Britt Adamson

List of Publications by Year in Descending Order

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	Enhanced prime editing systems by manipulating cellular determinants of editing outcomes. *Cell*, **2021**, 184, 5635-5652.e29	56.2	48
19	Mapping the genetic landscape of DNA double-strand break repair. *Cell*, **2021**, 184, 5653-5669.e25	56.2	12
18	Efficient C□-to-G□ base editors developed using CRISPRi screens, target-library analysis, and machine learning. *Nature Biotechnology*, **2021**, 39, 1414-1425	44.5	32
17	Pervasive functional translation of noncanonical human open reading frames. *Science*, **2020**, 367, 1140-1146	33.9	168
16	Combinatorial single-cell CRISPR screens by direct guide RNA capture and targeted sequencing. *Nature Biotechnology*, **2020**, 38, 954-961	44.5	85
15	Prime Editing: Precision Genome Editing by Reverse Transcription. *Molecular Cell*, **2020**, 77, 210-212	17.6	11
14	Molecular recording of mammalian embryogenesis. *Nature*, **2019**, 570, 77-82	50.4	140
13	Mapping the Genetic Landscape of Human Cells. *Cell*, **2018**, 174, 953-967.e22	56.2	136
12	Compact and highly active next-generation libraries for CRISPR-mediated gene repression and activation. *ELife*, **2016**, 5,	8.9	343
11	Perturb-Seq: Dissecting Molecular Circuits with Scalable Single-Cell RNA Profiling of Pooled Genetic Screens. *Cell*, **2016**, 167, 1853-1866.e17	56.2	675
10	A Multiplexed Single-Cell CRISPR Screening Platform Enables Systematic Dissection of the Unfolded Protein Response. *Cell*, **2016**, 167, 1867-1882.e21	56.2	518
9	A Systematic Analysis of Factors Localized to Damaged Chromatin Reveals PARP-Dependent Recruitment of Transcription Factors. *Cell Reports*, **2015**, 11, 1486-500	10.6	100
8	Genome-Scale CRISPR-Mediated Control of Gene Repression and Activation. *Cell*, **2014**, 159, 647-61	56.2	1556
7	Polyubiquitinated PCNA recruits the ZRANB3 translocase to maintain genomic integrity after replication stress. *Molecular Cell*, **2012**, 47, 396-409	17.6	194
6	A genome-wide homologous recombination screen identifies the RNA-binding protein RBMX as a component of the DNA-damage response. *Nature Cell Biology*, **2012**, 14, 318-28	23.4	300
5	A bioinformatics method identifies prominent off-targeted transcripts in RNAi screens. *Nature Methods*, **2012**, 9, 363-6	21.6	119
4	A chromatin localization screen reveals poly (ADP ribose)-regulated recruitment of the repressive polycomb and NuRD complexes to sites of DNA damage. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 18475-80	11.5	408

List of Publications

3	A genome-wide camptothecin sensitivity screen identifies a mammalian MMS22L-NFKBIL2 complex required for genomic stability. *Molecular Cell*, **2010**, 40, 645-57	17.6	81
2	Approaches to maximize sgRNA-barcode coupling in Perturb-seq screens		14
1	Mapping the Genetic Landscape of DNA Double-strand Break Repair		2