

Naoyuki Sugiyama

List of Publications by Year in descending order

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40
papers

4,334
citations

270111

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41
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docs citations

42
times ranked

6727
citing authors

#	ARTICLE	IF	CITATIONS
1	Calcium-dependent protein kinase 16 phosphorylates and activates the aquaporin PIP2;2 to regulate reversible flower opening in <i>Gentiana scabra</i> . <i>Plant Cell</i> , 2022, 34, 2652-2670.	3.1	12
2	Large-scale Discovery of Substrates of the Human Kinome. <i>Scientific Reports</i> , 2019, 9, 10503.	1.6	79
3	Algal Protein Kinase, Triacylglycerol Accumulation Regulator 1, Modulates Cell Viability and Gametogenesis in Carbon/Nitrogen-Imbalanced Conditions. <i>Plant and Cell Physiology</i> , 2019, 60, 916-930.	1.5	15
4	Comparative proteomics of <i>Helicobacter pylori</i> strains reveals geographical features rather than genomic variations. <i>Genes To Cells</i> , 2019, 24, 139-150.	0.5	6
5	The jPOST environment: an integrated proteomics data repository and database. <i>Nucleic Acids Research</i> , 2019, 47, D1218-D1224.	6.5	94
6	Phosphoproteomic profiling reveals ABA-responsive phosphosignaling pathways in <i>Physcomitrella patens</i> . <i>Plant Journal</i> , 2018, 94, 699-708.	2.8	48
7	jPOSTrepo: an international standard data repository for proteomes. <i>Nucleic Acids Research</i> , 2017, 45, D1107-D1111.	6.5	451
8	Identifications of Putative PKA Substrates with Quantitative Phosphoproteomics and Primary-Sequence-Based Scoring. <i>Journal of Proteome Research</i> , 2017, 16, 1825-1830.	1.8	26
9	Large-scale profiling of protein kinases for cellular signaling studies by mass spectrometry and other techniques. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2016, 130, 264-272.	1.4	10
10	Uncovering Phosphorylation-Based Specificities through Functional Interaction Networks. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 236-245.	2.5	68
11	LATS1 and LATS2 Phosphorylate CDC26 to Modulate Assembly of the Tetratricopeptide Repeat Subcomplex of APC/C. <i>PLoS ONE</i> , 2015, 10, e0118662.	1.1	12
12	PCK1 Regulates Integrin-Dependent Spindle Orientation via Protein Kinase A Regulatory Subunit KAPO and Myosin X. <i>Molecular and Cellular Biology</i> , 2015, 35, 1197-1208.	1.1	24
13	Systematic profiling of the bacterial phosphoproteome reveals bacterium-specific features of phosphorylation. <i>Science Signaling</i> , 2015, 8, rs10.	1.6	49
14	Extended Coverage of Singly and Multiply Phosphorylated Peptides from a Single Titanium Dioxide Microcolumn. <i>Analytical Chemistry</i> , 2015, 87, 10213-10221.	3.2	33
15	Inhibition of endocytic vesicle fusion by Plk1-mediated phosphorylation of vimentin during mitosis. <i>Cell Cycle</i> , 2014, 13, 126-137.	1.3	16
16	Phosphoproteome Analysis of Formalin-Fixed and Paraffin-Embedded Tissue Sections Mounted on Microscope Slides. <i>Journal of Proteome Research</i> , 2014, 13, 915-924.	1.8	45
17	p38-Mediated phosphorylation of Eps15 endocytic adaptor protein. <i>FEBS Letters</i> , 2014, 588, 131-137.	1.3	14
18	Large-Scale Identification of Phosphorylation Sites for Profiling Protein Kinase Selectivity. <i>Journal of Proteome Research</i> , 2014, 13, 3410-3419.	1.8	52

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19	Genetics and Phosphoproteomics Reveal a Protein Phosphorylation Network in the Abscisic Acid Signaling Pathway in <i>Arabidopsis thaliana</i> . <i>Science Signaling</i> , 2013, 6, rs8.	1.6	355
20	Temporal Profiling of Lapatinib-suppressed Phosphorylation Signals in EGFR/HER2 Pathways. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1741-1757.	2.5	55
21	Characterization of kinase inhibitors using different phosphorylation states of colony stimulating factor-1 receptor tyrosine kinase. <i>Journal of Biochemistry</i> , 2012, 151, 47-55.	0.9	17
22	Shotguns in the Front Line: Phosphoproteomics in Plants. <i>Plant and Cell Physiology</i> , 2012, 53, 118-124.	1.5	55
23	Phosphoproteomic Analysis of <i>Rhodospseudomonas palustris</i> Reveals the Role of Pyruvate Phosphate Dikinase Phosphorylation in Lipid Production. <i>Journal of Proteome Research</i> , 2012, 11, 5362-5375.	1.8	37
24	The Rice Proteogenomics Database OryzaPG-DB: Development, Expansion, and New Features. <i>Frontiers in Plant Science</i> , 2012, 3, 65.	1.7	17
25	LATS1/WARTS phosphorylates MYPT1 to counteract PLK1 and regulate mammalian mitotic progression. <i>Journal of Cell Biology</i> , 2012, 197, 625-641.	2.3	51
26	Human proteome analysis by using reversed phase monolithic silica capillary columns with enhanced sensitivity. <i>Journal of Chromatography A</i> , 2012, 1228, 292-297.	1.8	60
27	Mass spectrum sequential subtraction speeds up searching large peptide <sc>MS</sc> spectra datasets against large nucleotide databases for proteogenomics. <i>Genes To Cells</i> , 2012, 17, 633-644.	0.5	26
28	Microscale Phosphoproteome Analysis of 10 ⁶ Cells from Human Cancer Cell Lines. <i>Analytical Chemistry</i> , 2011, 83, 7698-7703.	3.2	68
29	Integrative Features of the Yeast Phosphoproteome and Protein-Protein Interaction Map. <i>PLoS Computational Biology</i> , 2011, 7, e1001064.	1.5	60
30	Detection of Rap1A as a yessotoxin binding protein from blood cell membranes. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2010, 20, 6443-6446.	1.0	11
31	Chemical dephosphorylation for identification of multiply phosphorylated peptides and phosphorylation site determination. <i>Rapid Communications in Mass Spectrometry</i> , 2010, 24, 2277-2282.	0.7	14
32	Large-Scale Comparative Phosphoproteomics Identifies Conserved Phosphorylation Sites in Plants. <i>Plant Physiology</i> , 2010, 153, 1161-1174.	2.3	361
33	Quantitative proteome and phosphoproteome analyses of cultured cells based on SILAC labeling without requirement of serum dialysis. <i>Molecular BioSystems</i> , 2010, 6, 594.	2.9	27
34	Identification of DNA-dependent Protein Kinase as a Cofactor for the Forkhead Transcription Factor FoxA2. <i>Journal of Biological Chemistry</i> , 2009, 284, 19915-19926.	1.6	8
35	Ser/Thr/Tyr phosphoproteome analysis of pathogenic and non-pathogenic <i>Pseudomonas</i> species. <i>Proteomics</i> , 2009, 9, 2764-2775.	1.3	107
36	Type 2C protein phosphatases directly regulate abscisic acid-activated protein kinases in <i>Arabidopsis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17588-17593.	3.3	980

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37	Successive and Selective Release of Phosphorylated Peptides Captured by Hydroxy Acid-Modified Metal Oxide Chromatography. <i>Journal of Proteome Research</i> , 2008, 7, 4585-4593.	1.8	110
38	Large-scale phosphorylation mapping reveals the extent of tyrosine phosphorylation in <i>Arabidopsis</i> . <i>Molecular Systems Biology</i> , 2008, 4, 193.	3.2	347
39	Automated Phosphoproteome Analysis for Cultured Cancer Cells by Two-Dimensional NanoLC-MS Using a Calcined Titania/C18 Biphasic Column. <i>Analytical Sciences</i> , 2008, 24, 161-166.	0.8	114
40	Phosphopeptide Enrichment by Aliphatic Hydroxy Acid-modified Metal Oxide Chromatography for Nano-LC-MS/MS in Proteomics Applications. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1103-1109.	2.5	397