

# Zhengtao Xiao

## List of Publications by Year in descending order

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Version: 2024-02-01

32  
papers

1,883  
citations

430874

18  
h-index

454955

30  
g-index

36  
all docs

36  
docs citations

36  
times ranked

3551  
citing authors

#	ARTICLE	IF	CITATIONS
1	Metabolic landscape of the tumor microenvironment at single cell resolution. Nature Communications, 2019, 10, 3763.	12.8	290
2	Disturbed mitochondrial dynamics in CD8+ TILs reinforce T cell exhaustion. Nature Immunology, 2020, 21, 1540-1551.	14.5	252
3	Transcriptional diversity and bioenergetic shift in human breast cancer metastasis revealed by single-cell RNA sequencing. Nature Cell Biology, 2020, 22, 310-320.	10.3	189
4	Genome-wide assessment of differential translations with ribosome profiling data. Nature Communications, 2016, 7, 11194.	12.8	179
5	Germinal-center development of memory B cells driven by IL-9 from follicular helper T cells. Nature Immunology, 2017, 18, 921-930.	14.5	132
6	Function of HNRNPC in breast cancer cells by controlling the dsRNA-induced interferon response. EMBO Journal, 2018, 37, .	7.8	131
7	De novo annotation and characterization of the translome with ribosome profiling data. Nucleic Acids Research, 2018, 46, e61-e61.	14.5	104
8	Oncogenic Properties of NEAT1 in Prostate Cancer Cells Depend on the CDC5L-AGRN Transcriptional Regulation Circuit. Cancer Research, 2018, 78, 4138-4149.	0.9	83
9	Tumor-induced reshuffling of lipid composition on the endoplasmic reticulum membrane sustains macrophage survival and pro-tumorigenic activity. Nature Immunology, 2021, 22, 1403-1415.	14.5	72
10	Dynamic mechanisms for pre-miRNA binding and export by Exportin-5. Rna, 2011, 17, 1511-1528.	3.5	55
11	Where do health benefits of flavonoids come from? Insights from flavonoid targets and their evolutionary history. Biochemical and Biophysical Research Communications, 2013, 434, 701-704.	2.1	54
12	ZEB1 Represses Neural Differentiation and Cooperates with CTBP2 to Dynamically Regulate Cell Migration during Neocortex Development. Cell Reports, 2019, 27, 2335-2353.e6.	6.4	49
13	Base- and Structure-Dependent DNA Dinucleotide-Carbon Nanotube Interactions: Molecular Dynamics Simulations and Thermodynamic Analysis. Journal of Physical Chemistry C, 2011, 115, 21546-21558.	3.1	37
14	Combined 3D-QSAR, Molecular Docking and Molecular Dynamics Study on Derivatives of Peptide Epoxyketone and Tyropeptin-Boronic Acid as Inhibitors Against the Î²5 Subunit of Human 20S Proteasome. International Journal of Molecular Sciences, 2011, 12, 1807-1835.	4.1	34
15	Survey of the translation shifts in hepatocellular carcinoma with ribosome profiling. Theranostics, 2019, 9, 4141-4155.	10.0	33
16	Mutual dependency between lncRNA LETN and protein NPM1 in controlling the nucleolar structure and functions sustaining cell proliferation. Cell Research, 2021, 31, 664-683.	12.0	30
17	Ribosome Profiling Reveals Genome-wide Cellular Translational Regulation upon Heat Stress in Escherichia coli. Genomics, Proteomics and Bioinformatics, 2017, 15, 324-330.	6.9	26
18	Dependency of the Cancer-Specific Transcriptional Regulation Circuitry on the Promoter DNA Methylome. Cell Reports, 2019, 26, 3461-3474.e5.	6.4	22

#	ARTICLE	IF	CITATIONS
19	Insight into the Structural Requirements of Benzothiadiazine Scaffold-Based Derivatives as Hepatitis C Virus NS5B Polymerase Inhibitors Using 3D-QSAR, Molecular Docking and Molecular Dynamics. <i>Current Medicinal Chemistry</i> , 2011, 18, 4019-4028.	2.4	16
20	Two TPX2-Dependent Switches Control the Activity of Aurora A. <i>PLoS ONE</i> , 2011, 6, e16757.	2.5	15
21	Development of in silico models for pyrazoles and pyrimidine derivatives as cyclin-dependent kinase 2 inhibitors. <i>Journal of Molecular Graphics and Modelling</i> , 2011, 30, 67-81.	2.4	15
22	Metabolism in the tumor microenvironment: insights from single-cell analysis. <i>Oncolmmunology</i> , 2020, 9, 1726556.	4.6	13
23	Studies of New Fused Benzazepine as Selective Dopamine D3 Receptor Antagonists Using 3D-QSAR, Molecular Docking and Molecular Dynamics. <i>International Journal of Molecular Sciences</i> , 2011, 12, 1196-1221.	4.1	10
24	RiboMiner: a toolset for mining multi-dimensional features of the translome with ribosome profiling data. <i>BMC Bioinformatics</i> , 2020, 21, 340.	2.6	10
25	Structural determinants of imidacloprid-based nicotinic acetylcholine receptor inhibitors identified using 3D-QSAR, docking and molecular dynamics. <i>Journal of Molecular Modeling</i> , 2012, 18, 2279-2289.	1.8	8
26	Molecular simulation of a series of benzothiazole PI3K $\alpha$ inhibitors: probing the relationship between structural features, anti-tumor potency and selectivity. <i>Journal of Molecular Modeling</i> , 2012, 18, 2943-2958.	1.8	8
27	Epigenomic links from metabolism $\alpha$ methionine and chromatin architecture. <i>Current Opinion in Chemical Biology</i> , 2021, 63, 11-18.	6.1	5
28	Molecular dynamics simulation of conformational heterogeneity in transportin 1. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 382-397.	2.6	4
29	Triangular Model Registration Algorithm Through Differential Topological Singularity Points by Helmholtz-Hodge Decomposition. <i>IEEE Access</i> , 2019, 7, 34776-34790.	4.2	2
30	&lt;em>De novo&lt;/em> Identification of Actively Translated Open Reading Frames with Ribosome Profiling Data. <i>Journal of Visualized Experiments</i> , 2022, , .	0.3	1
31	Abstract A2-54: DNA methylation-dependent transcription regulatory networks elucidate dynamics of transcription regulatory circuitry in cancers. , 2015, , .		0
32	Abstract B2-25: DNA methylation-dependent transcription regulatory networks elucidate dynamics of transcription regulatory circuitry in cancers. , 2015, , .		0