

# Guang Hu

## List of Publications by Year in descending order

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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	A NOD-Like Receptor Signaling-Based Gene Signature Identified as a Novel Prognostic Biomarker for Predicting Overall Survival of Colorectal Cancer Patients. <i>Current Bioinformatics</i> , 2022, 17, 77-88.	1.5	2
2	Structural Biology Meets Biomolecular Networks: The Post-AlphaFold Era. <i>Current Bioinformatics</i> , 2022, 17, 493-497.	1.5	2
3	Dissecting mutational allosteric effects in alkaline phosphatases associated with different Hypophosphatasia phenotypes: An integrative computational investigation. <i>PLoS Computational Biology</i> , 2022, 18, e1010009.	3.2	3
4	Biophysical Insight into the SARS-CoV2 Spike-ACE2 Interaction and Its Modulation by Hepcidin through a Multifaceted Computational Approach. <i>ACS Omega</i> , 2022, 7, 17024-17042.	3.5	9
5	Leveraging Protein Dynamics to Identify Functional Phosphorylation Sites using Deep Learning Models. <i>Journal of Chemical Information and Modeling</i> , 2022, 62, 3331-3345.	5.4	7
6	Network-Based Target Prioritization and Drug Candidate Identification for Multiple Sclerosis: From Analyzing "Omics Data" to Druggability Simulations. <i>ACS Chemical Neuroscience</i> , 2021, 12, 917-929.	3.5	5
7	Knowledge-Guided "Community Network" Analysis Reveals the Functional Modules and Candidate Targets in Non-Small-Cell Lung Cancer. <i>Cells</i> , 2021, 10, 402.	4.1	10
8	Editorial: Understanding Protein Dynamics, Binding and Allostery for Drug Design. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 681364.	3.5	2
9	Insights into Conformational Dynamics and Allostery in DNMT1-H3Ub/USP7 Interactions. <i>Molecules</i> , 2021, 26, 5153.	3.8	5
10	Identification of Allosteric Effects in Proteins by Elastic Network Models. <i>Methods in Molecular Biology</i> , 2021, 2253, 21-35.	0.9	7
11	Dynamics of Post-Translational Modification Inspires Drug Design in the Kinase Family. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 15111-15125.	6.4	13
12	Integration of network models and evolutionary analysis into high-throughput modeling of protein dynamics and allosteric regulation: theory, tools and applications. <i>Briefings in Bioinformatics</i> , 2020, 21, 815-835.	6.5	58
13	Role of protein-protein interactions in allosteric drug design for DNA methyltransferases. <i>Advances in Protein Chemistry and Structural Biology</i> , 2020, 121, 49-84.	2.3	5
14	Allosteric Regulation at the Crossroads of New Technologies: Multiscale Modeling, Networks, and Machine Learning. <i>Frontiers in Molecular Biosciences</i> , 2020, 7, 136.	3.5	44
15	USP7 negatively controls global DNA methylation by attenuating ubiquitinated histone-dependent DNMT1 recruitment. <i>Cell Discovery</i> , 2020, 6, 58.	6.7	23
16	Identifying Drug Targets in Pancreatic Ductal Adenocarcinoma Through Machine Learning, Analyzing Biomolecular Networks, and Structural Modeling. <i>Frontiers in Pharmacology</i> , 2020, 11, 534.	3.5	21
17	Comparative Dynamics and Functional Mechanisms of the CYP17A1 Tunnels Regulated by Ligand Binding. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 3632-3647.	5.4	17
18	The Discovery of a Putative Allosteric Site in the SARS-CoV-2 Spike Protein Using an Integrated Structural/Dynamic Approach. <i>Journal of Proteome Research</i> , 2020, 19, 4576-4586.	3.7	66

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19	Modulation of Toroidal Proteins Dynamics in Favor of Functional Mechanisms upon Ligand Binding. <i>Biophysical Journal</i> , 2020, 118, 1782-1794.	0.5	9
20	Probing Carbon Utilization of <i>Cordyceps militaris</i> by Sugar Transportome and Protein Structural Analysis. <i>Cells</i> , 2020, 9, 401.	4.1	13
21	Both intra and inter-domain interactions define the intrinsic dynamics and allosteric mechanism in DNMT1s. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 749-764.	4.1	20
22	Efficient simulation of isotope aggregated and fine structure by vector manipulation and change-making strategy. <i>International Journal of Mass Spectrometry</i> , 2019, 443, 70-76.	1.5	2
23	Dioxin and AHR impairs mesoderm gene expression and cardiac differentiation in human embryonic stem cells. <i>Science of the Total Environment</i> , 2019, 651, 1038-1046.	8.0	29
24	Deciphering the role of dimer interface in intrinsic dynamics and allosteric pathways underlying the functional transformation of DNMT3A. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2018, 1862, 1667-1679.	2.4	20
25	Nudt21 Controls Cell Fate by Connecting Alternative Polyadenylation to Chromatin Signaling. <i>Cell</i> , 2018, 172, 106-120.e21.	28.9	123
26	Transcription coactivator Cited1 acts as an inducer of trophoblast-like state from mouse embryonic stem cells through the activation of BMP signaling. <i>Cell Death and Disease</i> , 2018, 9, 924.	6.3	9
27	Modeling of PH Domains and Phosphoinositides Interactions and Beyond. <i>Advances in Experimental Medicine and Biology</i> , 2018, 1111, 19-32.	1.6	14
28	Node-Weighted Amino Acid Network Strategy for Characterization and Identification of Protein Functional Residues. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 2024-2032.	5.4	20
29	Recent Advances on the Network Models in Target-based Drug Discovery. <i>Current Topics in Medicinal Chemistry</i> , 2018, 18, 1031-1043.	2.1	13
30	Cnot3 enhances human embryonic cardiomyocyte proliferation by promoting cell cycle inhibitor mRNA degradation. <i>Scientific Reports</i> , 2017, 7, 1500.	3.3	10
31	An advanced MRI and MRSI data fusion scheme for enhancing unsupervised brain tumor differentiation. <i>Computers in Biology and Medicine</i> , 2017, 81, 121-129.	7.0	20
32	Rif1 promotes a repressive chromatin state to safeguard against endogenous retrovirus activation. <i>Nucleic Acids Research</i> , 2017, 45, 12723-12738.	14.5	49
33	Post-transcriptional regulation of the pluripotent state. <i>Current Opinion in Genetics and Development</i> , 2017, 46, 15-23.	3.3	35
34	Intrinsic Dynamics Analysis of a DNA Octahedron by Elastic Network Model. <i>Molecules</i> , 2017, 22, 145.	3.8	10
35	Comparative Study of Elastic Network Model and Protein Contact Network for Protein Complexes: The Hemoglobin Case. <i>BioMed Research International</i> , 2017, 2017, 1-15.	1.9	20
36	Network Proteomics: From Protein Structure to Protein-Protein Interaction. <i>BioMed Research International</i> , 2017, 2017, 1-1.	1.9	4

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37	DNA methyltransferase inhibitors: an updated patent review (2012-2015). <i>Expert Opinion on Therapeutic Patents</i> , 2016, 26, 1017-1030.	5.0	45
38	Protein-Protein Interface and Disease: Perspective from Biomolecular Networks. <i>Advances in Biochemical Engineering/Biotechnology</i> , 2016, 160, 57-74.	1.1	8
39	Remodeling super-enhancers and oncogenic transcription. <i>Cell Cycle</i> , 2016, 15, 3157-3158.	2.6	3
40	RNA polymerase II promoter-proximal pausing in mammalian long non-coding genes. <i>Genomics</i> , 2016, 108, 64-77.	2.9	44
41	CNOT3-Dependent mRNA Deadenylation Safeguards the Pluripotent State. <i>Stem Cell Reports</i> , 2016, 7, 897-910.	4.8	29
42	Biological Networks for Cancer Candidate Biomarkers Discovery. <i>Cancer Informatics</i> , 2016, 15s3, CIN.S39458.	1.9	13
43	INO80 governs superenhancer-mediated oncogenic transcription and tumor growth in melanoma. <i>Genes and Development</i> , 2016, 30, 1440-1453.	5.9	65
44	A Serial shRNA Screen for Roadblocks to Reprogramming Identifies the Protein Modifier SUMO2. <i>Stem Cell Reports</i> , 2016, 6, 704-716.	4.8	50
45	Protein Structure Network-based Drug Design. <i>Mini-Reviews in Medicinal Chemistry</i> , 2016, 16, 1330-1343.	2.4	5
46	Network Analysis of Protein Structures: The Comparison of Three Topologies. <i>Current Bioinformatics</i> , 2016, 11, 480-489.	1.5	8
47	Drug Design based on Protein Structure Network. <i>Mini-Reviews in Medicinal Chemistry</i> , 2016, , .	2.4	0
48	Knowledge-Based Analysis for Detecting Key Signaling Events from Time-Series Phosphoproteomics Data. <i>PLoS Computational Biology</i> , 2015, 11, e1004403.	3.2	32
49	Amino acid network for prediction of catalytic residues in enzymes: a comparison survey. <i>Current Protein and Peptide Science</i> , 2015, 17, 41-51.	1.4	8
50	Computational Analysis of the Binding Specificities of PH Domains. <i>BioMed Research International</i> , 2015, 2015, 1-11.	1.9	22
51	Pausing of RNA Polymerase II Regulates Mammalian Developmental Potential through Control of Signaling Networks. <i>Molecular Cell</i> , 2015, 58, 311-322.	9.7	155
52	Molecular Mechanism underlying PRMT1 Dimerization for SAM Binding and Methylase Activity. <i>Journal of Chemical Information and Modeling</i> , 2015, 55, 2623-2632.	5.4	30
53	Tumor Necrosis Factor- $\alpha$ as a Diagnostic Marker for Neonatal Sepsis: A Meta-Analysis. <i>Scientific World Journal</i> , The, 2014, 2014, 1-14.	2.1	26
54	Molecular design of DNA polyhedra based on genus. <i>Journal of Mathematical Chemistry</i> , 2014, 52, 2380-2394.	1.5	9

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55	Attractive target wave patterns in complex networks consisting of excitable nodes. Chinese Physics B, 2014, 23, 078906.	1.4	3
56	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
57	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
58	Residue interaction network analysis of Dronpa and a DNA clamp. Journal of Theoretical Biology, 2014, 348, 55-64.	1.7	63
59	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
60	Amino acid contact energy networks impact protein structure and evolution. Journal of Theoretical Biology, 2014, 355, 95-104.	1.7	18
61	Fip1 regulates mRNA alternative polyadenylation to promote stem cell self-renewal. EMBO Journal, 2014, 33, 878-889.	7.8	136
62	The construction of an amino acid network for understanding protein structure and function. Amino Acids, 2014, 46, 1419-1439.	2.7	92
63	SIRT1-Mediated Deacetylation of CRABP II Regulates Cellular Retinoic Acid Signaling and Modulates Embryonic Stem Cell Differentiation. Molecular Cell, 2014, 55, 843-855.	9.7	60
64	TRIM28 regulates RNA polymerase II promoter-proximal pausing and pause release. Nature Structural and Molecular Biology, 2014, 21, 876-883.	8.2	125
65	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
66	Amino Acid Network for the Discrimination of Native Protein Structures from Decoys. Current Protein and Peptide Science, 2014, 15, 522-528.	1.4	14
67	Post genome-wide association studies functional characterization of prostate cancer risk loci. BMC Genomics, 2013, 14, S9.	2.8	15
68	Identifying novel glioma associated pathways based on systems biology level meta-analysis. BMC Systems Biology, 2013, 7, S9.	3.0	10
69	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
70	Diagnosis Value of the Serum Amyloid A Test in Neonatal Sepsis: A Meta-Analysis. BioMed Research International, 2013, 2013, 1-9.	1.9	40
71	Synchronous firings in small-world networks of excitable nodes. Europhysics Letters, 2013, 102, 28001.	2.0	11
72	An analysis and validation pipeline for large-scale RNAi-based screens. Scientific Reports, 2013, 3, 1076.	3.3	5

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73	Translational Bioinformatics and Computational Systems Medicine. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-2.	1.3	5
74	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
75	Identification of Biomarkers for Pharmacological Activity. Translational Bioinformatics, 2013, , 189-205.	0.0	1
76	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
77	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
78	A primer on using pooled shRNA libraries for functional genomic screens. Acta Biochimica Et Biophysica Sinica, 2012, 44, 103-112.	2.0	24
79	Oct4GiP Reporter Assay to Study Genes that Regulate Mouse Embryonic Stem Cell Maintenance and Self-renewal. Journal of Visualized Experiments, 2012, , .	0.3	7
80	Identifying novel glioma associated pathways based on integrated &#x2018;omics&#x2019; data. , 2012, , .		0
81	NuRD and Pluripotency: A Complex Balancing Act. Cell Stem Cell, 2012, 10, 497-503.	11.1	99
82	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
83	Cnot1, Cnot2, and Cnot3 Maintain Mouse and Human ESC Identity and Inhibit Extraembryonic Differentiation. Stem Cells, 2012, 30, 910-922.	3.2	63
84	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
85	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
86	Activation of Multiple Proto-oncogenic Tyrosine Kinases in Breast Cancer via Loss of the PTPN12 Phosphatase. Cell, 2011, 144, 703-718.	28.9	246
87	Topological Analysis of Enzymatic Actions on DNA Polyhedral Links. Bulletin of Mathematical Biology, 2011, 73, 3030-3046.	1.9	6
88	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
89	A New Euler's Formula for DNA Polyhedra. PLoS ONE, 2011, 6, e26308.	2.5	16
90	The complexity of Platonic and Archimedean polyhedral links. Journal of Mathematical Chemistry, 2010, 48, 401-412.	1.5	8

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91	A genome-wide RNAi screen identifies a new transcriptional module required for self-renewal. <i>Genes and Development</i> , 2009, 23, 837-848.	5.9	354
92	The architecture of Platonic polyhedral links. <i>Journal of Mathematical Chemistry</i> , 2009, 46, 592-603.	1.5	30
93	Forward RNAi screens in primary human hematopoietic stem/progenitor cells. <i>Blood</i> , 2009, 113, 3690-3695.	1.4	32
94	SCF <sup>β2</sup> -TRCP controls oncogenic transformation and neural differentiation through REST degradation. <i>Nature</i> , 2008, 452, 370-374.	27.8	289
95	Cancer Proliferation Gene Discovery Through Functional Genomics. <i>Science</i> , 2008, 319, 620-624.	12.6	365
96	Second-generation shRNA libraries covering the mouse and human genomes. <i>Nature Genetics</i> , 2005, 37, 1281-1288.	21.4	582
97	A lentiviral microRNA-based system for single-copy polymerase II-regulated RNA interference in mammalian cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 13212-13217.	7.1	515
98	Characterization of R9AP, a Membrane Anchor for the Photoreceptor GTPase-Accelerating Protein, RGS9-1. <i>Methods in Enzymology</i> , 2004, 390, 178-196.	1.0	9
99	Identification of Protein Kinase C Isozymes Responsible for the Phosphorylation of Photoreceptor-specific RGS9-1 at Ser475. <i>Journal of Biological Chemistry</i> , 2003, 278, 8316-8325.	3.4	26
100	Activation of RGS9-1GTPase Acceleration by Its Membrane Anchor, R9AP. <i>Journal of Biological Chemistry</i> , 2003, 278, 14550-14554.	3.4	69
101	R9AP, a membrane anchor for the photoreceptor GTPase accelerating protein, RGS9-1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 9755-9760.	7.1	164
102	Phosphorylation of RGS9-1 by an Endogenous Protein Kinase in Rod Outer Segments. <i>Journal of Biological Chemistry</i> , 2001, 276, 22287-22295.	3.4	40