

# Pierre-Alain Binz

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

56  
papers

6,007  
citations

28  
h-index

73  
g-index

73  
ext. papers

6,862  
ext. citations

12  
avg. IF

4.51  
L-index

#	Paper	IF	Citations
56	Universal Spectrum Identifier for mass spectra. <i>Nature Methods</i> , <b>2021</b> , 18, 768-770	21.6	9
55	A new rat model of creatine transporter deficiency reveals behavioral disorder and altered brain metabolism. <i>Scientific Reports</i> , <b>2021</b> , 11, 1636	4.9	5
54	Exudative glutamine losses contribute to high needs after burn injury. <i>Journal of Parenteral and Enteral Nutrition</i> , <b>2021</b> ,	4.2	3
53	Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 2686-2692	5.6	11
52	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 4051-4066	5.6	26
51	Semisynthetic sensor proteins enable metabolic assays at the point of care. <i>Science</i> , <b>2018</b> , 361, 1122-1126	35.3	78
50	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 4288-4298	5.6	61
49	Tiered Human Integrated Sequence Search Databases for Shotgun Proteomics. <i>Journal of Proteome Research</i> , <b>2016</b> , 15, 4091-4100	5.6	16
48	Development of data representation standards by the human proteome organization proteomics standards initiative. <i>Journal of the American Medical Informatics Association: JAMIA</i> , <b>2015</b> , 22, 495-506	8.6	42
47	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 223-6	44.5	2053
46	Controlled vocabularies and ontologies in proteomics: overview, principles and practice. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2014</b> , 1844, 98-107	4	26
45	A standardized framing for reporting protein identifications in mzIdentML 1.2. <i>Proteomics</i> , <b>2014</b> , 14, 2389-99	4.8	16
44	The Minimal Information about a Proteomics Experiment (MIAPE) from the Proteomics Standards Initiative. <i>Methods in Molecular Biology</i> , <b>2014</b> , 1072, 765-80	1.4	23
43	Guidelines for reporting quantitative mass spectrometry based experiments in proteomics. <i>Journal of Proteomics</i> , <b>2013</b> , 95, 84-8	3.9	37
42	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2013</b> , 2013, bat009	5	56
41	Standard guidelines for the chromosome-centric human proteome project. <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 2005-13	5.6	121
40	Ten years of standardizing proteomic data: a report on the HUPO-PSI Spring Workshop: April 12-14th, 2012, San Diego, USA. <i>Proteomics</i> , <b>2012</b> , 12, 2767-72	4.8	15

39	The mzIdentML data standard for mass spectrometry-based proteomics results. <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, M111.014381	7.6	150
38	TraML--a standard format for exchange of selected reaction monitoring transition lists. <i>Molecular and Cellular Proteomics</i> , <b>2012</b> , 11, R111.015040	7.6	58
37	mzML--a community standard for mass spectrometry data. <i>Molecular and Cellular Proteomics</i> , <b>2011</b> , 10, R110.000133	7.6	424
36	Guidelines for reporting the use of gel image informatics in proteomics. <i>Nature Biotechnology</i> , <b>2010</b> , 28, 655-6	44.5	21
35	A simple workflow to increase MS2 identification rate by subsequent spectral library search. <i>Proteomics</i> , <b>2009</b> , 9, 1731-6	4.8	27
34	Getting a grip on proteomics data - Proteomics Data Collection (ProDaC). <i>Proteomics</i> , <b>2009</b> , 9, 3928-33	4.8	14
33	Second Joint HUPO publication and Proteomics Standards Initiative workshop. <i>Proteomics</i> , <b>2009</b> , 9, 4426-8	4.8	6
32	Annual spring meeting of the Proteomics Standards Initiative. <i>Proteomics</i> , <b>2009</b> , 9, 4429-32	4.8	8
31	X-Rank: a robust algorithm for small molecule identification using tandem mass spectrometry. <i>Analytical Chemistry</i> , <b>2009</b> , 81, 7604-10	7.8	65
30	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 889-96	44.5	417
29	Guidelines for reporting the use of mass spectrometry in proteomics. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 860-1	44.5	72
28	Guidelines for reporting the use of mass spectrometry informatics in proteomics. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 862	44.5	55
27	Guidelines for reporting the use of gel electrophoresis in proteomics. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 863-4	44.5	48
26	The PSI-MOD community standard for representation of protein modification data. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 864-6	44.5	104
25	Five years of progress in the Standardization of Proteomics Data 4th Annual Spring Workshop of the HUPO-Proteomics Standards Initiative April 23-25, 2007 Ecole Nationale Supérieure (ENS), Lyon, France. <i>Proteomics</i> , <b>2007</b> , 7, 3436-40	4.8	42
24	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , <b>2007</b> , 25, 887-93	44.5	583
23	Automated reprocessing pipeline for searching heterogeneous mass spectrometric data of the HUPO Brain Proteome Project pilot phase. <i>Proteomics</i> , <b>2006</b> , 6, 5015-29	4.8	50
22	ESF workshop on Sustainability and Governance of Web and GRID Resources in Functional Genomics <i>Comparative and Functional Genomics</i> , <b>2005</b> , 6, 307-10		

21 Mass Spectrometry in Proteomics **2005**, 135-169

20	MSight: an image analysis software for liquid chromatography-mass spectrometry. <i>Proteomics</i> , <b>2005</b> , 5, 2381-4	4.8	125
19	Gold coating of non-conductive membranes before matrix-assisted laser desorption/ionization tandem mass spectrometric analysis prevents charging effect. <i>Rapid Communications in Mass Spectrometry</i> , <b>2005</b> , 19, 605-10	2.2	28
18	The ESF Programme on Functional Genomics Workshop on Data Integration in Functional Genomics: Application to Biological Pathways <i>Comparative and Functional Genomics</i> , <b>2004</b> , 5, 148-55		1
17	The molecular scanner: concept and developments. <i>Current Opinion in Biotechnology</i> , <b>2004</b> , 15, 17-23	11.4	26
16	Data mining for mass-spectra based diagnosis and biomarker discovery. <i>Drug Discovery Today Biosilico</i> , <b>2004</b> , 2, 214-222		8
15	Mass spectrometry-based proteomics: current status and potential use in clinical chemistry. <i>Clinical Chemistry and Laboratory Medicine</i> , <b>2003</b> , 41, 1540-51	5.9	26
14	Peptide mass fingerprinting peak intensity prediction: extracting knowledge from spectra. <i>Proteomics</i> , <b>2002</b> , 2, 1374-91	4.8	44
13	Molecular scanner experiment with human plasma: improving protein identification by using intensity distributions of matching peptide masses. <i>Proteomics</i> , <b>2002</b> , 2, 1413-25	4.8	14
12	Conference Report: The ESF Programme on Integrated Approaches for Functional Genomics. Workshop on Data Integration in Functional Genomics and Proteomics <i>Comparative and Functional Genomics</i> , <b>2002</b> , 3, 16-21		2
11	Proteome Analysis. <i>Methods and Principles in Medicinal Chemistry</i> , <b>2001</b> , 69-118	0.4	1
10	The mouse SWISS-2D PAGE database: a tool for proteomics study of diabetes and obesity. <i>Proteomics</i> , <b>2001</b> , 1, 136-63	4.8	143
9	A clinical molecular scanner to study human proteome complexity. <i>Novartis Foundation Symposium</i> , <b>2000</b> , 229, 33-8; discussion 38-40		2
8	Modeling peptide mass fingerprinting data using the atomic composition of peptides. <i>Electrophoresis</i> , <b>1999</b> , 20, 3527-34	3.6	71
7	Improving protein identification from peptide mass fingerprinting through a parameterized multi-level scoring algorithm and an optimized peak detection. <i>Electrophoresis</i> , <b>1999</b> , 20, 3535-50	3.6	117
6	A molecular scanner to automate proteomic research and to display proteome images. <i>Analytical Chemistry</i> , <b>1999</b> , 71, 4981-8	7.8	118
5	Toward a clinical molecular scanner for proteome research: parallel protein chemical processing before and during western blot. <i>Analytical Chemistry</i> , <b>1999</b> , 71, 4800-7	7.8	119
4	High-throughput mass spectrometric discovery of protein post-translational modifications. <i>Journal of Molecular Biology</i> , <b>1999</b> , 289, 645-57	6.5	266

3	Modeling peptide mass fingerprinting data using the atomic composition of peptides <b>1999</b> , 20, 3527	2
2	Universal Spectrum Identifier for mass spectra	5
1	Proteomics Standards Initiative Extended FASTA Format (PEFF)	1