

Pierre-Alain Binz

List of Publications by Citations

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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	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014 , 32, 223-6	44.5	2053
55	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007 , 25, 887-93	44.5	583
54	mzML--a community standard for mass spectrometry data. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, R110.000133	7.6	424
53	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008 , 26, 889-96	44.5	417
52	High-throughput mass spectrometric discovery of protein post-translational modifications. <i>Journal of Molecular Biology</i> , 1999 , 289, 645-57	6.5	266
51	The mzIdentML data standard for mass spectrometry-based proteomics results. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.014381	7.6	150
50	The mouse SWISS-2D PAGE database: a tool for proteomics study of diabetes and obesity. <i>Proteomics</i> , 2001 , 1, 136-63	4.8	143
49	MSight: an image analysis software for liquid chromatography-mass spectrometry. <i>Proteomics</i> , 2005 , 5, 2381-4	4.8	125
48	Standard guidelines for the chromosome-centric human proteome project. <i>Journal of Proteome Research</i> , 2012 , 11, 2005-13	5.6	121
47	Toward a clinical molecular scanner for proteome research: parallel protein chemical processing before and during western blot. <i>Analytical Chemistry</i> , 1999 , 71, 4800-7	7.8	119
46	A molecular scanner to automate proteomic research and to display proteome images. <i>Analytical Chemistry</i> , 1999 , 71, 4981-8	7.8	118
45	Improving protein identification from peptide mass fingerprinting through a parameterized multi-level scoring algorithm and an optimized peak detection. <i>Electrophoresis</i> , 1999 , 20, 3535-50	3.6	117
44	The PSI-MOD community standard for representation of protein modification data. <i>Nature Biotechnology</i> , 2008 , 26, 864-6	44.5	104
43	Semisynthetic sensor proteins enable metabolic assays at the point of care. <i>Science</i> , 2018 , 361, 1122-1126	39.3	78
42	Guidelines for reporting the use of mass spectrometry in proteomics. <i>Nature Biotechnology</i> , 2008 , 26, 860-1	44.5	72
41	Modeling peptide mass fingerprinting data using the atomic composition of peptides. <i>Electrophoresis</i> , 1999 , 20, 3527-34	3.6	71
40	X-Rank: a robust algorithm for small molecule identification using tandem mass spectrometry. <i>Analytical Chemistry</i> , 2009 , 81, 7604-10	7.8	65

39	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017 , 16, 4288-4298	5.6	61
38	TraML--a standard format for exchange of selected reaction monitoring transition lists. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, R111.015040	7.6	58
37	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat009	5	56
36	Guidelines for reporting the use of mass spectrometry informatics in proteomics. <i>Nature Biotechnology</i> , 2008 , 26, 862	44.5	55
35	Automated reprocessing pipeline for searching heterogeneous mass spectrometric data of the HUPO Brain Proteome Project pilot phase. <i>Proteomics</i> , 2006 , 6, 5015-29	4.8	50
34	Guidelines for reporting the use of gel electrophoresis in proteomics. <i>Nature Biotechnology</i> , 2008 , 26, 863-4	44.5	48
33	Peptide mass fingerprinting peak intensity prediction: extracting knowledge from spectra. <i>Proteomics</i> , 2002 , 2, 1374-91	4.8	44
32	Development of data representation standards by the human proteome organization proteomics standards initiative. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015 , 22, 495-506	8.6	42
31	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> , 2007 , 7, 3436-40	4.8	42
30	Guidelines for reporting quantitative mass spectrometry based experiments in proteomics. <i>Journal of Proteomics</i> , 2013 , 95, 84-8	3.9	37
29	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> , 2005 , 19, 605-10	2.2	28
28	A simple workflow to increase MS2 identification rate by subsequent spectral library search. <i>Proteomics</i> , 2009 , 9, 1731-6	4.8	27
27	Controlled vocabularies and ontologies in proteomics: overview, principles and practice. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 98-107	4	26
26	The molecular scanner: concept and developments. <i>Current Opinion in Biotechnology</i> , 2004 , 15, 17-23	11.4	26
25	Mass spectrometry-based proteomics: current status and potential use in clinical chemistry. <i>Clinical Chemistry and Laboratory Medicine</i> , 2003 , 41, 1540-51	5.9	26
24	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018 , 17, 4051-4069	6	26
23	The Minimal Information about a Proteomics Experiment (MIAPE) from the Proteomics Standards Initiative. <i>Methods in Molecular Biology</i> , 2014 , 1072, 765-80	1.4	23
22	Guidelines for reporting the use of gel image informatics in proteomics. <i>Nature Biotechnology</i> , 2010 , 28, 655-6	44.5	21

21	Tiered Human Integrated Sequence Search Databases for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2016 , 15, 4091-4100	5.6	16
20	A standardized framing for reporting protein identifications in mzIdentML 1.2. <i>Proteomics</i> , 2014 , 14, 2389-99	4.8	16
19	Ten years of standardizing proteomic data: a report on the HUPO-PSI Spring Workshop: April 12-14th, 2012, San Diego, USA. <i>Proteomics</i> , 2012 , 12, 2767-72	4.8	15
18	Getting a grip on proteomics data - Proteomics Data Collection (ProDaC). <i>Proteomics</i> , 2009 , 9, 3928-33	4.8	14
17	Molecular scanner experiment with human plasma: improving protein identification by using intensity distributions of matching peptide masses. <i>Proteomics</i> , 2002 , 2, 1413-25	4.8	14
16	Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , 2019 , 18, 2686-2692	4.8	11
15	Universal Spectrum Identifier for mass spectra. <i>Nature Methods</i> , 2021 , 18, 768-770	21.6	9
14	Annual spring meeting of the Proteomics Standards Initiative. <i>Proteomics</i> , 2009 , 9, 4429-32	4.8	8
13	Data mining for mass-spectra based diagnosis and biomarker discovery. <i>Drug Discovery Today Biosilico</i> , 2004 , 2, 214-222		8
12	Second Joint HUPO publication and Proteomics Standards Initiative workshop. <i>Proteomics</i> , 2009 , 9, 4426-28	4.8	6
11	Universal Spectrum Identifier for mass spectra		5
10	A new rat model of creatine transporter deficiency reveals behavioral disorder and altered brain metabolism. <i>Scientific Reports</i> , 2021 , 11, 1636	4.9	5
9	Exudative glutamine losses contribute to high needs after burn injury. <i>Journal of Parenteral and Enteral Nutrition</i> , 2021 ,	4.2	3
8	A clinical molecular scanner to study human proteome complexity. <i>Novartis Foundation Symposium</i> , 2000 , 229, 33-8; discussion 38-40		2
7	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> , 2002 , 3, 16-21		2
6	Modeling peptide mass fingerprinting data using the atomic composition of peptides 1999 , 20, 3527		2
5	The ESF Programme on Functional Genomics Workshop on Data Integration in Functional Genomics: Application to Biological Pathways <i>Comparative and Functional Genomics</i> , 2004 , 5, 148-55		1
4	Proteome Analysis. <i>Methods and Principles in Medicinal Chemistry</i> , 2001 , 69-118	0.4	1

- 3 Proteomics Standards Initiative Extended FASTA Format (PEFF) 1
- 2 ESF workshop on Sustainability and Governance of Web and GRID Resources in Functional Genomics *Comparative and Functional Genomics*, **2005**, 6, 307-10
- 1 Mass Spectrometry in Proteomics **2005**, 135-169