Johan A Westerhuis

List of Publications by Year
in descending order

77 papers	7,323 citations	218381 26 h-index	66788 78 g-index
80 all docs	80 docs citations	80 times ranked	10712 citing authors

#	Article	IF	Citations
1	Effect of strigolactones on recruitment of the rice root-associated microbiome. FEMS Microbiology Ecology, 2022, 98, .	1.3	29
2	Elevation of fatty acid desaturaseÂ2 in esophageal adenocarcinoma increases polyunsaturated lipids and may exacerbate bile acidâ€induced DNA damage. Clinical and Translational Medicine, 2022, 12, e810.	1.7	6
3	A beginnerâ€™s guide to integrating multi-omics data from microbial communities. Biochemist, 2022, 44, 23-29.	0.2	5
4	Heterofusion: Fusing genomics data of different measurement scales. Journal of Chemometrics, 2021, 35, e3200.	0.7	5
5	Divide et impera: How disentangling common and distinctive variability in multiset data analysis can aid industrial process troubleshooting and understanding. Journal of Chemometrics, 2021, 35, e3266.	0.7	4
6	Generalized simultaneous component analysis of binary and quantitative data. Journal of Chemometrics, 2021, 35, e3312.	0.7	3
7	Systematic selection of competing metabolomics methods in a metabolite-sensory relationship study. Metabolomics, 2021, 17, 77.	1.4	3
8	Integration of omics data to unravel root microbiome recruitment. Current Opinion in Biotechnology, 2021, 70, 255-261.	3.3	20
9	Repeated measures ASCA+ for analysis of longitudinal intervention studies with multivariate outcome data. PLoS Computational Biology, 2021, 17, e1009585.	1.5	21
10	Targeted proteomic response to coffee consumption. European Journal of Nutrition, 2020, 59, 1529-1539.	1.8	2
11	Common and distinct variation in data fusion of designed experimental data. Metabolomics, 2020, 16, 2.	1.4	13
12	Separating common (global and local) and distinct variation in multiple mixed types data sets. Journal of Chemometrics, 2020, 34, e3197.	0.7	7
13	Increased comparability between RNA-Seq and microarray data by utilization of gene sets. PLoS Computational Biology, 2020, 16, e1008295.	1.5	18
14	Logistic principal component analysis via non-convex singular value thresholding. Chemometrics and Intelligent Laboratory Systems, 2020, 204, 104089.	1.8	9
15	Harmonization of quality metrics and power calculation in multi-omic studies. Nature Communications, 2020, 11, 3092.	5.8	43
16	Variable selection and validation in multivariate modelling. Bioinformatics, 2019, 35, 972-980.	1.8	122
17	Weighted sparse principal component analysis. Chemometrics and Intelligent Laboratory Systems, 2019, 195, 103875.	1.8	10
18	STATegra, a comprehensive multi-omics dataset of B-cell differentiation in mouse. Scientific Data, 2019, 6, 256.	2.4	26

#	Article	IF	Citations
19	Principal component analysis of binary genomics data. Briefings in Bioinformatics, 2019, 20, 317-329.	3.2	21
20	GCâ€“MS-based urinary organic acid profiling reveals multiple dysregulated metabolic pathways following experimental acute alcohol consumption. Scientific Reports, 2018, 8, 5775.	1.6	17
21	iTOP: inferring the topology of omics data. Bioinformatics, 2018, 34, i988-i996.	1.8	19
22	Lipidomic Response to Coffee Consumption. Nutrients, 2018, 10, 1851.	1.7	32
23	Fusing metabolomics data sets with heterogeneous measurement errors. PLoS ONE, 2018, 13, e0195939.	1.1	7
24	Training for translation between disciplines: a philosophy for life and data sciences curricula. Bioinformatics, 2018, 34, i4-i12.	1.8	5
25	The 1H-NMR-based metabolite profile of acute alcohol consumption: A metabolomics intervention study. PLoS ONE, 2018, 13, e0196850.	1.1	18
26	Metabolomics variable selection and classification in the presence of observations below the detection limit using an extension of ERp. BMC Bioinformatics, 2017, 18, 83.	1.2	6
27	Selecting the number of factors in principal component analysis by permutation testingâ€”Numerical and practical aspects. Journal of Chemometrics, 2017, 31, e2937.	0.7	22
28	Why orthogonal rotations might be not so orthogonal as you think. Journal of Chemometrics, 2017, 31, e2920.	0.7	1
29	Separating common from distinctive variation. BMC Bioinformatics, 2016, 17, 195.	1.2	18
30	Variable selection for binary classification using error rate p-values applied to metabolomics data. BMC Bioinformatics, 2016, 17, 33.	1.2	5
31	Gut microbial activity as influenced by fiber digestion: dynamic metabolomics in an in vitro colon simulator. Metabolomics, 2016, 12, 1.	1.4	17
32	Contribution towards a Metabolite Profile of the Detoxification of Benzoic Acid through Glycine Conjugation: An Intervention Study. PLoS ONE, 2016, 11, e0167309.	1.1	23
33	Using Petri nets for experimental design in a multi-organ elimination pathway. Computers in Biology and Medicine, 2015, 63, 19-27.	3.9	1
34	Analyzing metabolomics-based challenge tests. Metabolomics, 2015, 11, 50-63.	1.4	17
35	Network Identification of Hormonal Regulation. PLoS ONE, 2014, 9, e96284.	1.1	5
36	Reflections on univariate and multivariate analysis of metabolomics data. Metabolomics, 2014, 10, 361-374.	1.4	406

#	Article	IF	Citations
37	Variable importance in latent variable regression models. Journal of Chemometrics, 2014, 28, 615-622.	0.7	42
38	Population-based nutrikinetic modeling of polyphenol exposure. Metabolomics, 2014, 10, 1059-1073.	1.4	20
39	Identifying inhibitory compounds in lignocellulosic biomass hydrolysates using an exometabolomics approach. BMC Biotechnology, 2014, 14, 22.	1.7	55
40	Use of prior knowledge for the analysis of high-throughput transcriptomics and metabolomics data. BMC Systems Biology, 2014, 8, S2.	3.0	23
41	A technical note on challenge tests in human volunteers for multidimensional phenotyping. Chemometrics and Intelligent Laboratory Systems, 2014, 136, 81-84.	1.8	2
42	Application of NMR-based metabonomics suggests a relationship between betaine absorption and elevated creatine plasma concentrations in catheterised sows. British Journal of Nutrition, 2012, 107, 1603-1615.	1.2	15
43	Topology of Transcriptional Regulatory Networks: Testing and Improving. PLoS ONE, 2012, 7, e40082.	1.1	1
44	Double-check: validation of diagnostic statistics for PLS-DA models in metabolomics studies. Metabolomics, 2012, 8, 3-16.	1.4	622
45	Editorialâ€“data analysis in metabolomics. Metabolomics, 2012, 8, 1-2.	1.4	2
46	Metabolic fate of polyphenols in the human superorganism. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4531-4538.	3.3	448
47	New Figures of Merit for Comprehensive Functional Genomics Data: The Metabolomics Case. Analytical Chemistry, 2011, 83, 3267-3274.	3.2	22
48	Simplivariate Models: Uncovering the Underlying Biology in Functional Genomics Data. PLoS ONE, 2011, 6, e20747.	1.1	13
49	Data-processing strategies for metabolomics studies. TrAC - Trends in Analytical Chemistry, 2011, 30, 1685-1698.	5.8	164
50	ANOVAâ€“principal component analysis and ANOVAâ€“simultaneous component analysis: a comparison. Journal of Chemometrics, 2011, 25, 561-567.	0.7	119
51	Tracyâ€“Widom statistic for the largest eigenvalue of autoscaled real matrices. Journal of Chemometrics, 2011, 25, 644-652.	0.7	17
52	Multivariate paired data analysis: multilevel PLSDA versus OPLSDA. Metabolomics, 2010, 6, 119-128.	1.4	362
53	Multiâ€way analysis of flux distributions across multiple conditions. Journal of Chemometrics, 2009, 23, 406-420.	0.7	23
54	Metabolomics data exploration guided by prior knowledge. Analytica Chimica Acta, 2009, 651, 173-181.	2.6	28

#	Article	IF	Citations
55	Exploring the analysis of structured metabolomics data. Chemometrics and Intelligent Laboratory Systems, 2009, 98, 88-96.	1.8	27
56	Phenotyping Tea Consumers by Nutrikinetic Analysis of Polyphenolic End-Metabolites. Journal of Proteome Research, 2009, 8, 3317-3330.	1.8	89
57	Assessment of PLSDA cross validation. Metabolomics, 2008, 4, 81-89.	1.4	1,178
58	Discriminant Q2 (DQ2) for improved discrimination in PLSDA models. Metabolomics, 2008, 4, 293-296.	1.4	69
59	PARAFASCA: ASCA combined with PARAFAC for the analysis of metabolic fingerprinting data. Journal of Chemometrics, 2008, 22, 114-121.	0.7	52
60	The geometry of ASCA. Journal of Chemometrics, 2008, 22, 464-471.	0.7	19
61	Multilevel Data Analysis of a Crossover Designed Human Nutritional Intervention Study. Journal of Proteome Research, 2008, 7, 4483-4491.	1.8	158
62	Simplivariate Models: Ideas and First Examples. PLoS ONE, 2008, 3, e3259.	1.1	16
63	Grey component analysis. Journal of Chemometrics, 2007, 21, 474-485.	0.7	19
64	Statistical validation of megavariate effects in ASCA. BMC Bioinformatics, 2007, 8, 322.	1.2	137
65	Performance assessment and improvement of control charts for statistical batch process monitoring. Statistica Neerlandica, 2006, 60, 339-360.	0.9	14
66	Centering, scaling, and transformations: improving the biological information content of metabolomics data. BMC Genomics, 2006, 7, 142.	1.2	1,836
67	Maximum likelihood scaling (MALS). Journal of Chemometrics, 2006, 20, 120-127.	0.7	9
68	ASCA: analysis of multivariate data obtained from an experimental design. Journal of Chemometrics, 2005, 19, 469-481.	0.7	201
69	Model Selection and Optimal Sampling in High-Throughput Experimentation. Analytical Chemistry, 2004, 76, 3171-3178.	3.2	14
70	A framework for sequential multiblock component methods. Journal of Chemometrics, 2003, 17, 323-337.	0.7	190
71	Near-Infrared Spectroscopic Monitoring of a Series of Industrial Batch Processes Using a Bilinear Grey Model. Applied Spectroscopy, 2003, 57, 1007-1019.	1.2	18
72	Kinetic and mechanistic studies on the Heck reaction using real-time near infrared spectroscopy. Physical Chemistry Chemical Physics, 2003, 5, 4455-4460.	1.3	12

#	Article	IF	Citations
73	Monitoring of batch processes using spectroscopy. AIChE Journal, 2002, 48, 2283-2297.	1.8	53
74	Deflation in multiblock PLS. Journal of Chemometrics, 2001, 15, 485-493.	0.7	81
75	Modelling of spectroscopic batch process data using grey models to incorporate external information. Journal of Chemometrics, 2001, 15, 101-121.	0.7	38
76	Multiway multiblock component and covariates regression models. Journal of Chemometrics, 2000, 14, 301-331.	0.7	92
77	StandardizedQ-statistic for improved sensitivity in the monitoring of residuals in MSPC. Journal of Chemometrics, 2000, 14, 335-349.	0.7	34