Zhengtao Xiao

List of Publications by Year
in descending order

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	De novo Identification of Actively Translated Open Reading Frames with Ribosome Profiling Data. Journal of Visualized Experiments, 2022, , .	0.3	1
2	Epigenomic links from metabolism—methionine and chromatin architecture. Current Opinion in Chemical Biology, 2021, 63, 11-18.	6.1	5
3	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
4	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
5	Disturbed mitochondrial dynamics in CD8+ TILs reinforce T cell exhaustion. Nature Immunology, 2020, 21, 1540-1551.	14.5	252
6	RiboMiner: a toolset for mining multi-dimensional features of the translatome with ribosome profiling data. BMC Bioinformatics, 2020, 21, 340.	2.6	10
7	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
8	Metabolism in the tumor microenvironment: insights from single-cell analysis. OncoImmunology, 2020, 9, 1726556.	4.6	13
9	Survey of the translation shifts in hepatocellular carcinoma with ribosome profiling. Theranostics, 2019, 9, 4141-4155.	10.0	33
10	Metabolic landscape of the tumor microenvironment at single cell resolution. Nature Communications, 2019, 10, 3763.	12.8	290
11	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
12	Dependency of the Cancer-Specific Transcriptional Regulation Circuitry on the Promoter DNA Methylome. Cell Reports, 2019, 26, 3461-3474.e5.	6.4	22
13	Triangular Model Registration Algorithm Through Differential Topological Singularity Points by Helmholtz-Hodge Decomposition. IEEE Access, 2019, 7, 34776-34790.	4.2	2
14	De novo annotation and characterization of the translatome with ribosome profiling data. Nucleic Acids Research, 2018, 46, e61-e61.	14.5	104
15	Function of HNRNPC in breast cancer cells by controlling the dsRNA–induced interferon response. EMBO Journal, 2018, 37, .	7.8	131
16	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
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	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

#	Article	IF	Citations
19	Genome-wide assessment of differential translations with ribosome profiling data. Nature Communications, 2016, 7, 11194.	12.8	179
20	Abstract A2-54: DNA methylation-dependent transcription regulatory networks elucidate dynamics of transcription regulatory circuitry in cancers. , 2015, , .		0
21	Abstract B2-25: DNA methylation-dependent transcription regulatory networks elucidate dynamics of transcription regulatory circuitry in cancers. , 2015, , .		0
22	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
23	Molecular dynamics simulation of conformational heterogeneity in transportin 1. Proteins: Structure, Function and Bioinformatics, 2012, 80, 382-397.	2.6	4
24	Structural determinants of imidacloprid-based nicotinic acetylcholine receptor inhibitors identified using 3D-QSAR, docking and molecular dynamics. Journal of Molecular Modeling, 2012, 18, 2279-2289.	1.8	8
25	Molecular simulation of a series of benzothiazole PI3KÎ± inhibitors: probing the relationship between structural features, anti-tumor potency and selectivity. Journal of Molecular Modeling, 2012, 18, 2943-2958.	1.8	8
26	Base- and Structure-Dependent DNA Dinucleotideâ€"Carbon Nanotube Interactions: Molecular Dynamics Simulations and Thermodynamic Analysis. Journal of Physical Chemistry C, 2011, 115, 21546-21558.	3.1	37
27	Two TPX2-Dependent Switches Control the Activity of Aurora A. PLoS ONE, 2011, 6, e16757.	2.5	15
28	Development of in silico models for pyrazoles and pyrimidine derivatives as cyclin-dependent kinase 2 inhibitors. Journal of Molecular Graphics and Modelling, 2011, 30, 67-81.	2.4	15
29	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. Current Medicinal Chemistry, 2011, 18, 4019-4028.	2.4	16
30	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
31	Dynamic mechanisms for pre-miRNA binding and export by Exportin-5. Rna, 2011, 17, 1511-1528.	3.5	55
32	Studies of New Fused Benzazepine as Selective Dopamine D3 Receptor Antagonists Using 3D-QSAR, Molecular Docking and Molecular Dynamics. International Journal of Molecular Sciences, 2011, 12, 1196-1221.	4.1	10