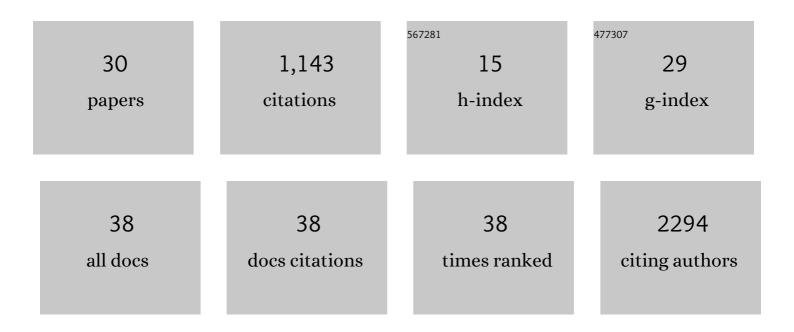
Xinghua Lu

List of Publications by Year in descending order

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XINCHUA LU

#	Article	IF	CITATIONS
1	MST4 Phosphorylation of ATG4B Regulates Autophagic Activity, Tumorigenicity, and Radioresistance in Glioblastoma. Cancer Cell, 2017, 32, 840-855.e8.	16.8	188
2	Phenotypic Plasticity of Invasive Edge Glioma Stem-like Cells in Response to Ionizing Radiation. Cell Reports, 2019, 26, 1893-1905.e7.	6.4	161
3	Precision Oncology beyond Targeted Therapy: Combining Omics Data with Machine Learning Matches the Majority of Cancer Cells to Effective Therapeutics. Molecular Cancer Research, 2018, 16, 269-278.	3.4	127
4	Investigating immune and non-immune cell interactions in head and neck tumors by single-cell RNA sequencing. Nature Communications, 2021, 12, 7338.	12.8	104
5	Learning a hierarchical representation of the yeast transcriptomic machinery using an autoencoder model. BMC Bioinformatics, 2016, 17, 9.	2.6	76
6	A regulatory circuit of miR-125b/miR-20b and Wnt signalling controls glioblastoma phenotypes through FZD6-modulated pathways. Nature Communications, 2016, 7, 12885.	12.8	72
7	Pharmacologic Suppression of B7-H4 Glycosylation Restores Antitumor Immunity in Immune-Cold Breast Cancers. Cancer Discovery, 2020, 10, 1872-1893.	9.4	66
8	Chitinase-3-like 1 protein complexes modulate macrophage-mediated immune suppression in glioblastoma. Journal of Clinical Investigation, 2021, 131, .	8.2	49
9	Unsupervised deep learning reveals prognostically relevant subtypes of glioblastoma. BMC Bioinformatics, 2017, 18, 381.	2.6	38
10	A novel strategy to block mitotic progression for targeted therapy. EBioMedicine, 2019, 49, 40-54.	6.1	33
11	Trans-species learning of cellular signaling systems with bimodal deep belief networks. Bioinformatics, 2015, 31, 3008-3015.	4.1	32
12	Systematic discovery of the functional impact of somatic genome alterations in individual tumors through tumor-specific causal inference. PLoS Computational Biology, 2019, 15, e1007088.	3.2	31
13	Genome-wide methylomic and transcriptomic analyses identify subtype-specific epigenetic signatures commonly dysregulated in glioma stem cells and glioblastoma. Epigenetics, 2018, 13, 432-448.	2.7	29
14	Interferon Î ² drives intestinal regeneration after radiation. Science Advances, 2021, 7, eabi5253.	10.3	20
15	eIF4E S209 phosphorylation licenses myc- and stress-driven oncogenesis. ELife, 2020, 9, .	6.0	19
16	ldentifying Driver Genomic Alterations in Cancers by Searching Minimum-Weight, Mutually Exclusive Sets. PLoS Computational Biology, 2015, 11, e1004257.	3.2	18
17	Integrating data and knowledge to identify functional modules of genes: a multilayer approach. BMC Bioinformatics, 2019, 20, 225.	2.6	11
18	From Data towards Knowledge: Revealing the Architecture of Signaling Systems by Unifying Knowledge Mining and Data Mining of Systematic Perturbation Data. PLoS ONE, 2013, 8, e61134.	2.5	11

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#	Article	IF	CITATIONS
19	Knowledge transfer via classification rules using functional mapping for integrative modeling of gene expression data. BMC Bioinformatics, 2015, 16, 226.	2.6	10
20	Learning to encode cellular responses to systematic perturbations with deep generative models. Npj Systems Biology and Applications, 2020, 6, 35.	3.0	7
21	From genome to phenome: Predicting multiple cancer phenotypes based on somatic genomic alterations via the genomic impact transformer. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2020, 25, 79-90.	0.7	7
22	Conceptualization of molecular findings by mining gene annotations. BMC Proceedings, 2013, 7, S2.	1.6	5
23	Integrating genome and functional genomics data to reveal perturbed signaling pathways in ovarian cancers. AMIA Summits on Translational Science Proceedings, 2012, 2012, 72-8.	0.4	5
24	Targeting Myc-driven stress vulnerability in mutant KRAS colorectal cancer. Molecular Biomedicine, 2022, 3, 10.	4.4	4
25	Discovering functional impacts of miRNAs in cancers using a causal deep learning model. BMC Medical Genomics, 2018, 11, 116.	1.5	3
26	Tumour-specific Causal Inference Discovers Distinct Disease Mechanisms Underlying Cancer Subtypes. Scientific Reports, 2019, 9, 13225.	3.3	3
27	Explicit representation of protein activity states significantly improves causal discovery of protein phosphorylation networks. BMC Bioinformatics, 2020, 21, 379.	2.6	3
28	Revealing common disease mechanisms shared by tumors of different tissues of origin through semantic representation of genomic alterations and topic modeling. BMC Genomics, 2017, 18, 105.	2.8	2
29	Testing of a machine learning (ML) model for ability to predict oxaliplatin and bevacizumab (bev) benefit in NRG Oncology/NSABP C-07 and C-08 Journal of Clinical Oncology, 2022, 40, 3607-3607.	1.6	1
30	De novo Prediction of Cell-Drug Sensitivities Using Deep Learning-based Graph Regularized Matrix Factorization. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2022, 27, 278-289.	0.7	0