Bas Van Breukelen

List of Publications by Year
in descending order

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	Highly Robust, Automated, and Sensitive Online TiO$_2$-Based Phosphoproteomics Applied To Study Endogenous Phosphorylation in *Drosophila melanogaster*. Journal of Proteome Research, 2008, 7, 687-697.	3.7	165
2	In-depth Qualitative and Quantitative Profiling of Tyrosine Phosphorylation Using a Combination of Phosphopeptide Immunoaffinity Purification and Stable Isotope Dimethyl Labeling. Molecular and Cellular Proteomics, 2010, 9, 84-99.	3.8	155
3	Profiling of N-Acetylated Protein Termini Provides In-depth Insights into the N-terminal Nature of the Proteome. Molecular and Cellular Proteomics, 2010, 9, 928-939.	3.8	113
4	Quantitative and Qualitative Proteome Characteristics Extracted from In-Depth Integrated Genomics and Proteomics Analysis. Cell Reports, 2013, 5, 1469-1478.	6.4	113
5	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. Journal of Proteome Research, 2006, 5, 1435-1447.	3.7	107
6	Current challenges in software solutions for mass spectrometry-based quantitative proteomics. Amino Acids, 2012, 43, 1087-1108.	2.7	101
7	Targeted Analysis of Protein Termini. Journal of Proteome Research, 2007, 6, 4634-4645.	3.7	93
8	An Augmented Multiple-Protease-Based Human Phosphopeptide Atlas. Cell Reports, 2015, 11, 1834-1843.	6.4	92
9	Improving SRM Assay Development: A Global Comparison between Triple Quadrupole, Ion Trap, and Higher Energy CID Peptide Fragmentation Spectra. Journal of Proteome Research, 2011, 10, 4334-4341.	3.7	90
10	Daily Rhythms in the Cyanobacterium Synechococcus elongatus Probed by High-resolution Mass Spectrometry–based Proteomics Reveals a Small Defined Set of Cyclic Proteins. Molecular and Cellular Proteomics, 2014, 13, 2042-2055.	3.8	83
11	Protease bias in absolute protein quantitation. Nature Methods, 2012, 9, 524-525.	19.0	80
12	Perturbation of the yeast N-acetyltransferase NatB induces elevation of protein phosphorylation levels. BMC Genomics, 2010, 11, 685.	2.8	77
13	Comparative phosphoproteomics reveals evolutionary and functional conservation of phosphorylation across eukaryotes. Genome Biology, 2008, 9, R144.	9.6	75
14	Online Automated *in Vivo* Zebrafish Phosphoproteomics: From Large-Scale Analysis Down to a Single Embryo. Journal of Proteome Research, 2008, 7, 1555-1564.	3.7	73
15	The Rep Protein of Adeno-Associated Virus Type 2 Interacts with Single-Stranded DNA-Binding Proteins That Enhance Viral Replication. Journal of Virology, 2004, 78, 441-453.	3.4	60
16	ROCK1 is a potential combinatorial drug target for BRAF mutant melanoma. Molecular Systems Biology, 2014, 10, 772.	7.2	48
17	A versatile peptide p***I*** calculator for phosphorylated and N-terminal acetylated peptides experimentally tested using peptide isoelectric focusing. Proteomics, 2008, 8, 4898-4906.	2.2	46
18	Multiplexed Proteomics Mapping of Yeast RNA Polymerase II and III Allows Near-Complete Sequence Coverage and Reveals Several Novel Phosphorylation Sites. Analytical Chemistry, 2008, 80, 3584-3592.	6.5	40

#	ARTICLE	IF	CITATIONS
19	Identification of Enriched PTM Crosstalk Motifs from Large-Scale Experimental Data Sets. Journal of Proteome Research, 2014, 13, 249-259.	3.7	40
20	StatQuant: a post-quantification analysis toolbox for improving quantitative mass spectrometry. Bioinformatics, 2009, 25, 1472-1473.	4.1	39
21	RockerBox: Analysis and Filtering of Massive Proteomics Search Results. Journal of Proteome Research, 2011, 10, 1420-1424.	3.7	28
22	Adenovirus Type 5 DNA Binding Protein Stimulates Binding of DNA Polymerase to the Replication Origin. Journal of Virology, 2003, 77, 915-922.	3.4	22
23	Deconvolution of overlapping isotopic clusters improves quantification of stable isotope–labeled peptides. Journal of Proteomics, 2011, 74, 2204-2209.	2.4	20
24	Proteome Adaptation of <i>Saccharomyces cerevisiae</i> to Severe Calorie Restriction in Retentostat Cultures. Journal of Proteome Research, 2014, 13, 3542-3553.	3.7	17
25	The Formation of a Flexible DNA-binding Protein Chain Is Required for Efficient DNA Unwinding and Adenovirus DNA Chain Elongation. Journal of Biological Chemistry, 2000, 275, 40897-40903.	3.4	16
26	Deep Proteome Profiling of Circulating Granulocytes Reveals Bactericidal/Permeability-Increasing Protein as a Biomarker for Severe Atherosclerotic Coronary Stenosis. Journal of Proteome Research, 2012, 11, 5235-5244.	3.7	16
27	Spatial Organization in Protein Kinase A Signaling Emerged at the Base of Animal Evolution. Journal of Proteome Research, 2015, 14, 2976-2987.	3.7	16
28	Targeted SCX Based Peptide Fractionation for Optimal Sequencing by Collision Induced, and Electron Transfer Dissociation. Journal of Proteomics and Bioinformatics, 2008, 01, 379-388.	0.4	14
29	Database independent proteomics analysis of the ostrich and human proteome. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 407-412.	7.1	13
30	Evaluating Experimental Bias and Completeness in Comparative Phosphoproteomics Analysis. PLoS ONE, 2011, 6, e23276.	2.5	12
31	High confidence and sensitivity four-dimensional fractionation for human plasma proteome analysis. Amino Acids, 2012, 43, 2199-2202.	2.7	11
32	<i>LysNDeNovo</i>: An algorithm enabling <i>de novo</i> sequencing of Lys–N generated peptides fragmented by electron transfer dissociation. Proteomics, 2010, 10, 1196-1201.	2.2	8