

Sebastien Gallien

List of Publications by Year in descending order

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38
papers

2,730
citations

218677

26
h-index

315739

38
g-index

40
all docs

40
docs citations

40
times ranked

4237
citing authors

#	ARTICLE	IF	CITATIONS
1	High-Density, Targeted Monitoring of Tyrosine Phosphorylation Reveals Activated Signaling Networks in Human Tumors. <i>Cancer Research</i> , 2021, 81, 2495-2509.	0.9	41
2	Absolute quantification of tumor antigens using embedded MHC-I isotopologue calibrants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	25
3	Standardization and harmonization of distributed multi-center proteotype analysis supporting precision medicine studies. <i>Nature Communications</i> , 2020, 11, 5248.	12.8	49
4	An α -matrix digestion procedure for AP-MS experiments dissects the interplay between complex-conserved and serotype-specific reactivities in Dengue virus-human plasma interactome. <i>Journal of Proteomics</i> , 2019, 193, 71-84.	2.4	3
5	The use of proteases complementary to trypsin to probe isoforms and modifications. <i>Proteomics</i> , 2016, 16, 715-728.	2.2	22
6	Parallel reaction monitoring using quadrupole-Orbitrap mass spectrometer: Principle and applications. <i>Proteomics</i> , 2016, 16, 2146-2159.	2.2	226
7	Dataset on protein composition of a human plasma sub-proteome able to modulate the Dengue 2 virus infection in Huh 7.5 cells. <i>Data in Brief</i> , 2016, 6, 352-358.	1.0	4
8	Hyphenation of fast liquid chromatography with high-resolution mass spectrometry for quantitative proteomics analyses. <i>TrAC - Trends in Analytical Chemistry</i> , 2016, 84, 144-150.	11.4	13
9	Novel interactions of domain III from the envelope glycoprotein of dengue 2 virus with human plasma proteins. <i>Journal of Proteomics</i> , 2016, 131, 205-213.	2.4	16
10	Quantification of SAA1 and SAA2 in lung cancer plasma using the isotype-specific PRM assays. <i>Proteomics</i> , 2015, 15, 3116-3125.	2.2	54
11	Advances in high-resolution quantitative proteomics: implications for clinical applications. <i>Expert Review of Proteomics</i> , 2015, 12, 489-498.	3.0	35
12	A quality control of proteomic experiments based on multiple isotopologous internal standards. <i>EuPA Open Proteomics</i> , 2015, 8, 16-21.	2.5	11
13	Large-Scale Targeted Proteomics Using Internal Standard Triggered-Parallel Reaction Monitoring (IS-PRM)*. <i>Molecular and Cellular Proteomics</i> , 2015, 14, 1630-1644.	3.8	164
14	Detection and quantification of proteins in clinical samples using high resolution mass spectrometry. <i>Methods</i> , 2015, 81, 15-23.	3.8	54
15	Recent advances in targeted proteomics for clinical applications. <i>Proteomics - Clinical Applications</i> , 2015, 9, 423-431.	1.6	56
16	Quantitative proteomics using the high resolution accurate mass capabilities of the quadrupole-orbitrap mass spectrometer. <i>Bioanalysis</i> , 2014, 6, 2159-2170.	1.5	15
17	Technical considerations for large-scale parallel reaction monitoring analysis. <i>Journal of Proteomics</i> , 2014, 100, 147-159.	2.4	153
18	A Simple Protocol To Routinely Assess the Uniformity of Proteomics Analyses. <i>Journal of Proteome Research</i> , 2014, 13, 2688-2695.	3.7	24

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19	Characterization of Protein Complexes using Targeted Proteomics. <i>Current Topics in Medicinal Chemistry</i> , 2014, 14, 344-350.	2.1	6
20	Targeted proteomics strategy applied to biomarker evaluation. <i>Proteomics - Clinical Applications</i> , 2013, 7, 739-747.	1.6	34
21	Selectivity of LC-MS/MS analysis: Implication for proteomics experiments. <i>Journal of Proteomics</i> , 2013, 81, 148-158.	2.4	123
22	Targeted Proteomic Quantification on Quadrupole-Orbitrap Mass Spectrometer. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1709-1723.	3.8	427
23	Phosphoproteome Exploration Reveals a Reformatting of Cellular Processes in Response to Low Sterol Biosynthetic Capacity in <i>Arabidopsis</i> . <i>Journal of Proteome Research</i> , 2012, 11, 1228-1239.	3.7	10
24	Highly multiplexed targeted proteomics using precise control of peptide retention time. <i>Proteomics</i> , 2012, 12, 1122-1133.	2.2	47
25	Mass spectrometry-based detection and quantification of plasma glycoproteins using selective reaction monitoring. <i>Nature Protocols</i> , 2012, 7, 859-871.	12.0	29
26	<i>In situ</i> proteo-metabolomics reveals metabolite secretion by the acid mine drainage bio-indicator, <i>Euglena mutabilis</i> . <i>ISME Journal</i> , 2012, 6, 1391-1402.	9.8	37
27	Taxonomic and functional prokaryote diversity in mildly arsenic-contaminated sediments. <i>Research in Microbiology</i> , 2011, 162, 877-887.	2.1	51
28	Metabolic diversity among main microorganisms inside an arsenic-rich ecosystem revealed by meta- and proteo-genomics. <i>ISME Journal</i> , 2011, 5, 1735-1747.	9.8	186
29	Enolases: storage compounds in seeds? Evidence from a proteomic comparison of zygotic and somatic embryos of <i>Cyclamen persicum</i> Mill.. <i>Plant Molecular Biology</i> , 2011, 75, 305-319.	3.9	36
30	Characterization of the Active Bacterial Community Involved in Natural Attenuation Processes in Arsenic-Rich Creek Sediments. <i>Microbial Ecology</i> , 2011, 61, 793-810.	2.8	67
31	Selected reaction monitoring applied to proteomics. <i>Journal of Mass Spectrometry</i> , 2011, 46, 298-312.	1.6	249
32	Physiological and proteomic characterization of manganese sensitivity and tolerance in rice (<i>Oryza</i>)	2.9	76
33	Ortho-proteogenomics: Multiple proteomes investigation through orthology and a new MS-based protocol. <i>Genome Research</i> , 2009, 19, 128-135.	5.5	99
34	Differential Membrane Proteome Analysis Reveals Novel Proteins Involved in the Degradation of Aromatic Compounds in <i>Geobacter metallireducens</i> . <i>Molecular and Cellular Proteomics</i> , 2009, 8, 2159-2169.	3.8	25
35	Characterization of leaf apoplastic peroxidases and metabolites in <i>Vigna unguiculata</i> in response to toxic manganese supply and silicon. <i>Journal of Experimental Botany</i> , 2009, 60, 1663-1678.	4.8	72
36	Identification and characterization of the tungsten-containing class of benzoyl-coenzyme A reductases. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 17687-17692.	7.1	112

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37	Cholest-4-En-3-One-1 ¹ -Dehydrogenase, a Flavoprotein Catalyzing the Second Step in Anoxic Cholesterol Metabolism. Applied and Environmental Microbiology, 2008, 74, 107-113.	3.1	47
38	Interrupted coding sequences in Mycobacterium smegmatis: authentic mutations or sequencing errors?. Genome Biology, 2007, 8, R20.	9.6	29