

# 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  | MST4 Phosphorylation of ATG4B Regulates Autophagic Activity, Tumorigenicity, and Radioresistance in Glioblastoma. <i>Cancer Cell</i> , 2017, 32, 840-855.e8.   | 16.8 | 188       |
| 2  | Phenotypic Plasticity of Invasive Edge Glioma Stem-like Cells in Response to Ionizing Radiation. <i>Cell Reports</i> , 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. <i>Molecular Cancer Research</i> , 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. <i>Nature Communications</i> , 2021, 12, 7338.  | 12.8 | 104       |
| 5  | Learning a hierarchical representation of the yeast transcriptomic machinery using an autoencoder model. <i>BMC Bioinformatics</i> , 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. <i>Nature Communications</i> , 2016, 7, 12885.                                 | 12.8 | 72        |
| 7  | Pharmacologic Suppression of B7-H4 Glycosylation Restores Antitumor Immunity in Immune-Cold Breast Cancers. <i>Cancer Discovery</i> , 2020, 10, 1872-1893.   | 9.4  | 66        |
| 8  | Chitinase-3-like 1 protein complexes modulate macrophage-mediated immune suppression in glioblastoma. <i>Journal of Clinical Investigation</i> , 2021, 131, .  | 8.2  | 49        |
| 9  | Unsupervised deep learning reveals prognostically relevant subtypes of glioblastoma. <i>BMC Bioinformatics</i> , 2017, 18, 381.  | 2.6  | 38        |
| 10 | A novel strategy to block mitotic progression for targeted therapy. <i>EBioMedicine</i> , 2019, 49, 40-54.   | 6.1  | 33        |
| 11 | Trans-species learning of cellular signaling systems with bimodal deep belief networks. <i>Bioinformatics</i> , 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. <i>PLoS Computational Biology</i> , 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. <i>Epigenetics</i> , 2018, 13, 432-448.      | 2.7  | 29        |
| 14 | Interferon $\beta$ drives intestinal regeneration after radiation. <i>Science Advances</i> , 2021, 7, eabi5253.  | 10.3 | 20        |
| 15 | eIF4E S209 phosphorylation licenses myc- and stress-driven oncogenesis. <i>ELife</i> , 2020, 9, .  | 6.0  | 19        |
| 16 | Identifying Driver Genomic Alterations in Cancers by Searching Minimum-Weight, Mutually Exclusive Sets. <i>PLoS Computational Biology</i> , 2015, 11, e1004257.  | 3.2  | 18        |
| 17 | Integrating data and knowledge to identify functional modules of genes: a multilayer approach. <i>BMC Bioinformatics</i> , 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. <i>PLoS ONE</i> , 2013, 8, e61134.                | 2.5  | 11        |

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|----|--|-----|-----------|
| 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         |