Catherine Cl Wong

List of Publications by Year in descending order

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57 papers

4,775 citations

32 h-index 56 g-index

57 all docs 57 docs citations

57 times ranked 7999 citing authors

#	Article	IF	CITATIONS
1	Immune response pattern across the asymptomatic, symptomatic and convalescent periods of COVID-19. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2022, 1870, 140736.	2.3	7
2	Recycling of autophagosomal components from autolysosomes by the recycler complex. Nature Cell Biology, 2022, 24, 497-512.	10.3	42
3	Upregulated YB-1 protein promotes glioblastoma growth through a YB-1/CCT4/mLST8/mTOR pathway. Journal of Clinical Investigation, 2022, 132, .	8.2	21
4	Retractosomes: small extracellular vesicles generated from broken-off retraction fibers. Cell Research, 2022, 32, 953-956.	12.0	11
5	HPF1 remodels the active site of PARP1 to enable the serine ADP-ribosylation of histones. Nature Communications, 2021, 12, 1028.	12.8	41
6	CBRPP: a new RNA-centric method to study RNA–protein interactions. RNA Biology, 2021, 18, 1608-1621.	3.1	19
7	The TOR–EIN2 axis mediates nuclear signalling to modulate plant growth. Nature, 2021, 591, 288-292.	27.8	70
8	Proteomic Analysis Identifies Prolonged Disturbances in Pathways Related to Cholesterol Metabolism and Myocardium Function in the COVID-19 Recovery Stage. Journal of Proteome Research, 2021, 20, 3463-3474.	3.7	21
9	Global profiling of RNA-binding protein target sites by LACE-seq. Nature Cell Biology, 2021, 23, 664-675.	10.3	40
10	Proteogenomics Integrating Novel Junction Peptide Identification Strategy Discovers Three Novel Protein Isoforms of Human NHSL1 and EEF1B2. Journal of Proteome Research, 2021, 20, 5294-5303.	3.7	2
11	O-glycosylation pattern of the SARS-CoV-2 spike protein reveals an "O-Follow-N―rule. Cell Research, 2021, 31, 1123-1125.	12.0	70
12	Mechanism of Microbial Metabolite Leupeptin in the Treatment of COVID-19 by Traditional Chinese Medicine Herbs. MBio, 2021, 12, e0222021.	4.1	23
13	A matter of perspectiveâ€"Cutting-edge technology-driven urine proteome in COVID-19. Urine, 2021, 3, 1-2.	4.0	2
14	Immune suppression in the early stage of COVID-19 disease. Nature Communications, 2020, 11, 5859.	12.8	161
15	Multiple Signaling Roles of CD3Îμ and Its Application in CAR-T Cell Therapy. Cell, 2020, 182, 855-871.e23.	28.9	91
16	TMT-Based Quantitative Proteomic Analysis Identification of Integrin Alpha 3 and Integrin Alpha 5 as Novel Biomarkers in Pathogenesis of Acute Aortic Dissection. BioMed Research International, 2020, 2020, 1-12.	1.9	10
17	Parallel Channels-Multidimensional Protein Identification Technology. Journal of the American Society for Mass Spectrometry, 2020, 31, 1440-1447.	2.8	5
18	Structural basis for catalysis and substrate specificity of human ACAT1. Nature, 2020, 581, 333-338.	27.8	66

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19	Quantitative Proteomics Analysis of Systemic Responses and Biological Mechanisms of ShuFengJieDu Capsule Using H1N1-Infected RAW264.7 Cells. ACS Omega, 2020, 5, 15417-15423.	3.5	6
20	câ€Jun NH2â€Terminal Protein Kinase Phosphorylates the Nrf2â€ECH Homology 6 Domain of Nuclear Factor Erythroid 2–Related Factor 2 and Downregulates Cytoprotective Genes in Acetaminophenâ€Induced Liver Injury in Mice. Hepatology, 2020, 71, 1787-1801.	7.3	50
21	Ate1-mediated posttranslational arginylation affects substrate adhesion and cell migration in <i>Dictyostelium discoideum</i> . Molecular Biology of the Cell, 2019, 30, 453-466.	2.1	14
22	Bax inhibitor 1 is a γ-secretase–independent presenilin-binding protein. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 141-147.	7.1	12
23	Eosinophil-derived CCL-6 impairs hematopoietic stem cell homeostasis. Cell Research, 2018, 28, 323-335.	12.0	26
24	Cryo-EM structure of human mTOR complex 2. Cell Research, 2018, 28, 518-528.	12.0	98
25	Nanoliter-Scale Oil-Air-Droplet Chip-Based Single Cell Proteomic Analysis. Analytical Chemistry, 2018, 90, 5430-5438.	6. 5	167
26	Architecture and subunit arrangement of the complete Saccharomyces cerevisiae COMPASS complex. Scientific Reports, 2018, 8, 17405.	3.3	14
27	SPSB1-mediated HnRNP A1 ubiquitylation regulates alternative splicing and cell migration in EGF signaling. Cell Research, 2017, 27, 540-558.	12.0	57
28	Extensive translation of circular RNAs driven by N6-methyladenosine. Cell Research, 2017, 27, 626-641.	12.0	1,367
29	Structural insights into POT1-TPP1 interaction and POT1 C-terminal mutations in human cancer. Nature Communications, 2017, 8, 14929.	12.8	71
30	CRISPR-Cas9-mediated genome editing in one blastomere of two-cell embryos reveals a novel Tet3 function in regulating neocortical development. Cell Research, 2017, 27, 815-829.	12.0	35
31	Cholesterol Modification of Smoothened Is Required for Hedgehog Signaling. Molecular Cell, 2017, 66, 154-162.e10.	9.7	169
32	The story of protein arginine methylation: characterization, regulation, and function. Expert Review of Proteomics, 2017, 14, 157-170.	3.0	63
33	pGlyco 2.0 enables precision N-glycoproteomics with comprehensive quality control and one-step mass spectrometry for intact glycopeptide identification. Nature Communications, 2017, 8, 438.	12.8	250
34	Therapeutic Mechanistic Studies of ShuFengJieDu Capsule in an Acute Lung Injury Animal Model Using Quantitative Proteomics Technology. Journal of Proteome Research, 2017, 16, 4009-4019.	3.7	41
35	Structural insight into the recognition of acetylated histone H3K56ac mediated by the bromodomain of CREBâ€binding protein. FEBS Journal, 2017, 284, 3422-3436.	4.7	16
36	HTLV-1 Tax Functions as a Ubiquitin E3 Ligase for Direct IKK Activation via Synthesis of Mixed-Linkage Polyubiquitin Chains. PLoS Pathogens, 2016, 12, e1005584.	4.7	20

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37	4.4 Ã Resolution Cryo-EM structure of human mTOR Complex 1. Protein and Cell, 2016, 7, 878-887.	11.0	69
38	pGlyco: a pipeline for the identification of intact N-glycopeptides by using HCD- and CID-MS/MS and MS3. Scientific Reports, 2016, 6, 25102.	3.3	84
39	The pseudokinase CaMKv is required for the activity-dependent maintenance of dendritic spines. Nature Communications, 2016, 7, 13282.	12.8	42
40	The 3.8 \tilde{A} structure of the U4/U6.U5 tri-snRNP: Insights into spliceosome assembly and catalysis. Science, 2016, 351, 466-475.	12.6	142
41	Structural basis for Sfm1 functioning as a protein arginine methyltransferase. Cell Discovery, 2015, 1, 15037.	6.7	21
42	Mixed Lineage Leukemia 5 (MLL5) Protein Stability Is Cooperatively Regulated by O-GlcNac Transferase (OGT) and Ubiquitin Specific Protease 7 (USP7). PLoS ONE, 2015, 10, e0145023.	2.5	49
43	The kinase MST4 limits inflammatory responses through direct phosphorylation of the adaptor TRAF6. Nature Immunology, 2015, 16, 246-257.	14.5	82
44	Casein Kinase 1 Promotes Initiation of Clathrin-Mediated Endocytosis. Developmental Cell, 2015, 32, 231-240.	7.0	43
45	The <scp>C</scp> rc protein participates in downâ€regulation of the <scp>L</scp> on gene to promote rhamnolipid production and <i>rhi>rhi> quorum sensing in <scp><i>P</i></scp><i>seudomonas aeruginosa</i>. Molecular Microbiology, 2015, 96, 526-547.</i>	2.5	42
46	An iridium(<scp>iii</scp>)-based irreversible protein–protein interaction inhibitor of BRD4 as a potent anticancer agent. Chemical Science, 2015, 6, 5400-5408.	7.4	125
47	Cleavage of amyloid precursor protein by an archaeal presenilin homologue PSH. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 3344-3349.	7.1	44
48	Structure of a yeast spliceosome at 3.6-angstrom resolution. Science, 2015, 349, 1182-1191.	12.6	314
49	AMPK-Dependent Phosphorylation of GAPDH Triggers Sirt1 Activation and Is Necessary for Autophagy upon Glucose Starvation. Molecular Cell, 2015, 60, 930-940.	9.7	222
50	The Specification and Global Reprogramming of Histone Epigenetic Marks during Gamete Formation and Early Embryo Development in C. elegans. PLoS Genetics, 2014, 10, e1004588.	3.5	39
51	Proteomics of <i>Pyrococcus furiosus</i> (<i>Pfu</i>): Identification of Extracted Proteins by Three Independent Methods. Journal of Proteome Research, 2013, 12, 763-770.	3.7	21
52	Casein kinase 1δ ε regulates clathrin―and actin―mediated endocytosis. FASEB Journal, 2013, 27, 553.25.	0.5	0
53	Proton and potassium affinities of aliphatic and N-methylated aliphatic \hat{l} ±-amino acids: Effect of alkyl chain length on relative stabilities of K+ bound zwitterionic complexes. International Journal of Mass Spectrometry, 2012, 316-318, 273-283.	1.5	9
54	Mining the Giardia genome and proteome for conserved and unique basal body proteins. International Journal for Parasitology, 2011, 41, 1079-1092.	3.1	48

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55	Arginylation and Methylation Double Up to Regulate Nuclear Proteins and Nuclear Architecture InAVivo. Chemistry and Biology, 2011, 18, 1369-1378.	6.0	37
56	Nbl1p: A Borealin/Dasra/CSC-1-like Protein Essential for Aurora/Ipl1 Complex Function and Integrity in <i>Saccharomyces cerevisiae</i> Molecular Biology of the Cell, 2009, 20, 1772-1784.	2.1	32
57	Global Analysis of Posttranslational Protein Arginylation. PLoS Biology, 2007, 5, e258.	5.6	132