

# Joost W Gouw

## List of Publications by Year in descending order

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Version: 2024-02-01

19  
papers

1,112  
citations

567281

15  
h-index

794594

19  
g-index

19  
all docs

19  
docs citations

19  
times ranked

1758  
citing authors

#	ARTICLE	IF	CITATIONS
1	MSQuant, an Open Source Platform for Mass Spectrometry-Based Quantitative Proteomics. <i>Journal of Proteome Research</i> , 2010, 9, 393-403.	3.7	237
2	Highly Robust, Automated, and Sensitive Online TiO <sub>2</sub> -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
3	Quantitative Proteomics by Metabolic Labeling of Model Organisms. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 11-24.	3.8	133
4	Expression Clustering Reveals Detailed Co-expression Patterns of Functionally Related Proteins during B Cell Differentiation. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 1297-1310.	3.8	78
5	Derivatization of small oligosaccharides prior to analysis by matrix-assisted laser desorption/ionization using glycidyltrimethylammonium chloride and Girard's reagent T. <i>Rapid Communications in Mass Spectrometry</i> , 2002, 16, 905-912.	1.5	68
6	Monitoring of changes in the membrane proteome during stationary phase adaptation of <i>Bacillus subtilis</i> using <i>in vivo</i> labeling techniques. <i>Proteomics</i> , 2008, 8, 2062-2076.	2.2	55
7	Optimizing Identification and Quantitation of <sup>15</sup> N-Labeled Proteins in Comparative Proteomics. <i>Analytical Chemistry</i> , 2008, 80, 7796-7803.	6.5	55
8	Alternative reading frame selection mediated by a tRNA-like domain of an internal ribosome entry site. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E630-9.	7.1	54
9	Comparative Phosphoproteomics of Zebrafish Fyn/Yes Morpholino Knockdown Embryos. <i>Molecular and Cellular Proteomics</i> , 2008, 7, 2176-2187.	3.8	53
10	In Vivo Stable Isotope Labeling of Fruit Flies Reveals Post-transcriptional Regulation in the Maternal-to-zygotic Transition. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1566-1578.	3.8	43
11	Straightforward and de Novo Peptide Sequencing by MALDI-MS/MS Using a Lys-N Metalloendopeptidase. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 650-660.	3.8	42
12	Metabolic Labeling of Model Organisms Using Heavy Nitrogen ( <sup>15</sup> N). <i>Methods in Molecular Biology</i> , 2011, 753, 29-42.	0.9	29
13	Identification of peptides with tolerogenic potential in a hydrolysed whey-based infant formula. <i>Clinical and Experimental Allergy</i> , 2018, 48, 1345-1353.	2.9	25
14	A Horizontally Acquired Transcription Factor Coordinates <i>Salmonella</i> Adaptations to Host Microenvironments. <i>MBio</i> , 2014, 5, e01727-14.	4.1	19
15	Target Profiling of a Small Library of Phosphodiesterase-5 (PDE5) Inhibitors using Chemical Proteomics. <i>ChemMedChem</i> , 2010, 5, 1927-1936.	3.2	17
16	Metaproteomic and 16S rRNA Gene Sequencing Analysis of the Infant Fecal Microbiome. <i>International Journal of Molecular Sciences</i> , 2019, 20, 1430.	4.1	12
17	A Highly Effective Component Vaccine against Nontyphoidal <i>Salmonella enterica</i> Infections. <i>MBio</i> , 2015, 6, e01421-15.	4.1	11
18	Response of the honey bee ( <i>Apis mellifera</i> ) proteome to Israeli acute paralysis virus (IAPV) infection. <i>Canadian Journal of Zoology</i> , 2015, 93, 711-720.	1.0	9

#	ARTICLE	IF	CITATIONS
19	MSQuant: A Platform for Stable Isotope-Based Quantitative Proteomics. <i>Methods in Molecular Biology</i> , 2012, 893, 511-522.	0.9	7