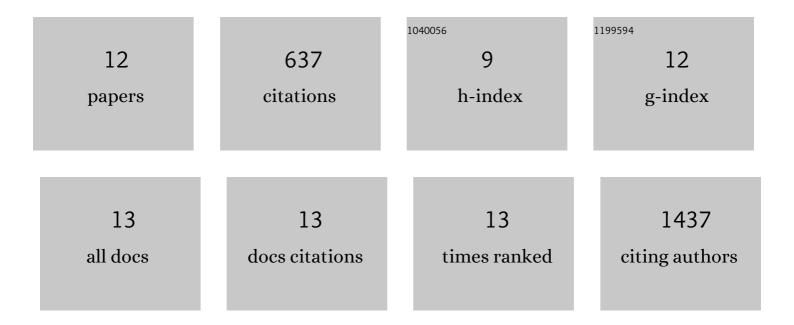
## Chang Xu

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/434923/publications.pdf Version: 2024-02-01



#	Article	IF	CITATIONS
1	Genomic and Epigenomic Profiling of High-Risk Intestinal Metaplasia Reveals Molecular Determinants of Progression to Gastric Cancer. Cancer Cell, 2018, 33, 137-150.e5.	16.8	175
2	Epigenomic profiling of primary gastric adenocarcinoma reveals super-enhancer heterogeneity. Nature Communications, 2016, 7, 12983.	12.8	123
3	<i>VHL</i> Deficiency Drives Enhancer Activation of Oncogenes in Clear Cell Renal Cell Carcinoma. Cancer Discovery, 2017, 7, 1284-1305.	9.4	111
4	Epigenomic Promoter Alterations Amplify Gene Isoform and Immunogenic Diversity in Gastric Adenocarcinoma. Cancer Discovery, 2017, 7, 630-651.	9.4	48
5	Long-read transcriptome sequencing reveals abundant promoter diversity in distinct molecular subtypes of gastric cancer. Genome Biology, 2021, 22, 44.	8.8	46
6	HoxC5 and miR-615-3p target newly evolved genomic regions to repress hTERT and inhibit tumorigenesis. Nature Communications, 2018, 9, 100.	12.8	38
7	Integrated paired-end enhancer profiling and whole-genome sequencing reveals recurrent <i>CCNE1</i> and <i>IGF2</i> enhancer hijacking in primary gastric adenocarcinoma. Gut, 2020, 69, 1039-1052.	12.1	36
8	<i>HNF4α</i> pathway mapping identifies wild-type <i>IDH1</i> as a targetable metabolic node in gastric cancer. Gut, 2020, 69, 231-242.	12.1	27
9	Genomic and epigenomic EBF1 alterations modulate TERT expression in gastric cancer. Journal of Clinical Investigation, 2020, 130, 3005-3020.	8.2	12
10	Integrative epigenomic and high-throughput functional enhancer profiling reveals determinants of enhancer heterogeneity in gastric cancer. Genome Medicine, 2021, 13, 158.	8.2	7
11	Chromatin Rewiring by Mismatch Repair Protein MSH2 Alters Cell Adhesion Pathways and Sensitivity to BET Inhibition in Gastric Cancer. Cancer Research, 2022, 82, 2538-2551.	0.9	7
12	Regulatory enhancer profiling of mesenchymal-type gastric cancer reveals subtype-specific epigenomic landscapes and targetable vulnerabilities. Gut, 2023, 72, 226-241.	12.1	6