Systematic Analysis of Factors Localized to Damaged Chromatin Reveals PARP-Dependent Recruitment of Transcription Factors. <i>Cell Reports</i> , 2015 , 11, 1486-500	10.6	100
8	Combinatorial single-cell CRISPR screens by direct guide RNA capture and targeted sequencing. <i>Nature Biotechnology</i> , 2020 , 38, 954-961	44.5	85
7	A genome-wide camptothecin sensitivity screen identifies a mammalian MMS22L-NFKBIL2 complex required for genomic stability. <i>Molecular Cell</i> , 2010 , 40, 645-57	17.6	81
6	Enhanced prime editing systems by manipulating cellular determinants of editing outcomes. <i>Cell</i> , 2021 , 184, 5635-5652.e29	56.2	48
5	Efficient C _T -to-G _T base editors developed using CRISPRi screens, target-library analysis, and machine learning. <i>Nature Biotechnology</i> , 2021 , 39, 1414-1425	44.5	32
4	Approaches to maximize sgRNA-barcode coupling in Perturb-seq screens		14

3	Mapping the genetic landscape of DNA double-strand break repair. <i>Cell</i> , 2021 , 184, 5653-5669.e25	56.2	12
2	Prime Editing: Precision Genome Editing by Reverse Transcription. <i>Molecular Cell</i> , 2020 , 77, 210-212	17.6	11
1	Mapping the Genetic Landscape of DNA Double-strand Break Repair		2