

Bas Van Breukelen

List of Publications by Year in descending order

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32
papers

1,883
citations

331670

21
h-index

414414

32
g-index

32
all docs

32
docs citations

32
times ranked

2964
citing authors

#	ARTICLE	IF	CITATIONS
1	Spatial Organization in Protein Kinase A Signaling Emerged at the Base of Animal Evolution. <i>Journal of Proteome Research</i> , 2015, 14, 2976-2987.	3.7	16
2	An Augmented Multiple-Protease-Based Human Phosphopeptide Atlas. <i>Cell Reports</i> , 2015, 11, 1834-1843.	6.4	92
3	Daily Rhythms in the Cyanobacterium <i>Synechococcus elongatus</i> Probed by High-resolution Mass Spectrometry-based Proteomics Reveals a Small Defined Set of Cyclic Proteins. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2042-2055.	3.8	83
4	ROCK1 is a potential combinatorial drug target for BRAF mutant melanoma. <i>Molecular Systems Biology</i> , 2014, 10, 772.	7.2	48
5	Identification of Enriched PTM Crosstalk Motifs from Large-Scale Experimental Data Sets. <i>Journal of Proteome Research</i> , 2014, 13, 249-259.	3.7	40
6	Proteome Adaptation of <i>Saccharomyces cerevisiae</i> to Severe Calorie Restriction in Retentostat Cultures. <i>Journal of Proteome Research</i> , 2014, 13, 3542-3553.	3.7	17
7	Quantitative and Qualitative Proteome Characteristics Extracted from In-Depth Integrated Genomics and Proteomics Analysis. <i>Cell Reports</i> , 2013, 5, 1469-1478.	6.4	113
8	Database independent proteomics analysis of the ostrich and human proteome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 407-412.	7.1	13
9	Deep Proteome Profiling of Circulating Granulocytes Reveals Bactericidal/Permeability-Increasing Protein as a Biomarker for Severe Atherosclerotic Coronary Stenosis. <i>Journal of Proteome Research</i> , 2012, 11, 5235-5244.	3.7	16
10	Current challenges in software solutions for mass spectrometry-based quantitative proteomics. <i>Amino Acids</i> , 2012, 43, 1087-1108.	2.7	101
11	High confidence and sensitivity four-dimensional fractionation for human plasma proteome analysis. <i>Amino Acids</i> , 2012, 43, 2199-2202.	2.7	11
12	Protease bias in absolute protein quantitation. <i>Nature Methods</i> , 2012, 9, 524-525.	19.0	80
13	RockerBox: Analysis and Filtering of Massive Proteomics Search Results. <i>Journal of Proteome Research</i> , 2011, 10, 1420-1424.	3.7	28
14	Deconvolution of overlapping isotopic clusters improves quantification of stable isotope-labeled peptides. <i>Journal of Proteomics</i> , 2011, 74, 2204-2209.	2.4	20
15	Evaluating Experimental Bias and Completeness in Comparative Phosphoproteomics Analysis. <i>PLoS ONE</i> , 2011, 6, e23276.	2.5	12
16	Improving SRM Assay Development: A Global Comparison between Triple Quadrupole, Ion Trap, and Higher Energy CID Peptide Fragmentation Spectra. <i>Journal of Proteome Research</i> , 2011, 10, 4334-4341.	3.7	90
17	Perturbation of the yeast N-acetyltransferase NatB induces elevation of protein phosphorylation levels. <i>BMC Genomics</i> , 2010, 11, 685.	2.8	77
18	LysNDeNovo: An algorithm enabling de novo sequencing of LysN generated peptides fragmented by electron transfer dissociation. <i>Proteomics</i> , 2010, 10, 1196-1201.	2.2	8

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19	In-depth Qualitative and Quantitative Profiling of Tyrosine Phosphorylation Using a Combination of Phosphopeptide Immunoaffinity Purification and Stable Isotope Dimethyl Labeling. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 84-99.	3.8	155
20	Profiling of N-Acetylated Protein Termini Provides In-depth Insights into the N-terminal Nature of the Proteome. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 928-939.	3.8	113
21	StatQuant: a post-quantification analysis toolbox for improving quantitative mass spectrometry. <i>Bioinformatics</i> , 2009, 25, 1472-1473.	4.1	39
22	A versatile peptide p<i>l</i> calculator for phosphorylated and N-terminal acetylated peptides experimentally tested using peptide isoelectric focusing. <i>Proteomics</i> , 2008, 8, 4898-4906.	2.2	46
23	Highly Robust, Automated, and Sensitive Online TiO ₂ -Based Phosphoproteomics Applied To Study Endogenous Phosphorylation in <i>Drosophila melanogaster</i> . <i>Journal of Proteome Research</i> , 2008, 7, 687-697.	3.7	165
24	Comparative phosphoproteomics reveals evolutionary and functional conservation of phosphorylation across eukaryotes. <i>Genome Biology</i> , 2008, 9, R144.	9.6	75
25	Online Automated <i>in Vivo</i> Zebrafish Phosphoproteomics: From Large-Scale Analysis Down to a Single Embryo. <i>Journal of Proteome Research</i> , 2008, 7, 1555-1564.	3.7	73
26	Multiplexed Proteomics Mapping of Yeast RNA Polymerase II and III Allows Near-Complete Sequence Coverage and Reveals Several Novel Phosphorylation Sites. <i>Analytical Chemistry</i> , 2008, 80, 3584-3592.	6.5	40
27	Targeted SCX Based Peptide Fractionation for Optimal Sequencing by Collision Induced, and Electron Transfer Dissociation. <i>Journal of Proteomics and Bioinformatics</i> , 2008, 01, 379-388.	0.4	14
28	Targeted Analysis of Protein Termini. <i>Journal of Proteome Research</i> , 2007, 6, 4634-4645.	3.7	93
29	Analysis of the cGMP/cAMP Interactome Using a Chemical Proteomics Approach in Mammalian Heart Tissue Validates Sphingosine Kinase Type 1-interacting Protein as a Genuine and Highly Abundant AKAP. <i>Journal of Proteome Research</i> , 2006, 5, 1435-1447.	3.7	107
30	The Rep Protein of Adeno-Associated Virus Type 2 Interacts with Single-Stranded DNA-Binding Proteins That Enhance Viral Replication. <i>Journal of Virology</i> , 2004, 78, 441-453.	3.4	60
31	Adenovirus Type 5 DNA Binding Protein Stimulates Binding of DNA Polymerase to the Replication Origin. <i>Journal of Virology</i> , 2003, 77, 915-922.	3.4	22
32	The Formation of a Flexible DNA-binding Protein Chain Is Required for Efficient DNA Unwinding and Adenovirus DNA Chain Elongation. <i>Journal of Biological Chemistry</i> , 2000, 275, 40897-40903.	3.4	16