

Shao-En Ong

List of Publications by Year in descending order

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69
papers

18,090
citations

109321

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h-index

110387

64
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76
all docs

76
docs citations

76
times ranked

22117
citing authors

#	ARTICLE	IF	CITATIONS
1	Water Droplet-in-Oil Digestion Method for Single-Cell Proteomics. <i>Analytical Chemistry</i> , 2022, 94, 10329-10336.	6.5	6
2	Phosphoproteomic Analysis as an Approach for Understanding Molecular Mechanisms of cAMP-Dependent Actions. <i>Molecular Pharmacology</i> , 2021, 99, 342-357.	2.3	5
3	Identifying Poly(ADP-ribose)-Binding Proteins with Photoaffinity-Based Proteomics. <i>Journal of the American Chemical Society</i> , 2021, 143, 3037-3042.	13.7	44
4	KiRNet: Kinase-centered network propagation of pharmacological screen results. <i>Cell Reports Methods</i> , 2021, 1, 100007.	2.9	8
5	Ion-Pairing with Triethylammonium Acetate Improves Solid-Phase Extraction of ADP-Ribosylated Peptides. <i>Journal of Proteome Research</i> , 2020, 19, 984-990.	3.7	3
6	A-kinase-anchoring protein 1 (dAKAP1)-based signaling complexes coordinate local protein synthesis at the mitochondrial surface. <i>Journal of Biological Chemistry</i> , 2020, 295, 10749-10765.	3.4	15
7	Pharmacoproteomics Identifies Kinase Pathways that Drive the Epithelial-Mesenchymal Transition and Drug Resistance in Hepatocellular Carcinoma. <i>Cell Systems</i> , 2020, 11, 196-207.e7.	6.2	24
8	Parallel Chemoselective Profiling for Mapping Protein Structure. <i>Cell Chemical Biology</i> , 2020, 27, 1084-1096.e4.	5.2	6
9	Kinobead/LC-MS Phosphokinome Profiling Enables Rapid Analyses of Kinase-Dependent Cell Signaling Networks. <i>Journal of Proteome Research</i> , 2020, 19, 1235-1247.	3.7	7
10	N-glycosylation of β 1D-adrenergic receptor N-terminal domain is required for correct trafficking, function, and biogenesis. <i>Scientific Reports</i> , 2020, 10, 7209.	3.3	8
11	ELTA: Enzymatic Labeling of Terminal ADP-Ribose. <i>Molecular Cell</i> , 2019, 73, 845-856.e5.	9.7	52
12	GPR124 regulates microtubule assembly, mitotic progression, and glioblastoma cell proliferation. <i>Glia</i> , 2019, 67, 1558-1570.	4.9	15
13	5-HT _{1B} Receptor-Mediated Activation of ERK1/2 Requires Both G β and β -Arrestin Proteins. <i>ACS Chemical Neuroscience</i> , 2019, 10, 3143-3153.	3.5	10
14	Depletion of dAKAP1 protein kinase A signaling islands from the outer mitochondrial membrane alters breast cancer cell metabolism and motility. <i>Journal of Biological Chemistry</i> , 2019, 294, 3152-3168.	3.4	17
15	An acquired scaffolding function of the DNAJ-PKAc fusion contributes to oncogenic signaling in fibrolamellar carcinoma. <i>ELife</i> , 2019, 8, .	6.0	48
16	FUS Regulates Activity of MicroRNA-Mediated Gene Silencing. <i>Molecular Cell</i> , 2018, 69, 787-801.e8.	9.7	76
17	Kinome chemoproteomics characterization of pyrrolo[3,4- <i>c</i>]pyrazoles as potent and selective inhibitors of glycogen synthase kinase 3. <i>Molecular Omics</i> , 2018, 14, 26-36.	2.8	14
18	Single nucleotide polymorphisms alter kinase anchoring and the subcellular targeting of A-kinase anchoring proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11465-E11474.	7.1	41

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19	Noncanonical translation via deadenylated 3' UTRs maintains primordial germ cells. <i>Nature Chemical Biology</i> , 2018, 14, 844-852.	8.0	5
20	Crystal Structure of the COMPASS H3K4 Methyltransferase Catalytic Module. <i>Cell</i> , 2018, 174, 1106-1116.e9.	28.9	75
21	Quantitative Determination of MAR Hydrolase Residue Specificity In Vitro by Tandem Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2018, 1813, 271-283.	0.9	0
22	Kinobead and Single-Shot LC-MS Profiling Identifies Selective PKD Inhibitors. <i>Journal of Proteome Research</i> , 2017, 16, 1216-1227.	3.7	36
23	ADP-ribosylhydrolase activity of Chikungunya virus macrodomain is critical for virus replication and virulence. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, 1666-1671.	7.1	147
24	Analyses of PDE-regulated phosphoproteomes reveal unique and specific cAMP-signaling modules in T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6240-E6249.	7.1	26
25	ADP-Ribosylated Peptide Enrichment and Site Identification: The Phosphodiesterase-Based Method. <i>Methods in Molecular Biology</i> , 2017, 1608, 79-93.	0.9	17
26	Proteomic Profiling of Protein Kinase Inhibitor Targets by Mass Spectrometry. <i>Methods in Molecular Biology</i> , 2017, 1636, 105-117.	0.9	7
27	Nudix hydrolases degrade protein-conjugated ADP-ribose. <i>Scientific Reports</i> , 2016, 5, 18271.	3.3	55
28	SCAP/SREBP pathway is required for the full steroidogenic response to cyclic AMP. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E5685-93.	7.1	37
29	ENPP1 processes protein ADP-ribosylation in vitro. <i>FEBS Journal</i> , 2016, 283, 3371-3388.	4.7	63
30	Studying mechanisms of cAMP and cyclic nucleotide phosphodiesterase signaling in Leydig cell function with phosphoproteomics. <i>Cellular Signalling</i> , 2016, 28, 764-778.	3.6	30
31	The Promise of Proteomics for the Study of ADP-Ribosylation. <i>Molecular Cell</i> , 2015, 58, 911-924.	9.7	181
32	APC/Cdh1 controls CtIP stability during the cell cycle and in response to DNA damage. <i>EMBO Journal</i> , 2014, 33, 2860-2879.	7.8	65
33	Rapid profiling of protein kinase inhibitors by quantitative proteomics. <i>MedChemComm</i> , 2014, 5, 363-369.	3.4	20
34	Huntingtin is associated with cytomatrix proteins at the presynaptic terminal. <i>Molecular and Cellular Neurosciences</i> , 2014, 63, 96-100.	2.2	16
35	Comparing SILAC- and Stable Isotope Dimethyl-Labeling Approaches for Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2014, 13, 4164-4174.	3.7	99
36	Phosphoproteomic Approach to Characterize Protein Mono- and Poly(ADP-ribosylation) Sites from Cells. <i>Journal of Proteome Research</i> , 2014, 13, 3510-3522.	3.7	108

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37	Identification of regulators of the innate immune response to cytosolic DNA and retroviral infection by an integrative approach. <i>Nature Immunology</i> , 2013, 14, 179-185.	14.5	104
38	GPR124 coupling and function in astrocytomas. <i>FASEB Journal</i> , 2013, 27, 1096.4.	0.5	0
39	Iron-dependent regulation of mitochondrial form and function. <i>FASEB Journal</i> , 2013, 27, lb65.	0.5	0
40	The expanding field of SILAC. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 404, 967-976.	3.7	78
41	AAK1 Identified as an Inhibitor of Neuregulin-1/ErbB4-Dependent Neurotrophic Factor Signaling Using Integrative Chemical Genomics and Proteomics. <i>Chemistry and Biology</i> , 2011, 18, 891-906.	6.0	34
42	CUB-domain-containing protein 1 (CDCP1) activates Src to promote melanoma metastasis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1379-1384.	7.1	84
43	A Mitotic Phosphorylation Feedback Network Connects Cdk1, Plk1, 53BP1, and Chk2 to Inactivate the G2/M DNA Damage Checkpoint. <i>PLoS Biology</i> , 2010, 8, e1000287.	5.6	201
44	MSQuant, an Open Source Platform for Mass Spectrometry-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 393-403.	3.7	237
45	DNA Damage Activates a Spatially Distinct Late Cytoplasmic Cell-Cycle Checkpoint Network Controlled by MK2-Mediated RNA Stabilization. <i>Molecular Cell</i> , 2010, 40, 34-49.	9.7	210
46	Identifying the proteins to which small-molecule probes and drugs bind in cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 4617-4622.	7.1	282
47	Empirical Bayes Analysis of Quantitative Proteomics Experiments. <i>PLoS ONE</i> , 2009, 4, e7454.	2.5	52
48	A Mitochondrial Protein Compendium Elucidates Complex I Disease Biology. <i>Cell</i> , 2008, 134, 112-123.	28.9	1,766
49	Proteomic screen defines the Polo-box domain interactome and identifies Rock2 as a Plk1 substrate. <i>EMBO Journal</i> , 2007, 26, 2262-2273.	7.8	223
50	Syk Is a New Target for AML Differentiation.. <i>Blood</i> , 2007, 110, 209-209.	1.4	6
51	Autophagy as a Target Pathway in Multiple Myeloma: A Forward Chemical Genetic Approach.. <i>Blood</i> , 2007, 110, 2510-2510.	1.4	0
52	A practical recipe for stable isotope labeling by amino acids in cell culture (SILAC). <i>Nature Protocols</i> , 2006, 1, 2650-2660.	12.0	816
53	Mass spectrometry-based proteomics turns quantitative. <i>Nature Chemical Biology</i> , 2005, 1, 252-262.	8.0	1,426
54	Nucleolar proteome dynamics. <i>Nature</i> , 2005, 433, 77-83.	27.8	1,061

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55	Temporal analysis of phosphotyrosine-dependent signaling networks by quantitative proteomics. <i>Nature Biotechnology</i> , 2004, 22, 1139-1145.	17.5	680
56	Identifying and quantifying in vivo methylation sites by heavy methyl SILAC. <i>Nature Methods</i> , 2004, 1, 119-126.	19.0	427
57	Trypsin Cleaves Exclusively C-terminal to Arginine and Lysine Residues. <i>Molecular and Cellular Proteomics</i> , 2004, 3, 608-614.	3.8	957
58	A proteomics strategy to elucidate functional protein-protein interactions applied to EGF signaling. <i>Nature Biotechnology</i> , 2003, 21, 315-318.	17.5	702
59	Properties of ¹³ C-Substituted Arginine in Stable Isotope Labeling by Amino Acids in Cell Culture (SILAC). <i>Journal of Proteome Research</i> , 2003, 2, 173-181.	3.7	439
60	Cloning of MASK, a Novel Member of the Mammalian Germinal Center Kinase III Subfamily, with Apoptosis-inducing Properties. <i>Journal of Biological Chemistry</i> , 2002, 277, 5929-5939.	3.4	53
61	Analysis of protein phosphorylation using mass spectrometry: deciphering the phosphoproteome. <i>Trends in Biotechnology</i> , 2002, 20, 261-268.	9.3	877
62	Using mass spectrometry for drug discovery. <i>Trends in Biotechnology</i> , 2002, 20, 227.	9.3	1
63	Stable Isotope Labeling by Amino Acids in Cell Culture, SILAC, as a Simple and Accurate Approach to Expression Proteomics. <i>Molecular and Cellular Proteomics</i> , 2002, 1, 376-386.	3.8	4,931
64	An integrated approach in the discovery and characterization of a novel nuclear protein over-expressed in liver and pancreatic tumors. <i>FEBS Letters</i> , 2001, 496, 109-116.	2.8	36
65	AU Binding Proteins Recruit the Exosome to Degrade ARE-Containing mRNAs. <i>Cell</i> , 2001, 107, 451-464.	28.9	803
66	An evaluation of the use of two-dimensional gel electrophoresis in proteomics. <i>New Biotechnology</i> , 2001, 18, 195-205.	2.7	143
67	Proteome analysis of a human hepatocellular carcinoma cell line, HCC-M: An update. <i>Electrophoresis</i> , 2001, 22, 2804-2811.	2.4	33
68	Proteomic Investigation of Metabolic Shift in Mammalian Cell Culture. <i>Biotechnology Progress</i> , 2001, 17, 1137-1144.	2.6	41
69	KiRNet: Integrated, Kinase-Centered Network Modeling Predicts Mechanisms Behind Phenotypic Associations. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0