Guang Hu

List of Publications by Year
in descending order

102 papers	6,017 citations	136950 32 h-index	76900 74 g-index
105 all docs	105 docs citations	105 times ranked	10232 citing authors

#	Article	IF	Citations
1	Second-generation shRNA libraries covering the mouse and human genomes. Nature Genetics, 2005, 37, 1281-1288.	21.4	582
2	The pINDUCER lentiviral toolkit for inducible RNA interference in vitro and in vivo. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 3665-3670.	7.1	570
3	A lentiviral microRNA-based system for single-copy polymerase II-regulated RNA interference in mammalian cells. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 13212-13217.	7.1	515
4	Cancer Proliferation Gene Discovery Through Functional Genomics. Science, 2008, 319, 620-624.	12.6	365
5	A genome-wide RNAi screen identifies a new transcriptional module required for self-renewal. Genes and Development, 2009, 23, 837-848.	5.9	354
6	SCFÎ²-TRCP controls oncogenic transformation and neural differentiation through REST degradation. Nature, 2008, 452, 370-374.	27.8	289
7	Activation of Multiple Proto-oncogenic Tyrosine Kinases in Breast Cancer via Loss of the PTPN12 Phosphatase. Cell, 2011, 144, 703-718.	28.9	246
8	Tyrosine phosphatase SHP2 promotes breast cancer progression and maintains tumor-initiating cells via activation of key transcription factors and a positive feedback signaling loop. Nature Medicine, 2012, 18, 529-537.	30.7	224
9	R9AP, a membrane anchor for the photoreceptor GTPase accelerating protein, RGS9-1. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 9755-9760.	7.1	164
10	Pausing of RNA Polymerase II Regulates Mammalian Developmental Potential through Control of Signaling Networks. Molecular Cell, 2015, 58, 311-322.	9.7	155
11	INO80 Facilitates Pluripotency Gene Activation in Embryonic Stem Cell Self-Renewal, Reprogramming, and Blastocyst Development. Cell Stem Cell, 2014, 14, 575-591.	11.1	148
12	Fip1 regulates mRNA alternative polyadenylation to promote stem cell self-renewal. EMBO Journal, 2014, 33, 878-889.	7.8	136
13	TRIM28 regulates RNA polymerase II promoter-proximal pausing and pause release. Nature Structural and Molecular Biology, 2014, 21, 876-883.	8.2	125
14	Nudt21 Controls Cell Fate by Connecting Alternative Polyadenylation to Chromatin Signaling. Cell, 2018, 172, 106-120.e21.	28.9	123
15	NuRD and Pluripotency: A Complex Balancing Act. Cell Stem Cell, 2012, 10, 497-503.	11.1	99
16	The construction of an amino acid network for understanding protein structure and function. Amino Acids, 2014, 46, 1419-1439.	2.7	92
17	The THO Complex Regulates Pluripotency Gene mRNA Export and Controls Embryonic Stem Cell Self-Renewal and Somatic Cell Reprogramming. Cell Stem Cell, 2013, 13, 676-690.	11.1	85
18	Acute depletion of Tet1-dependent 5-hydroxymethylcytosine levels impairs LIF/Stat3 signaling and results in loss of embryonic stem cell identity. Nucleic Acids Research, 2012, 40, 3364-3377.	14.5	84

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19	Activation of RGS9-1GTPase Acceleration by Its Membrane Anchor, R9AP. Journal of Biological Chemistry, 2003, 278, 14550-14554.	3.4	69
20	The Discovery of a Putative Allosteric Site in the SARS-CoV-2 Spike Protein Using an Integrated Structural/Dynamic Approach. Journal of Proteome Research, 2020, 19, 4576-4586.	3.7	66
21	INO80 governs superenhancer-mediated oncogenic transcription and tumor growth in melanoma. Genes and Development, 2016, 30, 1440-1453.	5.9	65
22	Cnot1, Cnot2, and Cnot3 Maintain Mouse and Human ESC Identity and Inhibit Extraembryonic Differentiation. Stem Cells, 2012, 30, 910-922.	3.2	63
23	Residue interaction network analysis of Dronpa and a DNA clamp. Journal of Theoretical Biology, 2014, 348, 55-64.	1.7	63
24	SIRT1-Mediated Deacetylation of CRABPII Regulates Cellular Retinoic Acid Signaling and Modulates Embryonic Stem Cell Differentiation. Molecular Cell, 2014, 55, 843-855.	9.7	60
25	Integration of network models and evolutionary analysis into high-throughput modeling of protein dynamics and allosteric regulation: theory, tools and applications. Briefings in Bioinformatics, 2020, 21, 815-835.	6.5	58
26	A Serial shRNA Screen for Roadblocks to Reprogramming Identifies the Protein Modifier SUMO2. Stem Cell Reports, 2016, 6, 704-716.	4.8	50
27	Rif1 promotes a repressive chromatin state to safeguard against endogenous retrovirus activation. Nucleic Acids Research, 2017, 45, 12723-12738.	14.5	49
28	DNA methyltransferase inhibitors: an updated patent review (2012-2015). Expert Opinion on Therapeutic Patents, 2016, 26, 1017-1030.	5.0	45
29	RNA polymerase II promoter-proximal pausing in mammalian long non-coding genes. Genomics, 2016, 108, 64-77.	2.9	44
30	Allosteric Regulation at the Crossroads of New Technologies: Multiscale Modeling, Networks, and Machine Learning. Frontiers in Molecular Biosciences, 2020, 7, 136.	3.5	44
31	Phosphorylation of RGS9-1 by an Endogenous Protein Kinase in Rod Outer Segments. Journal of Biological Chemistry, 2001, 276, 22287-22295.	3.4	40
32	Diagnosis Value of the Serum Amyloid A Test in Neonatal Sepsis: A Meta-Analysis. BioMed Research International, 2013, 2013, 1-9.	1.9	40
33	Post-transcriptional regulation of the pluripotent state. Current Opinion in Genetics and Development, 2017, 46, 15-23.	3.3	35
34	Forward RNAi screens in primary human hematopoietic stem/progenitor cells. Blood, 2009, 113, 3690-3695.	1.4	32
35	Knowledge-Based Analysis for Detecting Key Signaling Events from Time-Series Phosphoproteomics Data. PLoS Computational Biology, 2015, 11, e1004403.	3.2	32
36	The architecture of Platonic polyhedral links. Journal of Mathematical Chemistry, 2009, 46, 592-603.	1.5	30

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37	Molecular Mechanism underlying PRMT1 Dimerization for SAM Binding and Methylase Activity. Journal of Chemical Information and Modeling, 2015, 55, 2623-2632.	5.4	30
38	CNOT3-Dependent mRNA Deadenylation Safeguards the Pluripotent State. Stem Cell Reports, 2016, 7, 897-910.	4.8	29
39	Dioxin and AHR impairs mesoderm gene expression and cardiac differentiation in human embryonic stem cells. Science of the Total Environment, 2019, 651, 1038-1046.	8.0	29
40	Identification of Protein Kinase C Isozymes Responsible for the Phosphorylation of Photoreceptor-specific RGS9-1 at Ser475. Journal of Biological Chemistry, 2003, 278, 8316-8325.	3.4	26
41	Tumor Necrosis Factor-<i>Î±</i> as a Diagnostic Marker for Neonatal Sepsis: A Meta-Analysis. Scientific World Journal, The, 2014, 2014, 1-14.	2.1	26
42	Integrative framework for identification of key cell identity genes uncovers determinants of ES cell identity and homeostasis. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, E1581-90.	7.1	26
43	A primer on using pooled shRNA libraries for functional genomic screens. Acta Biochimica Et Biophysica Sinica, 2012, 44, 103-112.	2.0	24
44	USP7 negatively controls global DNA methylation by attenuating ubiquitinated histone-dependent DNMT1 recruitment. Cell Discovery, 2020, 6, 58.	6.7	23
45	Computational Analysis of the Binding Specificities of PH Domains. BioMed Research International, 2015, 2015, 1-11.	1.9	22
46	The Topology and Dynamics of Protein Complexes: Insights from Intra&ndash; Molecular Network Theory. Current Protein and Peptide Science, 2013, 14, 121-132.	1.4	22
47	Identifying Drug Targets in Pancreatic Ductal Adenocarcinoma Through Machine Learning, Analyzing Biomolecular Networks, and Structural Modeling. Frontiers in Pharmacology, 2020, 11, 534.	3.5	21
48	An advanced MRI and MRSI data fusion scheme for enhancing unsupervised brain tumor differentiation. Computers in Biology and Medicine, 2017, 81, 121-129.	7.0	20
49	Comparative Study of Elastic Network Model and Protein Contact Network for Protein Complexes: The Hemoglobin Case. BioMed Research International, 2017, 2017, 1-15.	1.9	20
50	Deciphering the role of dimer interface in intrinsic dynamics and allosteric pathways underlying the functional transformation of DNMT3A. Biochimica Et Biophysica Acta - General Subjects, 2018, 1862, 1667-1679.	2.4	20
51	Node-Weighted Amino Acid Network Strategy for Characterization and Identification of Protein Functional Residues. Journal of Chemical Information and Modeling, 2018, 58, 2024-2032.	5.4	20
52	Both intra and inter-domain interactions define the intrinsic dynamics and allosteric mechanism in DNMT1s. Computational and Structural Biotechnology Journal, 2020, 18, 749-764.	4.1	20
53	SVR_CAF: An integrated score function for detecting native protein structures among decoys. Proteins: Structure, Function and Bioinformatics, 2014, 82, 556-564.	2.6	18
54	Amino acid contact energy networks impact protein structure and evolution. Journal of Theoretical Biology, 2014, 355, 95-104.	1.7	18

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55	Comparative Dynamics and Functional Mechanisms of the CYP17A1 Tunnels Regulated by Ligand Binding. Journal of Chemical Information and Modeling, 2020, 60, 3632-3647.	5.4	17
56	A New Euler's Formula for DNA Polyhedra. PLoS ONE, 2011, 6, e26308.	2.5	16
57	Post genome-wide association studies functional characterization of prostate cancer risk loci. BMC Genomics, 2013, 14, S9.	2.8	15
58	Modeling of PH Domains and Phosphoinositides Interactions and Beyond. Advances in Experimental Medicine and Biology, 2018, 1111, 19-32.	1.6	14
59	Amino Acid Network for the Discrimination of Native Protein Structures from Decoys. Current Protein and Peptide Science, 2014, 15, 522-528.	1.4	14
60	Biological Networks for Cancer Candidate Biomarkers Discovery. Cancer Informatics, 2016, 15s3, CIN.S39458.	1.9	13
61	Probing Carbon Utilization of Cordyceps militaris by Sugar Transportome and Protein Structural Analysis. Cells, 2020, 9, 401.	4.1	13
62	Recent Advances on the Network Models in Target-based Drug Discovery. Current Topics in Medicinal Chemistry, 2018, 18, 1031-1043.	2.1	13
63	Dynamics of Post-Translational Modification Inspires Drug Design in the Kinase Family. Journal of Medicinal Chemistry, 2021, 64, 15111-15125.	6.4	13
64	The harmonic analysis of cylindrically symmetric proteins: A comparison of Dronpa and a DNA sliding clamp. Journal of Molecular Graphics and Modelling, 2012, 34, 28-37.	2.4	11
65	Synchronous firings in small-world networks of excitable nodes. Europhysics Letters, 2013, 102, 28001.	2.0	11
66	Identifying novel glioma associated pathways based on systems biology level meta-analysis. BMC Systems Biology, 2013, 7, S9.	3.0	10
67	Cnot3 enhances human embryonic cardiomyocyte proliferation by promoting cell cycle inhibitor mRNA degradation. Scientific Reports, 2017, 7, 1500.	3.3	10
68	Intrinsic Dynamics Analysis of a DNA Octahedron by Elastic Network Model. Molecules, 2017, 22, 145.	3.8	10
69	Knowledge-Guided â€œCommunity Networkâ€•Analysis Reveals the Functional Modules and Candidate Targets in Non-Small-Cell Lung Cancer. Cells, 2021, 10, 402.	4.1	10
70	Characterization of R9AP, a Membrane Anchor for the Photoreceptor GTPase-Accelerating Protein, RGS9-1. Methods in Enzymology, 2004, 390, 178-196.	1.0	9
71	Molecular design of DNA polyhedra based on genus. Journal of Mathematical Chemistry, 2014, 52, 2380-2394.	1.5	9
72	Transcription coactivator Cited1 acts as an inducer of trophoblast-like state from mouse embryonic stem cells through the activation of BMP signaling. Cell Death and Disease, 2018, 9, 924.	6.3	9

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73	Modulation of Toroidal Proteins Dynamics in Favor of Functional Mechanisms upon Ligand Binding. Biophysical Journal, 2020, 118, 1782-1794.	0.5	9
74	Biophysical Insight into the SARS-CoV2 Spike–ACE2 Interaction and Its Modulation by Hepcidin through a Multifaceted Computational Approach. ACS Omega, 2022, 7, 17024-17042.	3.5	9
75	The complexity of Platonic and Archimedean polyhedral links. Journal of Mathematical Chemistry, 2010, 48, 401-412.	1.5	8
76	Amino acid network for prediction of catalytic residues in enzymes: a comparison survey. Current Protein and Peptide Science, 2015, 17, 41-51.	1.4	8
77	Protein–Protein Interface and Disease: Perspective from Biomolecular Networks. Advances in Biochemical Engineering/Biotechnology, 2016, 160, 57-74.	1.1	8
78	Network Analysis of Protein Structures: The Comparison of Three Topologies. Current Bioinformatics, 2016, 11, 480-489.	1.5	8
79	Normal Mode Analysis of Trp RNA Binding Attenuation Protein: Structure and Collective Motions. Journal of Chemical Information and Modeling, 2011, 51, 2361-2371.	5.4	7
80	Oct4GiP Reporter Assay to Study Genes that Regulate Mouse Embryonic Stem Cell Maintenance and Self-renewal. Journal of Visualized Experiments, 2012, , .	0.3	7
81	Molecular Dynamic Simulation to Explore the Molecular Basis of Btk-PH Domain Interaction with Ins(1,3,4,5)P4. Scientific World Journal, The, 2013, 2013, 1-10.	2.1	7
82	Identification of Allosteric Effects in Proteins by Elastic Network Models. Methods in Molecular Biology, 2021, 2253, 21-35.	0.9	7
83	Leveraging Protein Dynamics to Identify Functional Phosphorylation Sites using Deep Learning Models. Journal of Chemical Information and Modeling, 2022, 62, 3331-3345.	5.4	7
84	Topological Analysis of Enzymatic Actions on DNA Polyhedral Links. Bulletin of Mathematical Biology, 2011, 73, 3030-3046.	1.9	6
85	An analysis and validation pipeline for large-scale RNAi-based screens. Scientific Reports, 2013, 3, 1076.	3.3	5
86	Translational Bioinformatics and Computational Systems Medicine. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-2.	1.3	5
87	Role of protein-protein interactions in allosteric drug design for DNA methyltransferases. Advances in Protein Chemistry and Structural Biology, 2020, 121, 49-84.	2.3	5
88	Network-Based Target Prioritization and Drug Candidate Identification for Multiple Sclerosis: From Analyzing "Omics Data" to Druggability Simulations. ACS Chemical Neuroscience, 2021, 12, 917-929.	3.5	5
89	Insights into Conformational Dynamics and Allostery in DNMT1-H3Ub/USP7 Interactions. Molecules, 2021, 26, 5153.	3.8	5
90	Protein Structure Network-based Drug Design. Mini-Reviews in Medicinal Chemistry, 2016, 16, 1330-1343.	2.4	5

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91	Network Proteomics: From Protein Structure to Protein-Protein Interaction. BioMed Research International, 2017, 2017, 1-1.	1.9	4
92	Attractive target wave patterns in complex networks consisting of excitable nodes. Chinese Physics B, 2014, 23, 078906.	1.4	3
93	Remodeling super-enhancers and oncogenic transcription. Cell Cycle, 2016, 15, 3157-3158.	2.6	3
94	Dissecting mutational allosteric effects in alkaline phosphatases associated with different Hypophosphatasia phenotypes: An integrative computational investigation. PLoS Computational Biology, 2022, 18, e1010009.	3.2	3
95	Efficient simulation of isotope aggregated and fine structure by vector manipulation and change-making strategy. International Journal of Mass Spectrometry, 2019, 443, 70-76.	1.5	2
96	Editorial: Understanding Protein Dynamics, Binding and Allostery for Drug Design. Frontiers in Molecular Biosciences, 2021, 8, 681364.	3.5	2
97	Use of Genome-Wide RNAi Screens to Identify Regulators of Embryonic Stem Cell Pluripotency and Self-Renewal. Methods in Molecular Biology, 2014, 1150, 163-173.	0.9	2
98	A NOD-Like Receptor Signaling-Based Gene Signature Identified as a Novel Prognostic Biomarker for Predicting Overall Survival of Colorectal Cancer Patients. Current Bioinformatics, 2022, 17, 77-88.	1.5	2
99	Structural Biology Meets Biomolecular Networks: The Post-AlphaFold Era. Current Bioinformatics, 2022, 17, 493-497.	1.5	2
100	Identification of Biomarkers for Pharmacological Activity. Translational Bioinformatics, 2013, , 189-205.	0.0	1
101	Identifying novel glioma associated pathways based on integrated ‘omics’ data. , 2012, , .		0
102	Drug Design based on Protein Structure Network. Mini-Reviews in Medicinal Chemistry, 2016, , .	2.4	0