

Julien Boccard

List of Publications by Year in descending order

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109
papers

3,897
citations

125106

35
h-index

162838

57
g-index

113
all docs

113
docs citations

113
times ranked

5624
citing authors

#	ARTICLE	IF	CITATIONS
1	Efficiently handling high-dimensional data from multifactorial designs with unequal group sizes using Rebalanced ASCA (RASCA). <i>Journal of Chemometrics</i> , 2023, 37, .	0.7	2
2	Longitudinal evaluation of multiple biomarkers for the detection of testosterone gel administration in women with normal menstrual cycle. <i>Drug Testing and Analysis</i> , 2022, 14, 833-850.	1.6	29
3	An integrated metabolomics and proteogenomics approach reveals molecular alterations following carbamazepine exposure in the male mussel <i>Mytilus galloprovincialis</i> . <i>Chemosphere</i> , 2022, 286, 131793.	4.2	15
4	Network principal component analysis: a versatile tool for the investigation of multigroup and multiblock datasets. <i>Bioinformatics</i> , 2021, 37, 1297-1303.	1.8	6
5	From a single steroid to the steroidome: Trends and analytical challenges. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2021, 206, 105797.	1.2	41
6	Metabotypes of <i>Pseudomonas aeruginosa</i> Correlate with Antibiotic Resistance, Virulence and Clinical Outcome in Cystic Fibrosis Chronic Infections. <i>Metabolites</i> , 2021, 11, 63.	1.3	20
7	Neuroinflammatory Response to TNF α and IL1 β Cytokines Is Accompanied by an Increase in Glycolysis in Human Astrocytes In Vitro. <i>International Journal of Molecular Sciences</i> , 2021, 22, 4065.	1.8	13
8	Gaining Insights Into Metabolic Networks Using Chemometrics and Bioinformatics: Chronic Kidney Disease as a Clinical Model. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 682559.	1.6	5
9	Steroid profiling by UHPLC-MS/MS in dried blood spots collected from healthy women with and without testosterone gel administration. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2021, 204, 114280.	1.4	24
10	Identification of a predictive metabolic signature of response to immune checkpoint inhibitors in non-small cell lung cancer: METABO-ICI clinical study protocol. <i>Respiratory Medicine and Research</i> , 2021, 80, 100845.	0.4	3
11	Approaches in metabolomics for regulatory toxicology applications. <i>Analyst</i> , The, 2021, 146, 1820-1834.	1.7	30
12	Wipe-sampling procedure optimisation for the determination of 23 antineoplastic drugs used in the hospital pharmacy. <i>European Journal of Hospital Pharmacy</i> , 2021, 28, 94-99.	0.5	5
13	Analysis of Metabolomics Data—A Chemometrics Perspective. , 2020, , 483-505.		2
14	Mass spectrometry metabolomic data handling for biomarker discovery. , 2020, , 369-388.		2
15	Implementation of liquid chromatography—high resolution mass spectrometry methods for untargeted metabolomic analyses of biological samples: A tutorial. <i>Analytica Chimica Acta</i> , 2020, 1105, 28-44.	2.6	83
16	Metabolomics approach reveals disruption of metabolic pathways in the marine bivalve <i>Mytilus galloprovincialis</i> exposed to a WWTP effluent extract. <i>Science of the Total Environment</i> , 2020, 712, 136551.	3.9	45
17	Profiling of anabolic androgenic steroids and selective androgen receptor modulators for interference with adrenal steroidogenesis. <i>Biochemical Pharmacology</i> , 2020, 172, 113781.	2.0	10
18	Supercritical fluid chromatography—mass spectrometry in routine anti-doping analyses: Estimation of retention time variability under reproducible conditions. <i>Journal of Chromatography A</i> , 2020, 1616, 460780.	1.8	11

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19	Steroid profile analysis by LC-HRMS in human seminal fluid. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2020, 1136, 121929.	1.2	13
20	Combining the advantages of multilevel and orthogonal partial least squares data analysis for longitudinal metabolomics: Application to kidney transplantation. <i>Analytica Chimica Acta</i> , 2020, 1099, 26-38.	2.6	7
21	Evaluation of Different Tandem MS Acquisition Modes to Support Metabolite Annotation in Human Plasma Using Ultra High-Performance Liquid Chromatography High-Resolution Mass Spectrometry for Untargeted Metabolomics. <i>Metabolites</i> , 2020, 10, 464.	1.3	9
22	Exploring blood alterations in chronic kidney disease and haemodialysis using metabolomics. <i>Scientific Reports</i> , 2020, 10, 19502.	1.6	14
23	Multifactorial Analysis of Environmental Metabolomic Data in Ecotoxicology: Wild Marine Mussel Exposed to WWTP Effluent as a Case Study. <i>Metabolites</i> , 2020, 10, 269.	1.3	19
24	Insights on the Structural and Metabolic Resistance of Potato (<i>Solanum tuberosum</i>) Cultivars to Tuber Black Dot (<i>Colletotrichum coccodes</i>). <i>Frontiers in Plant Science</i> , 2020, 11, 1287.	1.7	11
25	Development and validation of an UHPLC-MS/MS method for extended serum steroid profiling in female populations. <i>Bioanalysis</i> , 2020, 12, 753-768.	0.6	16
26	Applicability of Supercritical fluid chromatography-Mass spectrometry to metabolomics. II-Assessment of a comprehensive library of metabolites and evaluation of biological matrices. <i>Journal of Chromatography A</i> , 2020, 1620, 461021.	1.8	34
27	Cultivar, site or harvest date: the gordian knot of wine terroir. <i>Metabolomics</i> , 2020, 16, 52.	1.4	12
28	Comprehensive Examination of the Mouse Lung Metabolome Following <i>Mycobacterium tuberculosis</i> Infection Using a Multiplatform Mass Spectrometry Approach. <i>Journal of Proteome Research</i> , 2020, 19, 2053-2070.	1.8	35
29	Steroidomics for highlighting novel serum biomarkers of testosterone doping. <i>Bioanalysis</i> , 2019, 11, 1169-1185.	0.6	23
30	Processing of NMR and MS metabolomics data using chemometrics methods: a global tool for fungi biotransformation reactions monitoring. <i>Metabolomics</i> , 2019, 15, 107.	1.4	7
31	Choosing an Optimal Sample Preparation in <i>Caulobacter crescentus</i> for Untargeted Metabolomics Approaches. <i>Metabolites</i> , 2019, 9, 193.	1.3	11
32	Protein pathway analysis to study development-dependent effects of acute and repeated trimethyltin (TMT) treatments in 3D rat brain cell cultures. <i>Toxicology in Vitro</i> , 2019, 60, 281-292.	1.1	5
33	An Integrative Multi-Omics Workflow to Address Multifactorial Toxicology Experiments. <i>Metabolites</i> , 2019, 9, 79.	1.3	24
34	DynaStI: A Dynamic Retention Time Database for Steroidomics. <i>Metabolites</i> , 2019, 9, 85.	1.3	18
35	In vitro models to study insulin and glucocorticoids modulation of trimethyltin (TMT)-induced neuroinflammation and neurodegeneration, and in vivo validation in db/db mice. <i>Archives of Toxicology</i> , 2019, 93, 1649-1664.	1.9	11
36	Toward a better understanding of chronic kidney disease with complementary chromatographic methods hyphenated with mass spectrometry for improved polar metabolome coverage. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2019, 1116, 9-18.	1.2	15

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37	Removal of batch effects using stratified subsampling of metabolomic data for in vitro endocrine disruptors screening. <i>Talanta</i> , 2019, 195, 77-86.	2.9	10
38	A scoring approach for multi-platform acquisition in metabolomics. <i>Journal of Chromatography A</i> , 2019, 1592, 47-54.	1.8	40
39	UHPLC-HRMS Analysis for Steroid Profiling in Serum (Steroidomics). <i>Methods in Molecular Biology</i> , 2018, 1738, 261-278.	0.4	11
40	Steroid profiles in both blood serum and seminal plasma are not correlated and do not reflect sperm quality: Study on the male reproductive health of fifty young Swiss men. <i>Clinical Biochemistry</i> , 2018, 62, 39-46.	0.8	16
41	Metabolomics in chronic kidney disease: Strategies for extended metabolome coverage. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2018, 161, 313-325.	1.4	23
42	Integration of Metabolomic Data From Multiple Analytical Platforms: Towards Extensive Coverage of the Metabolome. <i>Comprehensive Analytical Chemistry</i> , 2018, , 477-504.	0.7	0
43	Dynamics of Metabolite Induction in Fungal Co-cultures by Metabolomics at Both Volatile and Non-volatile Levels. <i>Frontiers in Microbiology</i> , 2018, 9, 72.	1.5	40
44	Extracting Knowledge from MS Clinical Metabolomic Data: Processing and Analysis Strategies. <i>Methods in Molecular Biology</i> , 2018, 1730, 371-384.	0.4	1
45	Targeted metabolomics shows plasticity in the evolution of signaling lipids and uncovers old and new endocannabinoids in the plant kingdom. <i>Scientific Reports</i> , 2017, 7, 41177.	1.6	52
46	Steroid profiling in H295R cells to identify chemicals potentially disrupting the production of adrenal steroids. <i>Toxicology</i> , 2017, 381, 51-63.	2.0	42
47	Optimized selection of liquid chromatography conditions for wide range analysis of natural compounds. <i>Journal of Chromatography A</i> , 2017, 1504, 91-104.	1.8	28
48	Enhanced metabolite annotation via dynamic retention time prediction: Steroidogenesis alterations as a case study. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017, 1071, 11-18.	1.2	25
49	Indirect quantitative structure-retention relationship for steroid identification: A chemometric challenge at "Chimie 2016". <i>Chemometrics and Intelligent Laboratory Systems</i> , 2017, 160, 52-58.	1.8	2
50	High-resolution mass spectrometry as an alternative detection method to tandem mass spectrometry for the analysis of endogenous steroids in serum. <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2017, 1052, 34-42.	1.2	34
51	Metabolomic analysis of urine samples by UHPLC-QTOF-MS: Impact of normalization strategies. <i>Analytica Chimica Acta</i> , 2017, 955, 27-35.	2.6	129
52	Unravelling the effects of multiple experimental factors in metabolomics, analysis of human neural cells with hydrophilic interaction liquid chromatography hyphenated to high resolution mass spectrometry. <i>Journal of Chromatography A</i> , 2017, 1527, 53-60.	1.8	27
53	Statistical Correlations between HPLC Activity-Based Profiling Results and NMR/MS Microfraction Data to Deconvolute Bioactive Compounds in Mixtures. <i>Molecules</i> , 2016, 21, 259.	1.7	15
54	Ultra-high performance supercritical fluid chromatography coupled with quadrupole-time-of-flight mass spectrometry as a performing tool for bioactive analysis. <i>Journal of Chromatography A</i> , 2016, 1450, 101-111.	1.8	56

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55	Exploring Omics data from designed experiments using analysis of variance multiblock Orthogonal Partial Least Squares. <i>Analytica Chimica Acta</i> , 2016, 920, 18-28.	2.6	63
56	Structured plant metabolomics for the simultaneous exploration of multiple factors. <i>Scientific Reports</i> , 2016, 6, 37390.	1.6	39
57	Standardized LC \bar{A} –LC-ELSD Fractionation Procedure for the Identification of Minor Bioactives via the Enzymatic Screening of Natural Extracts. <i>Journal of Natural Products</i> , 2016, 79, 2856-2864.	1.5	7
58	High-throughput identification of monoclonal antibodies after compounding by UV spectroscopy coupled to chemometrics analysis. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 5915-5924.	1.9	11
59	Methods for Doping Detection. <i>Frontiers of Hormone Research</i> , 2016, 47, 153-167.	1.0	12
60	Longitudinal monitoring of endogenous steroids in human serum by UHPLC-MS/MS as a tool to detect testosterone abuse in sports. <i>Analytical and Bioanalytical Chemistry</i> , 2016, 408, 705-719.	1.9	57
61	Prediction of retention time in reversed-phase liquid chromatography as a tool for steroid identification. <i>Analytica Chimica Acta</i> , 2016, 916, 8-16.	2.6	58
62	Evaluation and identification of dioxin exposure biomarkers in human urine by high-resolution metabolomics, multivariate analysis and in vitro synthesis. <i>Toxicology Letters</i> , 2016, 240, 22-31.	0.4	27
63	Systematic evaluation of matrix effects in hydrophilic interaction chromatography versus reversed phase liquid chromatography coupled to mass spectrometry. <i>Journal of Chromatography A</i> , 2016, 1439, 42-53.	1.8	28
64	Evaluation of steroidomics by liquid chromatography hyphenated to mass spectrometry as a powerful analytical strategy for measuring human steroid perturbations. <i>Journal of Chromatography A</i> , 2016, 1430, 97-112.	1.8	80
65	Rumen microbial communities influence metabolic phenotypes in lambs. <i>Frontiers in Microbiology</i> , 2015, 6, 1060.	1.5	98
66	Integrating metabolomic data from multiple analytical platforms for a comprehensive characterisation of lemon essential oils. <i>Flavour and Fragrance Journal</i> , 2015, 30, 131-138.	1.2	14
67	Assessing Susceptibility to Epilepsy in Three Rat Strains Using Brain Metabolic Profiling Based on HRMAS NMR Spectroscopy and Chemometrics. <i>Journal of Proteome Research</i> , 2015, 14, 2177-2189.	1.8	21
68	Steroidomic Footprinting Based on Ultra-High Performance Liquid Chromatography Coupled with Qualitative and Quantitative High-Resolution Mass Spectrometry for the Evaluation of Endocrine Disrupting Chemicals in H295R Cells. <i>Chemical Research in Toxicology</i> , 2015, 28, 955-966.	1.7	24
69	Multi-way PLS regression: Monotony convergence of tri-linear PLS2 and optimality of parameters. <i>Computational Statistics and Data Analysis</i> , 2015, 83, 129-139.	0.7	10
70	Untargeted profiling of urinary steroid metabolites after testosterone ingestion: opening new perspectives for antidoping testing. <i>Bioanalysis</i> , 2014, 6, 2523-2536.	0.6	25
71	Differentiation of lemon essential oil based on volatile and non-volatile fractions with various analytical techniques: a metabolomic approach. <i>Food Chemistry</i> , 2014, 143, 325-335.	4.2	92
72	Multi-way PLS for discrimination: Compact form equivalent to the tri-linear PLS2 procedure and its monotony convergence. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2014, 133, 25-32.	1.8	18

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73	Comprehensive profiling and marker identification in non-volatile citrus oil residues by mass spectrometry and nuclear magnetic resonance. <i>Food Chemistry</i> , 2014, 150, 235-245.	4.2	26
74	Retention time prediction for dereplication of natural products (C _x H _y O _z) in LC-MS metabolite profiling. <i>Phytochemistry</i> , 2014, 108, 196-207.	1.4	44
75	Harnessing the complexity of metabolomic data with chemometrics. <i>Journal of Chemometrics</i> , 2014, 28, 1-9.	0.7	90
76	Quantitative monitoring of tamoxifen in human plasma extended to 40 metabolites using liquid-chromatography high-resolution mass spectrometry: new investigation capabilities for clinical pharmacology. <i>Analytical and Bioanalytical Chemistry</i> , 2014, 406, 2627-2640.	1.9	34
77	Iterative weighting of multiblock data in the orthogonal partial least squares framework. <i>Analytica Chimica Acta</i> , 2014, 813, 25-34.	2.6	9
78	Human urinary biomarkers of dioxin exposure: Analysis by metabolomics and biologically driven data dimensionality reduction. <i>Toxicology Letters</i> , 2014, 230, 234-243.	0.4	51
79	Mass Spectrometry Metabolomic Data Handling for Biomarker Discovery. , 2013, , 425-445.		11
80	Profiling of steroid metabolites after transdermal and oral administration of testosterone by ultra-high pressure liquid chromatography coupled to quadrupole time-of-flight mass spectrometry. <i>Journal of Steroid Biochemistry and Molecular Biology</i> , 2013, 138, 222-235.	1.2	67
81	Systematic comparison of sensitivity between hydrophilic interaction liquid chromatography and reversed phase liquid chromatography coupled with mass spectrometry. <i>Journal of Chromatography A</i> , 2013, 1312, 49-57.	1.8	73
82	Metabolomics reveals herbivore-induced metabolites of resistance and susceptibility in maize leaves and roots. <i>Plant, Cell and Environment</i> , 2013, 36, 621-639.	2.8	149
83	A consensus orthogonal partial least squares discriminant analysis (OPLS-DA) strategy for multiblock Omics data fusion. <i>Analytica Chimica Acta</i> , 2013, 769, 30-39.	2.6	246
84	New Insights in Pharmaceutical Analysis. <i>Chimia</i> , 2012, 66, 330.	0.3	2
85	Analysis of basic compounds by supercritical fluid chromatography: Attempts to improve peak shape and maintain mass spectrometry compatibility. <i>Journal of Chromatography A</i> , 2012, 1262, 205-213.	1.8	101
86	Method development for pharmaceuticals: Some solutions for tuning selectivity in reversed phase and hydrophilic interaction liquid chromatography. <i>Journal of Pharmaceutical and Biomedical Analysis</i> , 2012, 63, 95-105.	1.4	33
87	NMR- and UHPLC-MS correlation for identification of biomarkers from woods of <i>Vitis Vinifera</i> cultivar resistant to pathogens. <i>Planta Medica</i> , 2012, 78, .	0.7	0
88	Phenotypic and molecular characterization of proliferating and differentiated GnRH-expressing GnV-3 cells. <i>Molecular and Cellular Endocrinology</i> , 2011, 332, 97-105.	1.6	12
89	A steroidomic approach for biomarkers discovery in doping control. <i>Forensic Science International</i> , 2011, 213, 85-94.	1.3	66
90	Analytical aspects in doping control: Challenges and perspectives. <i>Forensic Science International</i> , 2011, 213, 49-61.	1.3	46

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91	Quantification of glucuronidated and sulfated steroids in human urine by ultra-high pressure liquid chromatography quadrupole time-of-flight mass spectrometry. <i>Analytical and Bioanalytical Chemistry</i> , 2011, 400, 503-516.	1.9	82
92	Analysis of experimental design with multivariate response: A contribution using multiblock techniques. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2011, 106, 65-72.	1.8	11
93	IEF pattern classificationâ€derived criteria for the identification of epoetinâ€ in urine. <i>Electrophoresis</i> , 2010, 31, 1918-1924.	1.3	11
94	Knowledge discovery in metabolomics: An overview of MS data handling. <i>Journal of Separation Science</i> , 2010, 33, 290-304.	1.3	158
95	Standard machine learning algorithms applied to UPLC-TOF/MS metabolic fingerprinting for the discovery of wound biomarkers in <i>Arabidopsis thaliana</i> . <i>Chemometrics and Intelligent Laboratory Systems</i> , 2010, 104, 20-27.	1.8	23
96	Mass spectrometryâ€based metabolomics oriented by correlation analysis for woundâ€induced molecule discovery: identification of a novel jasmonate glucoside. <i>Phytochemical Analysis</i> , 2010, 21, 95-101.	1.2	35
97	MS-based Plant Metabolomic Approaches for Biomarker Discovery. <i>Natural Product Communications</i> , 2009, 4, 1934578X0900401.	0.2	25
98	A 3D linear solvation energy model to quantify the affinity of flavonoid derivatives toward P-glycoprotein. <i>European Journal of Pharmaceutical Sciences</i> , 2009, 36, 254-264.	1.9	33
99	Breast cancer resistance protein (BCRP/ABCG2): New inhibitors and QSAR studies by a 3D linear solvation energy approach. <i>European Journal of Pharmaceutical Sciences</i> , 2009, 38, 39-46.	1.9	41
100	Metabolite profiling of plant extracts by ultra-high-pressure liquid chromatography at elevated temperature coupled to time-of-flight mass spectrometry. <i>Journal of Chromatography A</i> , 2009, 1216, 5660-5668.	1.8	61
101	MS-based plant metabolomic approaches for biomarker discovery. <i>Natural Product Communications</i> , 2009, 4, 1417-30.	0.2	31
102	UPLCâ€TOF-MS for plant metabolomics: A sequential approach for wound marker analysis in <i>Arabidopsis thaliana</i> . <i>Journal of Chromatography B: Analytical Technologies in the Biomedical and Life Sciences</i> , 2008, 871, 261-270.	1.2	96
103	Optimized liquid chromatographyâ€mass spectrometry approach for the isolation of minor stress biomarkers in plant extracts and their identification by capillary nuclear magnetic resonance. <i>Journal of Chromatography A</i> , 2008, 1180, 90-98.	1.8	97
104	Antimitotic and Antiproliferative Activities of Chalcones: Forward Structureâ€Activity Relationship. <i>Journal of Medicinal Chemistry</i> , 2008, 51, 2307-2310.	2.9	166
105	Plant Metabolomics â€ Strategies for Biomarker Detection, Isolation, and Identification. <i>Chimia</i> , 2008, 62, 685.	0.3	0
106	Development of a twoâ€step screening ESIâ€TOFâ€MS method for rapid determination of significant stressâ€induced metabolome modifications in plant leaf extracts: The wound response in <i>Arabidopsis thaliana</i> as a case study. <i>Journal of Separation Science</i> , 2007, 30, 2268-2278.	1.3	46
107	Multivariate data analysis of rapid LC-TOF/MS experiments from <i>Arabidopsis thaliana</i> stressed by wounding. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2007, 86, 189-197.	1.8	35
108	Synergy at the 'Ecole de Pharmacie GenÃve-Lausanne': Methodology Developments for the Treatment of Complex Metabolomic Datasets with Data Mining. <i>Chimia</i> , 2005, 59, 362-365.	0.3	1

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109	CD40-CD40 Ligand Disruption Does Not Prevent Hyperoxia-Induced Injury. American Journal of Pathology, 2002, 160, 67-71.	1.9	11