Shimin Shuai

List of Publications by Year in Descending Order

15 papers	722 citations	11 h-index	16 g-index
16 ext. papers	1,075 ext. citations	21.9 avg, IF	3.87 L-index

#	Paper	IF	Citations
15	PanCancer analysis of somatic mutations in repetitive regions reveals recurrent mutations in snRNA U2.. *Npj Genomic Medicine*, **2022**, 7, 19	6.2	1
14	Interruption of Klf5 acetylation in basal progenitor cells promotes luminal commitment by activating Notch signaling.. *Journal of Genetics and Genomics*, **2021**,	4	0
13	Candidate Cancer Driver Mutations in Distal Regulatory Elements and Long-Range Chromatin Interaction Networks. *Molecular Cell*, **2020**, 77, 1307-1321.e10	17.6	20
12	Combined burden and functional impact tests for cancer driver discovery using DriverPower. *Nature Communications*, **2020**, 11, 734	17.4	16
11	Integrative pathway enrichment analysis of multivariate omics data. *Nature Communications*, **2020**, 11, 735	17.4	53
10	Pathway and network analysis of more than 2500 whole cancer genomes. *Nature Communications*, **2020**, 11, 729	17.4	38
9	Analyses of non-coding somatic drivers in 2,658 cancer whole genomes. *Nature*, **2020**, 578, 102-111	50.4	220
8	Cancer LncRNA Census reveals evidence for deep functional conservation of long noncoding RNAs in tumorigenesis. *Communications Biology*, **2020**, 3, 56	6.7	77
7	The U1 spliceosomal RNA is recurrently mutated in multiple cancers. *Nature*, **2019**, 574, 712-716	50.4	79
6	MEDU-39. HIGHLY RECURRENT U1 SMALL NUCLEAR RNA HOTSPOT MUTATIONS DRIVE ALTERNATIVE SPLICING IN SONIC HEDGEHOG MEDULLOBLASTOMA. *Neuro-Oncology*, **2019**, 21, ii111-ii111	1	78
5	Recurrent noncoding U1 snRNA mutations drive cryptic splicing in SHH medulloblastoma. *Nature*, **2019**, 574, 707-711	50.4	78
4	Recurrent noncoding regulatory mutations in pancreatic ductal adenocarcinoma. *Nature Genetics*, **2017**, 49, 825-833	36.3	41
3	DriverPower: Combined burden and functional impact tests for cancer driver discovery		4
2	Candidate cancer driver mutations in superenhancers and long-range chromatin interaction networks		5
1	Discovery and characterization of coding and non-coding driver mutations in more than 2,500 whole cancer genomes		12