

Simone Lemeer

List of Publications by Year in descending order

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29
papers

3,508
citations

430874

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477307

29
g-index

29
all docs

29
docs citations

29
times ranked

6788
citing authors

#	ARTICLE	IF	CITATIONS
1	Widespread arginine phosphorylation in <i>Staphylococcus aureus</i> . <i>Molecular and Cellular Proteomics</i> , 2022, , 100232.	3.8	3
2	Histidine phosphorylation in human cells; a needle or phantom in the haystack?. <i>Nature Methods</i> , 2022, 19, 827-828.	19.0	8
3	In-Depth Characterization of the <i>Staphylococcus aureus</i> Phosphoproteome Reveals New Targets of Stk1. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100034.	3.8	24
4	Thermal Proteome Profiling in Zebrafish Reveals Effects of Napabucasin on Retinoic Acid Metabolism. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100033.	3.8	8
5	Meltome atlas thermal proteome stability across the tree of life. <i>Nature Methods</i> , 2020, 17, 495-503.	19.0	152
6	Loss of the Fanconi anemia-associated protein NIPA causes bone marrow failure. <i>Journal of Clinical Investigation</i> , 2020, 130, 2827-2844.	8.2	8
7	Gaining Confidence in the Elusive Histidine Phosphoproteome. <i>Analytical Chemistry</i> , 2019, 91, 5542-5547.	6.5	23
8	Phosphopeptide Fragmentation and Site Localization by Mass Spectrometry: An Update. <i>Analytical Chemistry</i> , 2019, 91, 126-141.	6.5	80
9	CTGF/VEGFA-activated Fibroblasts Promote Tumor Migration Through Micro-environmental Modulation. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1502-1514.	3.8	12
10	Defeating Major Contaminants in Fe ³⁺ - Immobilized Metal Ion Affinity Chromatography (IMAC) Phosphopeptide Enrichment. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 1028-1034.	3.8	68
11	Widespread bacterial protein histidine phosphorylation revealed by mass spectrometry-based proteomics. <i>Nature Methods</i> , 2018, 15, 187-190.	19.0	140
12	A New Tool to Reveal Bacterial Signaling Mechanisms in Antibiotic Treatment and Resistance. <i>Molecular and Cellular Proteomics</i> , 2018, 17, 2496-2507.	3.8	22
13	Proteomic tools to study drug function. <i>Current Opinion in Systems Biology</i> , 2018, 10, 9-18.	2.6	4
14	Adaptive Resistance to EGFR-Targeted Therapy by Calcium Signaling in NSCLC Cells. <i>Molecular Cancer Research</i> , 2018, 16, 1773-1784.	3.4	9
15	Lapatinib Resistance in Breast Cancer Cells Is Accompanied by Phosphorylation-Mediated Reprogramming of Glycolysis. <i>Cancer Research</i> , 2017, 77, 1842-1853.	0.9	79
16	Optimized Enrichment of Phosphoproteomes by Fe-IMAC Column Chromatography. <i>Methods in Molecular Biology</i> , 2017, 1550, 47-60.	0.9	26
17	MALDI-TOF and nESI Orbitrap MS/MS identify orthogonal parts of the phosphoproteome. <i>Proteomics</i> , 2016, 16, 1447-1456.	2.2	13
18	Comprehensive and Reproducible Phosphopeptide Enrichment Using Iron Immobilized Metal Ion Affinity Chromatography (Fe-IMAC) Columns. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 205-215.	3.8	111

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19	Evaluation of Kinase Activity Profiling Using Chemical Proteomics. <i>ACS Chemical Biology</i> , 2015, 10, 2743-2752.	3.4	32
20	Quantitative proteome profiling of human myoma and myometrium tissue reveals kinase expression signatures with potential for therapeutic intervention. <i>Proteomics</i> , 2015, 15, 356-364.	2.2	8
21	Proteomic analysis of phosphorylation in cancer. <i>Expert Review of Proteomics</i> , 2014, 11, 259-267.	3.0	44
22	Mass-spectrometry-based draft of the human proteome. <i>Nature</i> , 2014, 509, 582-587.	27.8	1,697
23	DMSO enhances electrospray response, boosting sensitivity of proteomic experiments. <i>Nature Methods</i> , 2013, 10, 989-991.	19.0	209
24	Comparing Immobilized Kinase Inhibitors and Covalent ATP Probes for Proteomic Profiling of Kinase Expression and Drug Selectivity. <i>Journal of Proteome Research</i> , 2013, 12, 1723-1731.	3.7	48
25	SCFFbxo9 and CK2 direct the cellular response to growth factor withdrawal via Tel2/Tti1 degradation and promote survival in multiple myeloma. <i>Nature Cell Biology</i> , 2013, 15, 72-81.	10.3	76
26	A large synthetic peptide and phosphopeptide reference library for mass spectrometry-based proteomics. <i>Nature Biotechnology</i> , 2013, 31, 557-564.	17.5	164
27	Phosphorylation site localization in peptides by MALDI MS/MS and the Mascot Delta Score. <i>Analytical and Bioanalytical Chemistry</i> , 2012, 402, 249-260.	3.7	23
28	Confident Phosphorylation Site Localization Using the Mascot Delta Score. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S12.	3.8	247
29	The phosphoproteomics data explosion. <i>Current Opinion in Chemical Biology</i> , 2009, 13, 414-420.	6.1	170