

# Changwei Shao

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4350627/publications.pdf>

Version: 2024-02-01

18  
papers

1,360  
citations

759233

12  
h-index

839539

18  
g-index

21  
all docs

21  
docs citations

21  
times ranked

2553  
citing authors

#	ARTICLE	IF	CITATIONS
1	ILF3 represses repeat-derived microRNAs targeting RIG-I mediated type I interferon response. <i>Journal of Molecular Biology</i> , 2022, 434, 167469.	4.2	2
2	ADAR1-mediated RNA editing links ganglioside catabolism to glioblastoma stem cell maintenance. <i>Journal of Clinical Investigation</i> , 2022, 132, .	8.2	27
3	Wiskott-Aldrich syndrome protein forms nuclear condensates and regulates alternative splicing. <i>Nature Communications</i> , 2022, 13, .	12.8	6
4	Widespread Alternative Splicing Changes in Metastatic Breast Cancer Cells. <i>Cells</i> , 2021, 10, 858.	4.1	10
5	Global Alternative Splicing Defects in Human Breast Cancer Cells. <i>Cancers</i> , 2021, 13, 3071.	3.7	6
6	Active retrotransposons help maintain pericentromeric heterochromatin required for faithful cell division. <i>Genome Research</i> , 2020, 30, 1570-1582.	5.5	9
7	Initiation of Parental Genome Reprogramming in Fertilized Oocyte by Splicing Kinase SRPK1-Catalyzed Protamine Phosphorylation. <i>Cell</i> , 2020, 180, 1212-1227.e14.	28.9	54
8	RBFOX2-miR-34a-JPH2 axis contributes to cardiac decompensation during heart failure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 6172-6180.	7.1	32
9	The Augmented R-Loop Is a Unifying Mechanism for Myelodysplastic Syndromes Induced by High-Risk Splicing Factor Mutations. <i>Molecular Cell</i> , 2018, 69, 412-425.e6.	9.7	203
10	Capturing the interactome of newly transcribed RNA. <i>Nature Methods</i> , 2018, 15, 213-220.	19.0	170
11	R-ChIP Using Inactive RNase H Reveals Dynamic Coupling of R-loops with Transcriptional Pausing at Gene Promoters. <i>Molecular Cell</i> , 2017, 68, 745-757.e5.	9.7	263
12	NEAT1 scaffolds RNA-binding proteins and the Microprocessor to globally enhance pri-miRNA processing. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 816-824.	8.2	165
13	SPOP-containing complex regulates SETD2 stability and H3K36me3-coupled alternative splicing. <i>Nucleic Acids Research</i> , 2017, 45, 92-105.	14.5	60
14	Distinct splicing signatures affect converged pathways in myelodysplastic syndrome patients carrying mutations in different splicing regulators. <i>Rna</i> , 2016, 22, 1535-1549.	3.5	40
15	Mechanisms for U2AF to define 5' splice sites and regulate alternative splicing in the human genome. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 997-1005.	8.2	150
16	Pseudo attP sites in favor of transgene integration and expression in cultured porcine cells identified by streptomyces phage phiC31 integrase. <i>BMC Molecular Biology</i> , 2013, 14, 20.	3.0	14
17	Nuclear Matrix Factor hnRNP U/SAF-A Exerts a Global Control of Alternative Splicing by Regulating U2 snRNP Maturation. <i>Molecular Cell</i> , 2012, 45, 656-668.	9.7	146
18	Construction and application of a built-in dual luciferase reporter for microRNA functional analysis. <i>Electronic Journal of Biotechnology</i> , 2011, 14, .	2.2	2