

# Pierre-Alain Binz

## List of Publications by Year in descending order

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Version: 2024-02-01

56  
papers

7,330  
citations

136950

32  
h-index

102487

66  
g-index

73  
all docs

73  
docs citations

73  
times ranked

13179  
citing authors

#	ARTICLE	IF	CITATIONS
1	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	17.5	2,505
2	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893.	17.5	694
3	mzML – a Community Standard for Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2011, 10, R110.000133.	3.8	555
4	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896.	17.5	506
5	High-throughput mass spectrometric discovery of protein post-translational modifications. <i>Journal of Molecular Biology</i> , 1999, 289, 645-657.	4.2	296
6	The mzIdentML Data Standard for Mass Spectrometry-Based Proteomics Results. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014381-1-M111.014381-10.	3.8	175
7	The mouse SWISS-2D PAGE database: a tool for proteomics study of diabetes and obesity. <i>Proteomics</i> , 2001, 1, 136-163.	2.2	155
8	Improving protein identification from peptide mass fingerprinting through a parameterized multi-level scoring algorithm and an optimized peak detection. <i>Electrophoresis</i> , 1999, 20, 3535-3550.	2.4	140
9	MSight: An image analysis software for liquid chromatography-mass spectrometry. <i>Proteomics</i> , 2005, 5, 2381-2384.	2.2	139
10	Standard Guidelines for the Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2012, 11, 2005-2013.	3.7	135
11	The PSI-MOD community standard for representation of protein modification data. <i>Nature Biotechnology</i> , 2008, 26, 864-866.	17.5	132
12	Toward a Clinical Molecular Scanner for Proteome Research: A Parallel Protein Chemical Processing before and during Western Blot. <i>Analytical Chemistry</i> , 1999, 71, 4800-4807.	6.5	128
13	A Molecular Scanner To Automate Proteomic Research and To Display Proteome Images. <i>Analytical Chemistry</i> , 1999, 71, 4981-4988.	6.5	127
14	Semisynthetic sensor proteins enable metabolic assays at the point of care. <i>Science</i> , 2018, 361, 1122-1126.	12.6	120
15	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017, 16, 4288-4298.	3.7	87
16	Guidelines for reporting the use of mass spectrometry in proteomics. <i>Nature Biotechnology</i> , 2008, 26, 860-861.	17.5	82
17	Modeling peptide mass fingerprinting data using the atomic composition of peptides. <i>Electrophoresis</i> , 1999, 20, 3527-3534.	2.4	79
18	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat009-bat009.	3.0	76

#	ARTICLE	IF	CITATIONS
19	X-Rank: A Robust Algorithm for Small Molecule Identification Using Tandem Mass Spectrometry. <i>Analytical Chemistry</i> , 2009, 81, 7604-7610.	6.5	72
20	TraML – A Standard Format for Exchange of Selected Reaction Monitoring Transition Lists. <i>Molecular and Cellular Proteomics</i> , 2012, 11, R111.015040.	3.8	65
21	Guidelines for reporting the use of mass spectrometry informatics in proteomics. <i>Nature Biotechnology</i> , 2008, 26, 862-862.	17.5	62
22	Guidelines for reporting the use of gel electrophoresis in proteomics. <i>Nature Biotechnology</i> , 2008, 26, 863-864.	17.5	61
23	Automated reprocessing pipeline for searching heterogeneous mass spectrometric data of the HUPO Brain Proteome Project pilot phase. <i>Proteomics</i> , 2006, 6, 5015-5029.	2.2	56
24	Peptide mass fingerprinting peak intensity prediction: Extracting knowledge from spectra. <i>Proteomics</i> , 2002, 2, 1374-1391.	2.2	54
25	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.	4.4	54
26	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	3.7	47
27	Universal Spectrum Identifier for mass spectra. <i>Nature Methods</i> , 2021, 18, 768-770.	19.0	47
28	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, 3436-3440.	2.2	46
29	Guidelines for reporting quantitative mass spectrometry based experiments in proteomics. <i>Journal of Proteomics</i> , 2013, 95, 84-88.	2.4	46
30	Controlled vocabularies and ontologies in proteomics: Overview, principles and practice. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 98-107.	2.3	36
31	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, 605-610.	1.5	35
32	Mass Spectrometry-Based Proteomics: Current Status and Potential Use in Clinical Chemistry. <i>Clinical Chemistry and Laboratory Medicine</i> , 2003, 41, 1540-51.	2.3	33
33	A simple workflow to increase MS2 identification rate by subsequent spectral library search. <i>Proteomics</i> , 2009, 9, 1731-1736.	2.2	32
34	The Minimal Information About a Proteomics Experiment (MIAPE) from the Proteomics Standards Initiative. <i>Methods in Molecular Biology</i> , 2014, 1072, 765-780.	0.9	31
35	The molecular scanner: concept and developments. <i>Current Opinion in Biotechnology</i> , 2004, 15, 17-23.	6.6	28
36	Tiered Human Integrated Sequence Search Databases for Shotgun Proteomics. <i>Journal of Proteome Research</i> , 2016, 15, 4091-4100.	3.7	24

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37	A standardized framing for reporting protein identifications in mzIdentML 1.2. <i>Proteomics</i> , 2014, 14, 2389-2399.	2.2	23
38	Guidelines for reporting the use of gel image informatics in proteomics. <i>Nature Biotechnology</i> , 2010, 28, 655-656.	17.5	22
39	Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , 2019, 18, 2686-2692.	3.7	22
40	A new rat model of creatine transporter deficiency reveals behavioral disorder and altered brain metabolism. <i>Scientific Reports</i> , 2021, 11, 1636.	3.3	18
41	Molecular scanner experiment with human plasma: Improving protein identification by using intensity distributions of matching peptide masses. <i>Proteomics</i> , 2002, 2, 1413-1425.	2.2	16
42	Ten Years of Standardizing Proteomic Data: A Report on the HUPOâ€PSI Spring Workshop. <i>Proteomics</i> , 2012, 12, 2767-2772.	2.2	16
43	Getting a grip on proteomics data â€“ Proteomics Data Collection (ProDaC). <i>Proteomics</i> , 2009, 9, 3928-3933.	2.2	15
44	Proteomics Standards Initiativeâ€™s ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidoforms. <i>Journal of Proteome Research</i> , 2022, 21, 1189-1195.	3.7	14
45	Report from the HarmoSter study: impact of calibration on comparability of LC-MS/MS measurement of circulating cortisol, 17OH-progesterone and aldosterone. <i>Clinical Chemistry and Laboratory Medicine</i> , 2022, 60, 726-739.	2.3	11
46	Data mining for mass-spectra based diagnosis and biomarker discovery. <i>Drug Discovery Today Biosilico</i> , 2004, 2, 214-222.	0.7	10
47	Exudative glutamine losses contribute to high needs after burn injury. <i>Journal of Parenteral and Enteral Nutrition</i> , 2022, 46, 782-788.	2.6	10
48	Annual Spring Meeting of the Proteomics Standards Initiative. <i>Proteomics</i> , 2009, 9, 4429-4432.	2.2	9
49	Creatine transporterâ€™ deficient rat model shows motor dysfunction, cerebellar alterations, and muscle creatine deficiency without muscle atrophy. <i>Journal of Inherited Metabolic Disease</i> , 2022, 45, 278-291.	3.6	7
50	Second Joint HUPO Publication and Proteomics Standards Initiative Workshop. <i>Proteomics</i> , 2009, 9, 4426-4428.	2.2	6
51	Conference Report: The ESF Programme on Integrated Approaches for Functional Genomics. Workshop on â€“Data Integration in Functional Genomics and Proteomicsâ€™. <i>Comparative and Functional Genomics</i> , 2002, 3, 16-21.	2.0	2
52	A Clinical Molecular Scanner to Study Human Proteome Complexity. <i>Novartis Foundation Symposium</i> , 2008, 229, 33-40.	1.1	2
53	Modeling peptide mass fingerprinting data using the atomic composition of peptides. <i>Electrophoresis</i> , 1999, 20, 3527-3534.	2.4	2
54	The ESF Programme on Functional Genomics Workshop on â€“Data Integration in Functional Genomics: Application to Biological Pathwaysâ€™. <i>Comparative and Functional Genomics</i> , 2004, 5, 148-155.	2.0	1

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55	ESF Workshop on "Sustainability and Governance of Web and GRID Resources in Functional Genomics". Comparative and Functional Genomics, 2005, 6, 307-310.	2.0	0
56	Mass Spectrometry in Proteomics. , 2005, , 135-169.		0