

Corey E Bakalarski

List of Publications by Year in descending order

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Version: 2024-02-01

20
papers

8,557
citations

471509

17
h-index

752698

20
g-index

20
all docs

20
docs citations

20
times ranked

15483
citing authors

#	ARTICLE	IF	CITATIONS
1	ATM and ATR Substrate Analysis Reveals Extensive Protein Networks Responsive to DNA Damage. <i>Science</i> , 2007, 316, 1160-1166.	12.6	2,689
2	Global Survey of Phosphotyrosine Signaling Identifies Oncogenic Kinases in Lung Cancer. <i>Cell</i> , 2007, 131, 1190-1203.	28.9	2,139
3	A quantitative atlas of mitotic phosphorylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 10762-10767.	7.1	1,435
4	The mitochondrial deubiquitinase USP30 opposes parkin-mediated mitophagy. <i>Nature</i> , 2014, 510, 370-375.	27.8	660
5	Loss of the Tumor Suppressor BAP1 Causes Myeloid Transformation. <i>Science</i> , 2012, 337, 1541-1546.	12.6	355
6	Optimization and Use of Peptide Mass Measurement Accuracy in Shotgun Proteomics. <i>Molecular and Cellular Proteomics</i> , 2006, 5, 1326-1337.	3.8	253
7	A Proteomic Strategy for Gaining Insights into Protein Sumoylation in Yeast. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 246-254.	3.8	227
8	Proteomic Profiling of ClpXP Substrates after DNA Damage Reveals Extensive Instability within SOS Regulon. <i>Molecular Cell</i> , 2006, 22, 193-204.	9.7	172
9	Improved Quantitative Mass Spectrometry Methods for Characterizing Complex Ubiquitin Signals. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M110.003756.	3.8	124
10	The Impact of Peptide Abundance and Dynamic Range on Stable-Isotope-Based Quantitative Proteomic Analyses. <i>Journal of Proteome Research</i> , 2008, 7, 4756-4765.	3.7	111
11	Enhanced Analysis of Metastatic Prostate Cancer Using Stable Isotopes and High Mass Accuracy Instrumentation. <i>Journal of Proteome Research</i> , 2006, 5, 1224-1231.	3.7	71
12	The effects of mass accuracy, data acquisition speed, and search algorithm choice on peptide identification rates in phosphoproteomics. <i>Analytical and Bioanalytical Chemistry</i> , 2007, 389, 1409-1419.	3.7	64
13	Characterizing Ubiquitination Sites by Peptide-based Immunoaffinity Enrichment. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1529-1540.	3.8	55
14	Catch-and-Release Reagents for Broad-scale Quantitative Proteomics Analyses. <i>Journal of Proteome Research</i> , 2007, 6, 1482-1491.	3.7	54
15	Phosphoproteomic characterization of DNA damage response in melanoma cells following MEK/PI3K dual inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 19426-19431.	7.1	51
16	A Biologist's Field Guide to Multiplexed Quantitative Proteomics. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 1489-1497.	3.8	50
17	Complementary Proteomic Tools for the Dissection of Apoptotic Proteolysis Events. <i>Journal of Proteome Research</i> , 2012, 11, 2947-2954.	3.7	23
18	Ubiquitination profiling identifies sensitivity factors for IAP antagonist treatment. <i>Biochemical Journal</i> , 2015, 466, 45-54.	3.7	9

#	ARTICLE	IF	CITATIONS
19	Discovery of a caspase cleavage motif antibody reveals insights into noncanonical inflammasome function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	8
20	Rapid, semi-automated protein terminal characterization using ISDetect. <i>Nature Biotechnology</i> , 2016, 34, 811-813.	17.5	7