

Xinghua Lu

List of Publications by Year in descending order

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Version: 2024-02-01

30
papers

1,143
citations

567281

15
h-index

477307

29
g-index

38
all docs

38
docs citations

38
times ranked

2294
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	Targeting Myc-driven stress vulnerability in mutant KRAS colorectal cancer. Molecular Biomedicine, 2022, 3, 10.	4.4	4
3	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
4	Chitinase-3-like 1 protein complexes modulate macrophage-mediated immune suppression in glioblastoma. Journal of Clinical Investigation, 2021, 131, .	8.2	49
5	Interferon β drives intestinal regeneration after radiation. Science Advances, 2021, 7, eabi5253.	10.3	20
6	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
7	Explicit representation of protein activity states significantly improves causal discovery of protein phosphorylation networks. BMC Bioinformatics, 2020, 21, 379.	2.6	3
8	Pharmacologic Suppression of B7-H4 Glycosylation Restores Antitumor Immunity in Immune-Cold Breast Cancers. Cancer Discovery, 2020, 10, 1872-1893.	9.4	66
9	Learning to encode cellular responses to systematic perturbations with deep generative models. Npj Systems Biology and Applications, 2020, 6, 35.	3.0	7
10	eIF4E S209 phosphorylation licenses myc- and stress-driven oncogenesis. ELife, 2020, 9, .	6.0	19
11	From genome to phenotype: 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
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	A novel strategy to block mitotic progression for targeted therapy. EBioMedicine, 2019, 49, 40-54.	6.1	33
14	Tumour-specific Causal Inference Discovers Distinct Disease Mechanisms Underlying Cancer Subtypes. Scientific Reports, 2019, 9, 13225.	3.3	3
15	Integrating data and knowledge to identify functional modules of genes: a multilayer approach. BMC Bioinformatics, 2019, 20, 225.	2.6	11
16	Phenotypic Plasticity of Invasive Edge Glioma Stem-like Cells in Response to Ionizing Radiation. Cell Reports, 2019, 26, 1893-1905.e7.	6.4	161
17	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
18	Discovering functional impacts of miRNAs in cancers using a causal deep learning model. BMC Medical Genomics, 2018, 11, 116.	1.5	3

#	ARTICLE	IF	CITATIONS
19	Genome-wide methylomic and transcriptomic analyses identify subtype-specific epigenetic signatures commonly dysregulated in glioma stem cells and glioblastoma. <i>Epigenetics</i> , 2018, 13, 432-448.	2.7	29
20	MST4 Phosphorylation of ATG4B Regulates Autophagic Activity, Tumorigenicity, and Radioresistance in Glioblastoma. <i>Cancer Cell</i> , 2017, 32, 840-855.e8.	16.8	188
21	Revealing common disease mechanisms shared by tumors of different tissues of origin through semantic representation of genomic alterations and topic modeling. <i>BMC Genomics</i> , 2017, 18, 105.	2.8	2
22	Unsupervised deep learning reveals prognostically relevant subtypes of glioblastoma. <i>BMC Bioinformatics</i> , 2017, 18, 381.	2.6	38
23	A regulatory circuit of miR-125b/miR-20b and Wnt signalling controls glioblastoma phenotypes through FZD6-modulated pathways. <i>Nature Communications</i> , 2016, 7, 12885.	12.8	72
24	Learning a hierarchical representation of the yeast transcriptomic machinery using an autoencoder model. <i>BMC Bioinformatics</i> , 2016, 17, 9.	2.6	76
25	Identifying Driver Genomic Alterations in Cancers by Searching Minimum-Weight, Mutually Exclusive Sets. <i>PLoS Computational Biology</i> , 2015, 11, e1004257.	3.2	18
26	Trans-species learning of cellular signaling systems with bimodal deep belief networks. <i>Bioinformatics</i> , 2015, 31, 3008-3015.	4.1	32
27	Knowledge transfer via classification rules using functional mapping for integrative modeling of gene expression data. <i>BMC Bioinformatics</i> , 2015, 16, 226.	2.6	10
28	Conceptualization of molecular findings by mining gene annotations. <i>BMC Proceedings</i> , 2013, 7, S2.	1.6	5
29	From Data towards Knowledge: Revealing the Architecture of Signaling Systems by Unifying Knowledge Mining and Data Mining of Systematic Perturbation Data. <i>PLoS ONE</i> , 2013, 8, e61134.	2.5	11
30	Integrating genome and functional genomics data to reveal perturbed signaling pathways in ovarian cancers. <i>AMIA Summits on Translational Science Proceedings</i> , 2012, 2012, 72-8.	0.4	5