

Jinfeng Liu

List of Publications by Year in descending order

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71
papers

15,540
citations

41344

49
h-index

82547

72
g-index

73
all docs

73
docs citations

73
times ranked

27353
citing authors

#	ARTICLE	IF	CITATIONS
1	Entospletinib in Combination with Induction Chemotherapy in Previously Untreated Acute Myeloid Leukemia: Response and Predictive Significance of <i>HOXA9</i> and <i>MEIS1</i> Expression. <i>Clinical Cancer Research</i> , 2020, 26, 5852-5859.	7.0	28
2	Tumor suppressor BAP1 is essential for thymic development and proliferative responses of T lymphocytes. <i>Science Immunology</i> , 2018, 3, .	11.9	25
3	Ubiquitin ligase COP1 coordinates transcriptional programs that control cell type specification in the developing mouse brain. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 11244-11249.	7.1	22
4	Single-cell RNA sequencing identifies distinct mouse medial ganglionic eminence cell types. <i>Scientific Reports</i> , 2017, 7, 45656.	3.3	67
5	Transcription factor Etv5 is essential for the maintenance of alveolar type II cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 3903-3908.	7.1	94
6	Repression of Stress-Induced LINE-1 Expression Protects Cancer Cell Subpopulations from Lethal Drug Exposure. <i>Cancer Cell</i> , 2017, 32, 221-237.e13.	16.8	177
7	Proline Starvation Induces Unresolved ER Stress and Hinders mTORC1-Dependent Tumorigenesis. <i>Cell Metabolism</i> , 2016, 24, 753-761.	16.2	85
8	Phosphorylation and linear ubiquitin direct A20 inhibition of inflammation. <i>Nature</i> , 2015, 528, 370-375.	27.8	227
9	β -Cell Insulin Secretion Requires the Ubiquitin Ligase COP1. <i>Cell</i> , 2015, 163, 1457-1467.	28.9	43
10	A comprehensive transcriptional portrait of human cancer cell lines. <i>Nature Biotechnology</i> , 2015, 33, 306-312.	17.5	556
11	Diverse modes of genomic alteration in hepatocellular carcinoma. <i>Genome Biology</i> , 2014, 15, 436.	8.8	100
12	Regulation of proximal T cell receptor signaling and tolerance induction by deubiquitinase Usp9X. <i>Journal of Experimental Medicine</i> , 2014, 211, 1947-1955.	8.5	53
13	Integrated exome and transcriptome sequencing reveals ZAK isoform usage in gastric cancer. <i>Nature Communications</i> , 2014, 5, 3830.	12.8	77
14	MBASED: allele-specific expression detection in cancer tissues and cell lines. <i>Genome Biology</i> , 2014, 15, 405.	8.8	112
15	An integrative analysis of colon cancer identifies an essential function for PRPF6 in tumor growth. <i>Genes and Development</i> , 2014, 28, 1068-1084.	5.9	95
16	Diverse modes of genomic alterations in hepatocellular carcinoma. <i>Genome Biology</i> , 2014, 15, 436.	9.6	4
17	Integrative analysis of two cell lines derived from a non-small-lung cancer patient—a panomics approach. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2014, , 75-86.	0.7	4
18	Large-scale integrative network-based analysis identifies common pathways disrupted by copy number alterations across cancers. <i>BMC Genomics</i> , 2013, 14, 440.	2.8	21

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19	Phosphorylation of Dishevelled by Protein Kinase RIPK4 Regulates Wnt Signaling. <i>Science</i> , 2013, 339, 1441-1445.	12.6	93
20	Deletion of <i>Asxl1</i> results in myelodysplasia and severe developmental defects in vivo. <i>Journal of Experimental Medicine</i> , 2013, 210, 2641-2659.	8.5	278
21	Host genetic background impacts modulation of the TLR4 pathway by RON in tissue-associated macrophages. <i>Immunology and Cell Biology</i> , 2013, 91, 451-460.	2.3	24
22	FGFR3 Stimulates Stearoyl CoA Desaturase 1 Activity to Promote Bladder Tumor Growth. <i>Cancer Research</i> , 2012, 72, 5843-5855.	0.9	73
23	Genome and transcriptome sequencing of lung cancers reveal diverse mutational and splicing events. <i>Genome Research</i> , 2012, 22, 2315-2327.	5.5	177
24	Phosphorylation of NLRP4 is critical for inflammasome activation. <i>Nature</i> , 2012, 490, 539-542.	27.8	254
25	The effects of hepatitis B virus integration into the genomes of hepatocellular carcinoma patients. <i>Genome Research</i> , 2012, 22, 593-601.	5.5	257
26	Loss of the Tumor Suppressor BAP1 Causes Myeloid Transformation. <i>Science</i> , 2012, 337, 1541-1546.	12.6	355
27	Solution NMR structure of the ribosomal protein RPL35A from <i>Pyrococcus furiosus</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 1901-1906.	2.6	3
28	COP1 is a tumour suppressor that causes degradation of ETS transcription factors. <i>Nature</i> , 2011, 474, 403-406.	27.8	143
29	Non-canonical inflammasome activation targets caspase-11. <i>Nature</i> , 2011, 479, 117-121.	27.8	2,072
30	USP1 Deubiquitinates ID Proteins to Preserve a Mesenchymal Stem Cell Program in Osteosarcoma. <i>Cell</i> , 2011, 146, 918-930.	28.9	212
31	Deubiquitinase USP37 Is Activated by CDK2 to Antagonize APC/CDH1 and Promote S Phase Entry. <i>Molecular Cell</i> , 2011, 42, 511-523.	9.7	131
32	Sensitivity to antitubulin chemotherapeutics is regulated by MCL1 and FBW7. <i>Nature</i> , 2011, 471, 110-114.	27.8	682
33	Inferring disease and gene set associations with rank coherence in networks. <i>Bioinformatics</i> , 2011, 27, 2692-2699.	4.1	37
34	Distinct Involvement of the Gab1 and Grb2 Adaptor Proteins in Signal Transduction by the Related Receptor Tyrosine Kinases RON and MET. <i>Journal of Biological Chemistry</i> , 2011, 286, 32762-32774.	3.4	21
35	Deubiquitinase USP9X stabilizes MCL1 and promotes tumour cell survival. <i>Nature</i> , 2010, 463, 103-107.	27.8	529
36	The mutation spectrum revealed by paired genome sequences from a lung cancer patient. <i>Nature</i> , 2010, 465, 473-477.	27.8	453

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37	Association of C-Terminal Ubiquitin Hydrolase BRCA1-Associated Protein 1 with Cell Cycle Regulator Host Cell Factor 1. <i>Molecular and Cellular Biology</i> , 2009, 29, 2181-2192.	2.3	187
38	NMR and X-RAY structures of human E2-like ubiquitin-fold modifier conjugating enzyme 1 (UFC1) reveal structural and functional conservation in the metazoan UFM1-UBA5-UFC1 ubiquitination pathway. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 127-136.	1.2	26
39	Structural genomics is the largest contributor of novel structural leverage. <i>Journal of Structural and Functional Genomics</i> , 2009, 10, 181-191.	1.2	69
40	Understanding the physical properties that control protein crystallization by analysis of large-scale experimental data. <i>Nature Biotechnology</i> , 2009, 27, 51-57.	17.5	133
41	Axl as a potential therapeutic target in cancer: role of Axl in tumor growth, metastasis and angiogenesis. <i>Oncogene</i> , 2009, 28, 3442-3455.	5.9	253
42	Solution NMR structure of the SOS response protein YnzC from <i>Bacillus subtilis</i> . <i>Proteins: Structure, Function and Bioinformatics</i> , 2008, 72, 526-530.	2.6	14
43	Natural selection of protein structural and functional properties: a SNP perspective. <i>Genome Biology</i> , 2008, 9, R69.	9.6	54
44	Microphthalmia-Associated Transcription Factor Is a Critical Transcriptional Regulator of Melanoma Inhibitor of Apoptosis in Melanomas. <i>Cancer Research</i> , 2008, 68, 3124-3132.	0.9	99
45	Natively Unstructured Loops Differ from Other Loops. <i>PLoS Computational Biology</i> , 2007, 3, e140.	3.2	84
46	Membrane protein prediction methods. <i>Methods</i> , 2007, 41, 460-474.	3.8	104
47	Solution NMR structure of <i>Escherichia coli</i> ytfP expands the structural coverage of the UPF0131 protein domain family. <i>Proteins: Structure, Function and Bioinformatics</i> , 2007, 68, 789-795.	2.6	4
48	Novel leverage of structural genomics. <i>Nature Biotechnology</i> , 2007, 25, 849-851.	17.5	59
49	Distinguishing Protein-Coding from Non-Coding RNAs through Support Vector Machines. <i>PLoS Genetics</i> , 2006, 2, e29.	3.5	133
50	Solution structure of <i>Archaeoglobus fulgidis</i> peptidyl-tRNA hydrolase (Pth2) provides evidence for an extensive conserved family of Pth2 enzymes in archaea, bacteria, and eukaryotes. <i>Protein Science</i> , 2005, 14, 2849-2861.	7.6	25
51	The 2.35 Å structure of the TenA homolog from <i>Pyrococcus furiosus</i> supports an enzymatic function in thiamine metabolism. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2005, 61, 589-598.	2.5	12
52	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
53	Comparisons of NMR Spectral Quality and Success in Crystallization Demonstrate that NMR and X-ray Crystallography Are Complementary Methods for Small Protein Structure Determination. <i>Journal of the American Chemical Society</i> , 2005, 127, 16505-16511.	13.7	72
54	CHOP: parsing proteins into structural domains. <i>Nucleic Acids Research</i> , 2004, 32, W569-W571.	14.5	30

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55	Sequence-based prediction of protein domains. <i>Nucleic Acids Research</i> , 2004, 32, 3522-3530.	14.5	73
56	Predicting transmembrane beta-barrels in proteomes. <i>Nucleic Acids Research</i> , 2004, 32, 2566-2577.	14.5	137
57	The PredictProtein server. <i>Nucleic Acids Research</i> , 2004, 32, W321-W326.	14.5	1,246
58	Letter to the Editor: ¹ H, ¹³ C and ¹⁵ N assignments for the <i>Archaeoglobus fulgidis</i> protein AF2095. <i>Journal of Biomolecular NMR</i> , 2004, 30, 107-108.	2.8	1
59	Automatic target selection for structural genomics on eukaryotes. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 188-200.	2.6	62
60	The protein target list of the Northeast Structural Genomics Consortium. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 56, 181-187.	2.6	34
61	CHOP proteins into structural domain-like fragments. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 678-688.	2.6	68
62	Automatic prediction of protein function. <i>Cellular and Molecular Life Sciences</i> , 2003, 60, 2637-2650.	5.4	225
63	Domains, motifs and clusters in the protein universe. <i>Current Opinion in Chemical Biology</i> , 2003, 7, 5-11.	6.1	87
64	Solution NMR structure of the 30S ribosomal protein S28E from <i>Pyrococcus horikoshii</i> . <i>Protein Science</i> , 2003, 12, 2823-2830.	7.6	20
65	NORSp: predictions of long regions without regular secondary structure. <i>Nucleic Acids Research</i> , 2003, 31, 3833-3835.	14.5	124
66	The PredictProtein server. <i>Nucleic Acids Research</i> , 2003, 31, 3300-3304.	14.5	176
67	PEP: Predictions for Entire Proteomes. <i>Nucleic Acids Research</i> , 2003, 31, 410-413.	14.5	29
68	Target space for structural genomics revisited. <i>Bioinformatics</i> , 2002, 18, 922-933.	4.1	71
69	The Genome of <i>M. acetivorans</i> Reveals Extensive Metabolic and Physiological Diversity. <i>Genome Research</i> , 2002, 12, 532-542.	5.5	573
70	Loopy Proteins Appear Conserved in Evolution. <i>Journal of Molecular Biology</i> , 2002, 322, 53-64.	4.2	187
71	Comparing function and structure between entire proteomes. <i>Protein Science</i> , 2001, 10, 1970-1979.	7.6	248