Heng Zhu

List of Publications by Year in descending order

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		30070	24982
123	12,731	54	109
papers	citations	h-index	g-index
147	147	147	18662
all docs	docs citations	times ranked	citing authors

#	Article	IF	CITATIONS
1	Global analysis of protein phosphorylation in yeast. Nature, 2005, 438, 679-684.	27.8	915
2	Protein chip technology. Current Opinion in Chemical Biology, 2003, 7, 55-63.	6.1	861
3	Analysis of yeast protein kinases using protein chips. Nature Genetics, 2000, 26, 283-289.	21.4	810
4	Integrated Proteogenomic Characterization of Human High-Grade Serous Ovarian Cancer. Cell, 2016, 166, 755-765.	28.9	804
5	Distribution, recognition and regulation of non-CpG methylation in the adult mammalian brain. Nature Neuroscience, 2014, 17, 215-222.	14.8	663
6	Transcription factors as readers and effectors of DNA methylation. Nature Reviews Genetics, 2016, 17, 551-565.	16.3	482
7	Protein arrays and microarrays. Current Opinion in Chemical Biology, 2001, 5, 40-45.	6.1	376
8	Profiling the Human Protein-DNA Interactome Reveals ERK2 as a Transcriptional RepressorÂof Interferon Signaling. Cell, 2009, 139, 610-622.	28.9	352
9	Proteomics. Annual Review of Biochemistry, 2003, 72, 783-812.	11.1	332
10	DNA methylation presents distinct binding sites for human transcription factors. ELife, 2013, 2, e00726.	6.0	292
11	Protein Acetylation Microarray Reveals that NuA4 Controls Key Metabolic Target Regulating Gluconeogenesis. Cell, 2009, 136, 1073-1084.	28.9	279
12	A nuclease that mediates cell death induced by DNA damage and poly(ADP-ribose) polymerase-1. Science, 2016, 354, .	12.6	266
13	Opposing Roles for the IncRNA Haunt and Its Genomic Locus in Regulating HOXA Gene Activation during Embryonic Stem Cell Differentiation. Cell Stem Cell, 2015, 16, 504-516.	11.1	247
14	Finding new components of the target of rapamycin (TOR) signaling network through chemical genetics and proteome chips. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 16594-16599.	7.1	225
15	Regulation of Gene Expression by a Metabolic Enzyme. Science, 2004, 306, 482-484.	12.6	223
16	Lectin microarrays identify cell-specific and functionally significant cell surface glycan markers. Glycobiology, 2008, 18, 761-769.	2.5	184
17	Zika-Virus-Encoded NS2A Disrupts Mammalian Cortical Neurogenesis by Degrading Adherens Junction Proteins. Cell Stem Cell, 2017, 21, 349-358.e6.	11.1	163
18	Structural Features of Transcription Factors Associating with Nucleosome Binding. Molecular Cell, 2019, 75, 921-932.e6.	9.7	158

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19	Construction of human activityâ€based phosphorylation networks. Molecular Systems Biology, 2013, 9, 655.	7.2	153
20	Conserved Herpesvirus Kinases Target the DNA Damage Response Pathway and TIP60 Histone Acetyltransferase to Promote Virus Replication. Cell Host and Microbe, 2011, 10, 390-400.	11.0	148
21	Regulation of CK2 by phosphorylation and O-GlcNAcylation revealed by semisynthesis. Nature Chemical Biology, 2012, 8, 262-269.	8.0	148
22	EnhancerAtlas: a resource for enhancer annotation and analysis in 105 human cell/tissue types. Bioinformatics, 2016, 32, 3543-3551.	4.1	148
23	Overview of Protein Microarrays. Current Protocols in Protein Science, 2013, 72, Unit 27.1.	2.8	144
24	Rapid Identification of Monospecific Monoclonal Antibodies Using a Human Proteome Microarray. Molecular and Cellular Proteomics, 2012, 11, O111.016253.	3.8	136
25	Acetylation of Yeast AMPK Controls Intrinsic Aging Independently of Caloric Restriction. Cell, 2011, 146, 969-979.	28.9	133
26	Characterization of tissue-specific differential DNA methylation suggests distinct modes of positive and negative gene expression regulation. BMC Genomics, 2015, 16, 49.	2.8	132
27	Severe acute respiratory syndrome diagnostics using a coronavirus protein microarray. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4011-4016.	7.1	131
28	The long noncoding RNA Six3OS acts in trans to regulate retinal development by modulating Six3 activity. Neural Development, 2011, 6, 32.	2.4	128
29	Emetine inhibits Zika and Ebola virus infections through two molecular mechanisms: inhibiting viral replication and decreasing viral entry. Cell Discovery, 2018, 4, 31.	6.7	128
30	Systematic identification of arsenic-binding proteins reveals that hexokinase-2 is inhibited by arsenic. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15084-15089.	7.1	126
31	A proteome chip approach reveals new DNA damage recognition activities in Escherichia coli. Nature Methods, 2008, 5, 69-74.	19.0	121
32	PhosphoNetworks: a database for human phosphorylation networks. Bioinformatics, 2014, 30, 141-142.	4.1	106
33	RNA-binding proteins that inhibit RNA virus infection. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 3129-3134.	7.1	97
34	MeDReaders: a database for transcription factors that bind to methylated DNA. Nucleic Acids Research, 2018, 46, D146-D151.	14.5	94
35	Protein chip fabrication by capture of nascent polypeptides. Nature Biotechnology, 2006, 24, 1253-1254.	17.5	90
36	Liver Transplantation for Severe Alcoholic Hepatitis, Updated Lessons from the World's Largest Series. Journal of the American College of Surgeons, 2018, 226, 549-557.	0.5	90

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37	hPDI: a database of experimental human protein–DNA interactions. Bioinformatics, 2010, 26, 287-289.	4.1	86
38	Identification of Serum Biomarkers for Gastric Cancer Diagnosis Using a Human Proteome Microarray. Molecular and Cellular Proteomics, 2016, 15, 614-623.	3.8	82
39	Identification of New Autoantigens for Primary Biliary Cirrhosis Using Human Proteome Microarrays. Molecular and Cellular Proteomics, 2012, 11, 669-680.	3.8	80
40	Global analysis of the glycoproteome in <i>Saccharomyces cerevisiae</i> reveals new roles for protein glycosylation in eukaryotes. Molecular Systems Biology, 2009, 5, 308.	7.2	79
41	Lin28A Binds Active Promoters and Recruits Tet1 to Regulate Gene Expression. Molecular Cell, 2016, 61, 153-160.	9.7	74
42	â€~Omic' approaches for unraveling signaling networks. Current Opinion in Cell Biology, 2002, 14, 173-179.	5.4	73
43	Activation of diverse signalling pathways by oncogenic PIK3CA mutations. Nature Communications, 2014, 5, 4961.	12.8	72
44	Protein Microarrays. BioTechniques, 2006, 40, 423-429.	1.8	71
45	Novel Autoimmune Hepatitis-Specific Autoantigens Identified Using Protein Microarray Technology. Journal of Proteome Research, 2010, 9, 30-39.	3.7	71
46	Detection and Verification of Glycosylation Patterns of Glycoproteins from Clinical Specimens Using Lectin Microarrays and Lectin-Based Immunosorbent Assays. Analytical Chemistry, 2011, 83, 8509-8516.	6.5	71
47	Functional Dissection of a HECT Ubiquitin E3 Ligase. Molecular and Cellular Proteomics, 2008, 7, 35-45.	3.8	70
48	Protein Array-based Approaches for Biomarker Discovery in Cancer. Genomics, Proteomics and Bioinformatics, 2017, 15, 73-81.	6.9	70
49	Applications of Protein Microarray Technology. Combinatorial Chemistry and High Throughput Screening, 2007, 10, 706-718.	1.1	67
50	Protein Array Identification of Substrates of the Epstein-Barr Virus Protein Kinase BGLF4. Journal of Virology, 2009, 83, 5219-5231.	3.4	67
51	Notch3 Interactome Analysis Identified WWP2 as a Negative Regulator of Notch3 Signaling in Ovarian Cancer. PLoS Genetics, 2014, 10, e1004751.	3.5	64
52	Identification of Novel Serological Biomarkers for Inflammatory Bowel Disease Using Escherichia coli Proteome Chip. Molecular and Cellular Proteomics, 2009, 8, 1765-1776.	3.8	63
53	Identification of Serological Biomarkers for Early Diagnosis of Lung Cancer Using a Protein Array-Based Approach. Molecular and Cellular Proteomics, 2017, 16, 2069-2078.	3.8	63
54	Functional protein microarray technology. Wiley Interdisciplinary Reviews: Systems Biology and Medicine, 2011, 3, 255-268.	6.6	62

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55	Functional Characterization of Schizophrenia-Associated Variation in CACNA1C. PLoS ONE, 2016, 11, e0157086.	2.5	61
56	A toolbox of immunoprecipitation-grade monoclonal antibodies to human transcription factors. Nature Methods, 2018, 15, 330-338.	19.0	58
57	A Protein Array Screen for Kaposi's Sarcoma-Associated Herpesvirus LANA Interactors Links LANA to TIP60, PP2A Activity, and Telomere Shortening. Journal of Virology, 2012, 86, 5179-5191.	3.4	56
58	SUMO Binding by the Epstein-Barr Virus Protein Kinase BGLF4 Is Crucial for BGLF4 Function. Journal of Virology, 2012, 86, 5412-5421.	3.4	56
59	YcgC represents a new protein deacetylase family in prokaryotes. ELife, 2015, 4, .	6.0	52
60	Identification of Novel Biomarkers for Behcet Disease Diagnosis Using Human Proteome Microarray Approach. Molecular and Cellular Proteomics, 2017, 16, 147-156.	3.8	49
61	Protein Arrays on Patterned Porous Gold Substrates Interrogated with Mass Spectrometry:  Detection of Peptides in Plasma. Analytical Chemistry, 2008, 80, 1448-1458.	6.5	47
62	Integrative analysis of tissue-specific methylation and alternative splicing identifies conserved transcription factor binding motifs. Nucleic Acids Research, 2013, 41, 8503-8514.	14.5	46
63	Applications in high-content functional protein microarrays. Current Opinion in Chemical Biology, 2016, 30, 21-27.	6.1	46
64	Developments and Applications of Functional Protein Microarrays. Molecular and Cellular Proteomics, 2020, 19, 916-927.	3.8	45
65	Autoantibody Profiling of Glioma Serum Samples to Identify Biomarkers Using Human Proteome Arrays. Scientific Reports, 2015, 5, 13895.	3.3	43
66	Methylated cis-regulatory elements mediate KLF4-dependent gene transactivation and cell migration. ELife, 2017, 6, .	6.0	39
67	Applications of Functional Protein Microarrays in Basic and Clinical Research. Advances in Genetics, 2012, 79, 123-155.	1.8	38
68	A Human Proteome Microarray Identifies that the Heterogeneous Nuclear Ribonucleoprotein K (hnRNP) Tj ETQq0 Proteomics, 2014, 13, 84-92.	0 0 rgBT /0 3.8	Overlock 10 37
69	Targeting UDP-α-d-glucose 6-dehydrogenase inhibits glioblastoma growth and migration. Oncogene, 2018, 37, 2615-2629.	5.9	37
70	Profiling Lipid–protein Interactions Using Nonquenched Fluorescent Liposomal Nanovesicles and Proteome Microarrays. Molecular and Cellular Proteomics, 2012, 11, 1177-1190.	3.8	36
71	Toward a systems-level view of dynamic phosphorylation networks. Frontiers in Genetics, 2014, 5, 263.	2.3	36
72	Single-Cell Co-expression Analysis Reveals Distinct Functional Modules, Co-regulation Mechanisms and Clinical Outcomes. PLoS Computational Biology, 2016, 12, e1004892.	3.2	36

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73	Phosphorylation of the Chromatin Binding Domain of KSHV LANA. PLoS Pathogens, 2012, 8, e1002972.	4.7	32
74	New Centromere Autoantigens Identified in Systemic Sclerosis Using Centromere Protein Microarrays. Journal of Rheumatology, 2013, 40, 461-468.	2.0	30
75	Parkinson-Associated SNCA Enhancer Variants Revealed by Open Chromatin in Mouse Dopamine Neurons. American Journal of Human Genetics, 2018, 103, 874-892.	6.2	30
76	Insight into novel RNA-binding activities via large-scale analysis of lncRNA-bound proteome and IDH1-bound transcriptome. Nucleic Acids Research, 2019, 47, 2244-2262.	14.5	29
77	A Human Proteome Array Approach to Identifying Key Host Proteins Targeted by Toxoplasma Kinase ROP18. Molecular and Cellular Proteomics, 2017, 16, 469-484.	3.8	28
78	Heterozygous IDH1R132H/WT created by "single base editing―inhibits human astroglial cell growth by downregulating YAP. Oncogene, 2018, 37, 5160-5174.	5.9	27
79	Characterization of the SUMO-Binding Activity of the Myeloproliferative and Mental Retardation (MYM)-Type Zinc Fingers in ZNF261 and ZNF198. PLoS ONE, 2014, 9, e105271.	2.5	27
80	A protein chip approach for high-throughput antigen identification and characterization. Proteomics, 2007, 7, 2151-2161.	2.2	24
81	Global Identification of Small Ubiquitin-related Modifier (SUMO) Substrates Reveals Crosstalk between SUMOylation and Phosphorylation Promotes Cell Migration. Molecular and Cellular Proteomics, 2018, 17, 871-888.	3.8	24
82	Integration of IgA and IgG Autoantigens Improves Performance of Biomarker Panels for Early Diagnosis of Lung Cancer. Molecular and Cellular Proteomics, 2020, 19, 490-500.	3.8	23
83	Discovery of a Potent GLUT Inhibitor from a Library of Rapafucins by Using 3D Microarrays. Angewandte Chemie - International Edition, 2019, 58, 17158-17162.	13.8	22
84	An all-to-all approach to the identification of sequence-specific readers for epigenetic DNA modifications on cytosine. Nature Communications, 2021, 12, 795.	12.8	22
85	Autoantibody Profiling on Human Proteome Microarray for Biomarker Discovery in Cerebrospinal Fluid and Sera of Neuropsychiatric Lupus. PLoS ONE, 2015, 10, e0126643.	2.5	20
86	Characterization of monoclonal antibody's binding kinetics using oblique-incidence reflectivity difference approach. MAbs, 2015, 7, 110-119.	5.2	20
87	Evaluation of autoantibody signatures in meningioma patients using human proteome arrays. Oncotarget, 2017, 8, 58443-58456.	1.8	20
88	Discovery and Validation of a Serologic Autoantibody Panel for Early Diagnosis of Esophageal Squamous Cell Carcinoma. Cancer Epidemiology Biomarkers and Prevention, 2019, 28, 1454-1460.	2.5	20
89	Multiplexed Biomarker Panels Discriminate Zika and Dengue Virus Infection in Humans. Molecular and Cellular Proteomics, 2018, 17, 349-356.	3.8	19
90	Proteome-wide Tyrosine Phosphorylation Analysis Reveals Dysregulated Signaling Pathways in Ovarian Tumors. Molecular and Cellular Proteomics, 2019, 18, 448-460.	3.8	19

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91	Profiling the Dynamics of a Human Phosphorylome Reveals New Components in HGF/c-Met Signaling. PLoS ONE, 2013, 8, e72671.	2.5	19
92	Functional genomics identifies novel genes essential for clear cell renal cell carcinoma tumor cell proliferation and migration. Oncotarget, 2014, 5, 5320-5334.	1.8	18
93	Measuring Ligand Binding Kinetics to Membrane Proteins Using Virion Nano-oscillators. Journal of the American Chemical Society, 2018, 140, 11495-11501.	13.7	17
94	VirD: A Virion Display Array for Profiling Functional Membrane Proteins. Analytical Chemistry, 2013, 85, 8046-8054.	6.5	16
95	Global Analysis of SUMO-Binding Proteins Identifies SUMOylation as a Key Regulator of the INO80 Chromatin Remodeling Complex. Molecular and Cellular Proteomics, 2017, 16, 812-823.	3.8	15
96	Analysis of KLF4 regulated genes in cancer cells reveals a role of DNA methylation in promoterenhancer interactions. Epigenetics, 2018, 13, 751-768.	2.7	15
97	High-Throughput Chip Assay for Investigating <i>Escherichia coli</i> Interaction with the Blood–Brain Barrier Using Microbial and Human Proteome Microarrays (Dual-Microarray) Tj ETQq1 1 0.784314	rgB\$ Ove	erl a5 k 10 Tf 5
98	Functional protein microarray as molecular decathlete: A versatile player in clinical proteomics. Proteomics - Clinical Applications, 2012, 6, 548-562.	1.6	13
99	Systematic Prediction of Scaffold Proteins Reveals New Design Principles in Scaffold-Mediated Signal Transduction. PLoS Computational Biology, 2015, 11, e1004508.	3.2	13
100	Development and application of a high-content virion display human GPCR array. Nature Communications, 2019, 10, 1997.	12.8	13
101	ldentification of Novel Serological Autoantibodies in Takayasu Arteritis Patients Using HuProt Arrays. Molecular and Cellular Proteomics, 2021, 20, 100036.	3.8	13
102	Characterization of Protein-DNA Interactions Using Protein Microarrays. Cold Spring Harbor Protocols, 2011, 2011, pdb.prot5614-pdb.prot5614.	0.3	12
103	ldentification of SUMO E3 Ligase-Specific Substrates Using the HuProt Human Proteome Microarray. Methods in Molecular Biology, 2015, 1295, 455-463.	0.9	11
104	A Screen for Extracellular Signal-Regulated Kinase-Primed Glycogen Synthase Kinase 3 Substrates Identifies the p53 Inhibitor iASPP. Journal of Virology, 2015, 89, 9232-9241.	3.4	10
105	DNA Binding and Condensation Properties of the Herpes Simplex Virus Type 1 Triplex Protein VP19C. PLoS ONE, 2014, 9, e104640.	2.5	9
106	The NIH Protein Capture Reagents Program (PCRP): a standardized protein affinity reagent toolbox. Nature Methods, 2016, 13, 805-806.	19.0	9
107	Protein Microarrays: Flexible Tools for Scientific Innovation. Cold Spring Harbor Protocols, 2016, 2016, pdb.top081471.	0.3	9
108	A Functional Protein Microarray Approach to Characterizing Posttranslational Modifications on Lysine Residues. Methods in Molecular Biology, 2011, 723, 213-223.	0.9	9

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109	Functional protein microarray: an ideal platform for investigating protein binding property. Frontiers in Biology, 2012, 7, 336-349.	0.7	8
110	ScaPD: a database for human scaffold proteins. BMC Bioinformatics, 2017, 18, 386.	2.6	8
111	An Integrated Systems Biology Approach Identifies the Proteasome as A Critical Host Machinery for ZIKV and DENV Replication. Genomics, Proteomics and Bioinformatics, 2021, 19, 108-122.	6.9	7
112	Multifaceted Regulation of Akt by Diverse C-Terminal Post-translational Modifications. ACS Chemical Biology, 2022, 17, 68-76.	3.4	7
113	Characterization of Protein–Protein Interactions Using Protein Microarrays. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot087965.	0.3	6
114	Microarray-Based Phospho-Proteomic Profiling of Complex Biological Systems. Translational Oncology, 2016, 9, 124-129.	3.7	6
115	CRYÎ ² B2 enhances tumorigenesis through upregulation of nucleolin in triple negative breast cancer. Oncogene, 2021, 40, 5752-5763.	5.9	6
116	Enzymatic analysis of WWP2 E3 ubiquitin ligase using protein microarrays identifies autophagy-related substrates. Journal of Biological Chemistry, 2022, 298, 101854.	3.4	6
117	AAgMarker 1.0: a resource of serological autoantigen biomarkers for clinical diagnosis and prognosis of various human diseases. Nucleic Acids Research, 2018, 46, D886-D893.	14.5	5
118	Characterization of RNA-Binding Proteins Using Protein Microarrays. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot087973.	0.3	3
119	Protein Microarrays and Liposome: A Method for Studying Lipid–Protein Interactions. Methods in Molecular Biology, 2019, 2003, 191-199.	0.9	3
120	Posttranslational Modification Assays on Functional Protein Microarrays. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot087999.	0.3	2
121	Characterization of Lipid–Protein Interactions Using Nonquenched Fluorescent Liposomal Nanovesicles and Yeast Proteome Microarrays. Cold Spring Harbor Protocols, 2016, 2016, pdb.prot087981.	0.3	1
122	Virion Display: A Highâ€Throughput Method to Express Functional Membrane Proteins. Current Protocols in Molecular Biology, 2020, 132, e126.	2.9	0
123	A protein chip approach to unraveling networks and pathways. FASEB Journal, 2009, 23, 328.2.	0.5	0