

Heng Zhu

List of Publications by Year in descending order

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Version: 2024-02-01

123
papers

12,731
citations

30070

54
h-index

24982

109
g-index

147
all docs

147
docs citations

147
times ranked

18662
citing authors

#	ARTICLE	IF	CITATIONS
1	Enzymatic analysis of WWP2 E3 ubiquitin ligase using protein microarrays identifies autophagy-related substrates. <i>Journal of Biological Chemistry</i> , 2022, 298, 101854.	3.4	6
2	Multifaceted Regulation of Akt by Diverse C-Terminal Post-translational Modifications. <i>ACS Chemical Biology</i> , 2022, 17, 68-76.	3.4	7
3	Identification of Novel Serological Autoantibodies in Takayasu Arteritis Patients Using HuProt Arrays. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100036.	3.8	13
4	An Integrated Systems Biology Approach Identifies the Proteasome as A Critical Host Machinery for ZIKV and DENV Replication. <i>Genomics, Proteomics and Bioinformatics</i> , 2021, 19, 108-122.	6.9	7
5	An all-to-all approach to the identification of sequence-specific readers for epigenetic DNA modifications on cytosine. <i>Nature Communications</i> , 2021, 12, 795.	12.8	22
6	CRY ² B2 enhances tumorigenesis through upregulation of nucleolin in triple negative breast cancer. <i>Oncogene</i> , 2021, 40, 5752-5763.	5.9	6
7	Virion Display: A High-Throughput Method to Express Functional Membrane Proteins. <i>Current Protocols in Molecular Biology</i> , 2020, 132, e126.	2.9	0
8	Integration of IgA and IgG Autoantigens Improves Performance of Biomarker Panels for Early Diagnosis of Lung Cancer. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 490-500.	3.8	23
9	Developments and Applications of Functional Protein Microarrays. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 916-927.	3.8	45
10	Structural Features of Transcription Factors Associating with Nucleosome Binding. <i>Molecular Cell</i> , 2019, 75, 921-932.e6.	9.7	158
11	Discovery of a Potent GLUT Inhibitor from a Library of Rapafucins by Using 3D Microarrays. <i>Angewandte Chemie - International Edition</i> , 2019, 58, 17158-17162.	13.8	22
12	Insight into novel RNA-binding activities via large-scale analysis of lncRNA-bound proteome and IDH1-bound transcriptome. <i>Nucleic Acids Research</i> , 2019, 47, 2244-2262.	14.5	29
13	Protein Microarrays and Liposome: A Method for Studying Lipid-Protein Interactions. <i>Methods in Molecular Biology</i> , 2019, 2003, 191-199.	0.9	3
14	Discovery and Validation of a Serologic Autoantibody Panel for Early Diagnosis of Esophageal Squamous Cell Carcinoma. <i>Cancer Epidemiology Biomarkers and Prevention</i> , 2019, 28, 1454-1460.	2.5	20
15	Development and application of a high-content virion display human GPCR array. <i>Nature Communications</i> , 2019, 10, 1997.	12.8	13
16	Proteome-wide Tyrosine Phosphorylation Analysis Reveals Dysregulated Signaling Pathways in Ovarian Tumors. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 448-460.	3.8	19
17	AAGMarker 1.0: a resource of serological autoantigen biomarkers for clinical diagnosis and prognosis of various human diseases. <i>Nucleic Acids Research</i> , 2018, 46, D886-D893.	14.5	5
18	Targeting UDP-glucose 6-dehydrogenase inhibits glioblastoma growth and migration. <i>Oncogene</i> , 2018, 37, 2615-2629.	5.9	37

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19	Global Identification of Small Ubiquitin-related Modifier (SUMO) Substrates Reveals Crosstalk between SUMOylation and Phosphorylation Promotes Cell Migration. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 871-888.	3.8	24
20	Liver Transplantation for Severe Alcoholic Hepatitis, Updated Lessons from the World's Largest Series. <i>Journal of the American College of Surgeons</i> , 2018, 226, 549-557.	0.5	90
21	MeDReaders: a database for transcription factors that bind to methylated DNA. <i>Nucleic Acids Research</i> , 2018, 46, D146-D151.	14.5	94
22	A toolbox of immunoprecipitation-grade monoclonal antibodies to human transcription factors. <i>Nature Methods</i> , 2018, 15, 330-338.	19.0	58
23	Multiplexed Biomarker Panels Discriminate Zika and Dengue Virus Infection in Humans. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 349-356.	3.8	19
24	Parkinson-Associated SNCA Enhancer Variants Revealed by Open Chromatin in Mouse Dopamine Neurons. <i>American Journal of Human Genetics</i> , 2018, 103, 874-892.	6.2	30
25	Heterozygous IDH1R132H/WT created by single base editing inhibits human astroglial cell growth by downregulating YAP. <i>Oncogene</i> , 2018, 37, 5160-5174.	5.9	27
26	Analysis of KLF4 regulated genes in cancer cells reveals a role of DNA methylation in promoter-enhancer interactions. <i>Epigenetics</i> , 2018, 13, 751-768.	2.7	15
27	High-Throughput Chip Assay for Investigating <i>Escherichia coli</i> Interaction with the Blood-Brain Barrier Using Microbial and Human Proteome Microarrays (Dual-Microarray) <i>Journal of Proteomics</i> , 2018, 11, 107-118.	0.784314	10
28	Measuring Ligand Binding Kinetics to Membrane Proteins Using Virion Nano-oscillators. <i>Journal of the American Chemical Society</i> , 2018, 140, 11495-11501.	13.7	17
29	Emetine inhibits Zika and Ebola virus infections through two molecular mechanisms: inhibiting viral replication and decreasing viral entry. <i>Cell Discovery</i> , 2018, 4, 31.	6.7	128
30	A Human Proteome Array Approach to Identifying Key Host Proteins Targeted by Toxoplasma Kinase ROP18. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 469-484.	3.8	28
31	Global Analysis of SUMO-Binding Proteins Identifies SUMOylation as a Key Regulator of the INO80 Chromatin Remodeling Complex. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 812-823.	3.8	15
32	Protein Array-based Approaches for Biomarker Discovery in Cancer. <i>Genomics, Proteomics and Bioinformatics</i> , 2017, 15, 73-81.	6.9	70
33	Identification of Serological Biomarkers for Early Diagnosis of Lung Cancer Using a Protein Array-Based Approach. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 2069-2078.	3.8	63
34	Zika-Virus-Encoded NS2A Disrupts Mammalian Cortical Neurogenesis by Degrading Adherens Junction Proteins. <i>Cell Stem Cell</i> , 2017, 21, 349-358.e6.	11.1	163
35	Identification of Novel Biomarkers for Behcet Disease Diagnosis Using Human Proteome Microarray Approach. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 147-156.	3.8	49
36	Methylated cis-regulatory elements mediate KLF4-dependent gene transactivation and cell migration. <i>ELife</i> , 2017, 6, .	6.0	39

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37	ScaPD: a database for human scaffold proteins. <i>BMC Bioinformatics</i> , 2017, 18, 386.	2.6	8
38	Evaluation of autoantibody signatures in meningioma patients using human proteome arrays. <i>Oncotarget</i> , 2017, 8, 58443-58456.	1.8	20
39	Single-Cell Co-expression Analysis Reveals Distinct Functional Modules, Co-regulation Mechanisms and Clinical Outcomes. <i>PLoS Computational Biology</i> , 2016, 12, e1004892.	3.2	36
40	Characterization of Lipid-Protein Interactions Using Nonquenched Fluorescent Liposomal Nanovesicles and Yeast Proteome Microarrays. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot087981.	0.3	1
41	The NIH Protein Capture Reagents Program (PCRP): a standardized protein affinity reagent toolbox. <i>Nature Methods</i> , 2016, 13, 805-806.	19.0	9
42	Characterization of RNA-Binding Proteins Using Protein Microarrays. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot087973.	0.3	3
43	Posttranslational Modification Assays on Functional Protein Microarrays. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot087999.	0.3	2
44	Protein Microarrays: Flexible Tools for Scientific Innovation. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.top081471.	0.3	9
45	Characterization of Protein-Protein Interactions Using Protein Microarrays. <i>Cold Spring Harbor Protocols</i> , 2016, 2016, pdb.prot087965.	0.3	6
46	A nuclease that mediates cell death induced by DNA damage and poly(ADP-ribose) polymerase-1. <i>Science</i> , 2016, 354, .	12.6	266
47	Transcription factors as readers and effectors of DNA methylation. <i>Nature Reviews Genetics</i> , 2016, 17, 551-565.	16.3	482
48	EnhancerAtlas: a resource for enhancer annotation and analysis in 105 human cell/tissue types. <i>Bioinformatics</i> , 2016, 32, 3543-3551.	4.1	148
49	Microarray-Based Phospho-Proteomic Profiling of Complex Biological Systems. <i>Translational Oncology</i> , 2016, 9, 124-129.	3.7	6
50	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. <i>Cell</i> , 2016, 166, 755-765.	28.9	804
51	Lin28A Binds Active Promoters and Recruits Tet1 to Regulate Gene Expression. <i>Molecular Cell</i> , 2016, 61, 153-160.	9.7	74
52	Applications in high-content functional protein microarrays. <i>Current Opinion in Chemical Biology</i> , 2016, 30, 21-27.	6.1	46
53	Identification of Serum Biomarkers for Gastric Cancer Diagnosis Using a Human Proteome Microarray. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 614-623.	3.8	82
54	Functional Characterization of Schizophrenia-Associated Variation in CACNA1C. <i>PLoS ONE</i> , 2016, 11, e0157086.	2.5	61

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55	Autoantibody Profiling of Glioma Serum Samples to Identify Biomarkers Using Human Proteome Arrays. <i>Scientific Reports</i> , 2015, 5, 13895.	3.3	43
56	Autoantibody Profiling on Human Proteome Microarray for Biomarker Discovery in Cerebrospinal Fluid and Sera of Neuropsychiatric Lupus. <i>PLoS ONE</i> , 2015, 10, e0126643.	2.5	20
57	Systematic Prediction of Scaffold Proteins Reveals New Design Principles in Scaffold-Mediated Signal Transduction. <i>PLoS Computational Biology</i> , 2015, 11, e1004508.	3.2	13
58	Identification of SUMO E3 Ligase-Specific Substrates Using the HuProt Human Proteome Microarray. <i>Methods in Molecular Biology</i> , 2015, 1295, 455-463.	0.9	11
59	A Screen for Extracellular Signal-Regulated Kinase-Primed Glycogen Synthase Kinase 3 Substrates Identifies the p53 Inhibitor iASPP. <i>Journal of Virology</i> , 2015, 89, 9232-9241.	3.4	10
60	Characterization of tissue-specific differential DNA methylation suggests distinct modes of positive and negative gene expression regulation. <i>BMC Genomics</i> , 2015, 16, 49.	2.8	132
61	Opposing Roles for the lncRNA Haunt and Its Genomic Locus in Regulating HOXA Gene Activation during Embryonic Stem Cell Differentiation. <i>Cell Stem Cell</i> , 2015, 16, 504-516.	11.1	247
62	Characterization of monoclonal antibody's binding kinetics using oblique-incidence reflectivity difference approach. <i>MAbs</i> , 2015, 7, 110-119.	5.2	20
63	Systematic identification of arsenic-binding proteins reveals that hexokinase-2 is inhibited by arsenic. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 15084-15089.	7.1	126
64	YcgC represents a new protein deacetylase family in prokaryotes. <i>ELife</i> , 2015, 4, .	6.0	52
65	DNA Binding and Condensation Properties of the Herpes Simplex Virus Type 1 Triplex Protein VP19C. <i>PLoS ONE</i> , 2014, 9, e104640.	2.5	9
66	Notch3 Interactome Analysis Identified WWP2 as a Negative Regulator of Notch3 Signaling in Ovarian Cancer. <i>PLoS Genetics</i> , 2014, 10, e1004751.	3.5	64
67	Toward a systems-level view of dynamic phosphorylation networks. <i>Frontiers in Genetics</i> , 2014, 5, 263.	2.3	36
68	A Human Proteome Microarray Identifies that the Heterogeneous Nuclear Ribonucleoprotein K (hnRNP) Tj ETQq0 0 0 rgBT /Overlock 10 Proteomics, 2014, 13, 84-92.	3.8	37
69	Distribution, recognition and regulation of non-CpG methylation in the adult mammalian brain. <i>Nature Neuroscience</i> , 2014, 17, 215-222.	14.8	663
70	PhosphoNetworks: a database for human phosphorylation networks. <i>Bioinformatics</i> , 2014, 30, 141-142.	4.1	106
71	Activation of diverse signalling pathways by oncogenic PIK3CA mutations. <i>Nature Communications</i> , 2014, 5, 4961.	12.8	72
72	Characterization of the SUMO-Binding Activity of the Myeloproliferative and Mental Retardation (MYM)-Type Zinc Fingers in ZNF261 and ZNF198. <i>PLoS ONE</i> , 2014, 9, e105271.	2.5	27

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73	Functional genomics identifies novel genes essential for clear cell renal cell carcinoma tumor cell proliferation and migration. <i>Oncotarget</i> , 2014, 5, 5320-5334.	1.8	18
74	Construction of human activityâ€based phosphorylation networks. <i>Molecular Systems Biology</i> , 2013, 9, 655.	7.2	153
75	Overview of Protein Microarrays. <i>Current Protocols in Protein Science</i> , 2013, 72, Unit 27.1.	2.8	144
76	VirD: A Virion Display Array for Profiling Functional Membrane Proteins. <i>Analytical Chemistry</i> , 2013, 85, 8046-8054.	6.5	16
77	New Centromere Autoantigens Identified in Systemic Sclerosis Using Centromere Protein Microarrays. <i>Journal of Rheumatology</i> , 2013, 40, 461-468.	2.0	30
78	Integrative analysis of tissue-specific methylation and alternative splicing identifies conserved transcription factor binding motifs. <i>Nucleic Acids Research</i> , 2013, 41, 8503-8514.	14.5	46
79	Profiling the Dynamics of a Human Phosphorylome Reveals New Components in HGF/c-Met Signaling. <i>PLoS ONE</i> , 2013, 8, e72671.	2.5	19
80	DNA methylation presents distinct binding sites for human transcription factors. <i>ELife</i> , 2013, 2, e00726.	6.0	292
81	Phosphorylation of the Chromatin Binding Domain of KSHV LANA. <i>PLoS Pathogens</i> , 2012, 8, e1002972.	4.7	32
82	Identification of New Autoantigens for Primary Biliary Cirrhosis Using Human Proteome Microarrays. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 669-680.	3.8	80
83	Profiling Lipidâ€protein Interactions Using Nonquenched Fluorescent Liposomal Nanovesicles and Proteome Microarrays. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1177-1190.	3.8	36
84	Rapid Identification of Monospecific Monoclonal Antibodies Using a Human Proteome Microarray. <i>Molecular and Cellular Proteomics</i> , 2012, 11, O111.016253.	3.8	136
85	Regulation of CK2 by phosphorylation and O-GlcNAcylation revealed by semisynthesis. <i>Nature Chemical Biology</i> , 2012, 8, 262-269.	8.0	148
86	A Protein Array Screen for Kaposi's Sarcoma-Associated Herpesvirus LANA Interactors Links LANA to TIP60, PP2A Activity, and Telomere Shortening. <i>Journal of Virology</i> , 2012, 86, 5179-5191.	3.4	56
87	SUMO Binding by the Epstein-Barr Virus Protein Kinase BGLF4 Is Crucial for BGLF4 Function. <i>Journal of Virology</i> , 2012, 86, 5412-5421.	3.4	56
88	Applications of Functional Protein Microarrays in Basic and Clinical Research. <i>Advances in Genetics</i> , 2012, 79, 123-155.	1.8	38
89	Functional protein microarray as molecular decathlete: A versatile player in clinical proteomics. <i>Proteomics - Clinical Applications</i> , 2012, 6, 548-562.	1.6	13
90	Functional protein microarray: an ideal platform for investigating protein binding property. <i>Frontiers in Biology</i> , 2012, 7, 336-349.	0.7	8

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91	Detection and Verification of Glycosylation Patterns of Glycoproteins from Clinical Specimens Using Lectin Microarrays and Lectin-Based Immunosorbent Assays. <i>Analytical Chemistry</i> , 2011, 83, 8509-8516.	6.5	71
92	Characterization of Protein-DNA Interactions Using Protein Microarrays. <i>Cold Spring Harbor Protocols</i> , 2011, 2011, pdb.prot5614-pdb.prot5614.	0.3	12
93	Acetylation of Yeast AMPK Controls Intrinsic Aging Independently of Caloric Restriction. <i>Cell</i> , 2011, 146, 969-979.	28.9	133
94	Conserved Herpesvirus Kinases Target the DNA Damage Response Pathway and TIP60 Histone Acetyltransferase to Promote Virus Replication. <i>Cell Host and Microbe</i> , 2011, 10, 390-400.	11.0	148
95	The long noncoding RNA Six3OS acts in trans to regulate retinal development by modulating Six3 activity. <i>Neural Development</i> , 2011, 6, 32.	2.4	128
96	Functional protein microarray technology. <i>Wiley Interdisciplinary Reviews: Systems Biology and Medicine</i> , 2011, 3, 255-268.	6.6	62
97	A Functional Protein Microarray Approach to Characterizing Posttranslational Modifications on Lysine Residues. <i>Methods in Molecular Biology</i> , 2011, 723, 213-223.	0.9	9
98	hPDI: a database of experimental human protein-DNA interactions. <i>Bioinformatics</i> , 2010, 26, 287-289.	4.1	86
99	Novel Autoimmune Hepatitis-Specific Autoantigens Identified Using Protein Microarray Technology. <i>Journal of Proteome Research</i> , 2010, 9, 30-39.	3.7	71
100	Protein Array Identification of Substrates of the Epstein-Barr Virus Protein Kinase BGLF4. <i>Journal of Virology</i> , 2009, 83, 5219-5231.	3.4	67
101	Global analysis of the glycoproteome in <i>Saccharomyces cerevisiae</i> reveals new roles for protein glycosylation in eukaryotes. <i>Molecular Systems Biology</i> , 2009, 5, 308.	7.2	79
102	Identification of Novel Serological Biomarkers for Inflammatory Bowel Disease Using Escherichia coli Proteome Chip. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1765-1776.	3.8	63
103	Protein Acetylation Microarray Reveals that NuA4 Controls Key Metabolic Target Regulating Gluconeogenesis. <i>Cell</i> , 2009, 136, 1073-1084.	28.9	279
104	Profiling the Human Protein-DNA Interactome Reveals ERK2 as a Transcriptional Repressor of Interferon Signaling. <i>Cell</i> , 2009, 139, 610-622.	28.9	352
105	A protein chip approach to unraveling networks and pathways. <i>FASEB Journal</i> , 2009, 23, 328.2.	0.5	0
106	A proteome chip approach reveals new DNA damage recognition activities in Escherichia coli. <i>Nature Methods</i> , 2008, 5, 69-74.	19.0	121
107	Protein Arrays on Patterned Porous Gold Substrates Interrogated with Mass Spectrometry: Detection of Peptides in Plasma. <i>Analytical Chemistry</i> , 2008, 80, 1448-1458.	6.5	47
108	Lectin microarrays identify cell-specific and functionally significant cell surface glycan markers. <i>Glycobiology</i> , 2008, 18, 761-769.	2.5	184

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109	Functional Dissection of a HECT Ubiquitin E3 Ligase. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 35-45.	3.8	70
110	RNA-binding proteins that inhibit RNA virus infection. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 3129-3134.	7.1	97
111	Applications of Protein Microarray Technology. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2007, 10, 706-718.	1.1	67
112	A protein chip approach for high-throughput antigen identification and characterization. <i>Proteomics</i> , 2007, 7, 2151-2161.	2.2	24
113	Protein Microarrays. <i>BioTechniques</i> , 2006, 40, 423-429.	1.8	71
114	Protein chip fabrication by capture of nascent polypeptides. <i>Nature Biotechnology</i> , 2006, 24, 1253-1254.	17.5	90
115	Severe acute respiratory syndrome diagnostics using a coronavirus protein microarray. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 4011-4016.	7.1	131
116	Global analysis of protein phosphorylation in yeast. <i>Nature</i> , 2005, 438, 679-684.	27.8	915
117	Finding new components of the target of rapamycin (TOR) signaling network through chemical genetics and proteome chips. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 16594-16599.	7.1	225
118	Regulation of Gene Expression by a Metabolic Enzyme. <i>Science</i> , 2004, 306, 482-484.	12.6	223
119	Protein chip technology. <i>Current Opinion in Chemical Biology</i> , 2003, 7, 55-63.	6.1	861
120	Proteomics. <i>Annual Review of Biochemistry</i> , 2003, 72, 783-812.	11.1	332
121	â€”Omicâ€™ approaches for unraveling signaling networks. <i>Current Opinion in Cell Biology</i> , 2002, 14, 173-179.	5.4	73
122	Protein arrays and microarrays. <i>Current Opinion in Chemical Biology</i> , 2001, 5, 40-45.	6.1	376
123	Analysis of yeast protein kinases using protein chips. <i>Nature Genetics</i> , 2000, 26, 283-289.	21.4	810