Pierre-Alain Binz

List of Publications by Year
in descending order

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	Exudative glutamine losses contribute to high needs after burn injury. Journal of Parenteral and Enteral Nutrition, 2022, 46, 782-788.	2.6	10
2	Report from the HarmoSter study: impact of calibration on comparability of LC-MS/MS measurement of circulating cortisol, 17OH-progesterone and aldosterone. Clinical Chemistry and Laboratory Medicine, 2022, 60, 726-739.	2.3	11
3	Proteomics Standards Initiative's ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidoforms. Journal of Proteome Research, 2022, 21, 1189-1195.	3.7	14
4	Creatine transporter–deficient rat model shows motor dysfunction, cerebellar alterations, and muscle creatine deficiency without muscle atrophy. Journal of Inherited Metabolic Disease, 2022, 45, 278-291.	3.6	7
5	A new rat model of creatine transporter deficiency reveals behavioral disorder and altered brain metabolism. Scientific Reports, 2021, 11, 1636.	3.3	18
6	Universal Spectrum Identifier for mass spectra. Nature Methods, 2021, 18, 768-770.	19.0	47
7	Proteomics Standards Initiative Extended FASTA Format. Journal of Proteome Research, 2019, 18, 2686-2692.	3.7	22
8	Expanding the Use of Spectral Libraries in Proteomics. Journal of Proteome Research, 2018, 17, 4051-4060.	3.7	47
9	Semisynthetic sensor proteins enable metabolic assays at the point of care. Science, 2018, 361, 1122-1126.	12.6	120
10	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. Journal of Proteome Research, 2017, 16, 4288-4298.	3.7	87
11	Tiered Human Integrated Sequence Search Databases for Shotgun Proteomics. Journal of Proteome Research, 2016, 15, 4091-4100.	3.7	24
12	Development of data representation standards by the human proteome organization proteomics standards initiative. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 495-506.	4.4	54
13	A standardized framing for reporting protein identifications in mzIdentML 1.2. Proteomics, 2014, 14, 2389-2399.	2.2	23
14	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. Nature Biotechnology, 2014, 32, 223-226.	17.5	2,505
15	Controlled vocabularies and ontologies in proteomics: Overview, principles and practice. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 98-107.	2.3	36
16	The Minimal Information About a Proteomics Experiment (MIAPE) from the Proteomics Standards Initiative. Methods in Molecular Biology, 2014, 1072, 765-780.	0.9	31
17	Guidelines for reporting quantitative mass spectrometry based experiments in proteomics. Journal of Proteomics, 2013, 95, 84-88.	2.4	46
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	The mzIdentML Data Standard for Mass Spectrometry-Based Proteomics Results. Molecular and Cellular Proteomics, 2012, 11, M111.014381-1-M111.014381-10.	3.8	175
20	TraMLâ€"A Standard Format for Exchange of Selected Reaction Monitoring Transition Lists. Molecular and Cellular Proteomics, 2012, 11, R111.015040.	3.8	65
21	Standard Guidelines for the Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2012, 11, 2005-2013.	3.7	135
22	Ten Years of Standardizing Proteomic Data: A Report on the HUPOâ€PSI Spring Workshop. Proteomics, 2012, 12, 2767-2772.	2.2	16
23	mzMLâ€"a Community Standard for Mass Spectrometry Data. Molecular and Cellular Proteomics, 2011, 10, R110.000133.	3.8	555
24	Guidelines for reporting the use of gel image informatics in proteomics. Nature Biotechnology, 2010, 28, 655-656.	17.5	22
25	A simple workflow to increase MS2 identification rate by subsequent spectral library search. Proteomics, 2009, 9, 1731-1736.	2.2	32
26	Getting a grip on proteomics data â€" Proteomics Data Collection (ProDaC). Proteomics, 2009, 9, 3928-3933.	2.2	15
27	Second Joint HUPO Publication and Proteomics Standards Initiative Workshop. Proteomics, 2009, 9, 4426-4428.	2.2	6
28	Annual Spring Meeting of the Proteomics Standards Initiative. Proteomics, 2009, 9, 4429-4432.	2.2	9
29	X-Rank: A Robust Algorithm for Small Molecule Identification Using Tandem Mass Spectrometry. Analytical Chemistry, 2009, 81, 7604-7610.	6.5	72
30	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. Nature Biotechnology, 2008, 26, 889-896.	17.5	506
31	Guidelines for reporting the use of mass spectrometry in proteomics. Nature Biotechnology, 2008, 26, 860-861.	17.5	82
32	Guidelines for reporting the use of mass spectrometry informatics in proteomics. Nature Biotechnology, 2008, 26, 862-862.	17.5	62
33	Guidelines for reporting the use of gel electrophoresis in proteomics. Nature Biotechnology, 2008, 26, 863-864.	17.5	61
34	The PSI-MOD community standard for representation of protein modification data. Nature Biotechnology, 2008, 26, 864-866.	17.5	132
35	A Clinical Molecular Scanner to Study Human Proteome Complexity. Novartis Foundation Symposium, 2008, 229, 33-40.	1.1	2
36	Five years of progress in the Standardization of Proteomics Data 4th Annual Spring Workshop of the HUPO-Proteomics Standards Initiative April 23â€"25, 2007 Ecole Nationale SupÃ©rieure (ENS), Lyon, France. Proteomics, 2007, 7, 3436-3440.	2.2	46

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37	The minimum information about a proteomics experiment (MIAPE). Nature Biotechnology, 2007, 25, 887-893.	17.5	694
38	Automated reprocessing pipeline for searching heterogeneous mass spectrometric data of the HUPO Brain Proteome Project pilot phase. Proteomics, 2006, 6, 5015-5029.	2.2	56
39	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
40	Mass Spectrometry in Proteomics. , 2005, , 135-169.		0
41	MSight: An image analysis software for liquid chromatography-mass spectrometry. Proteomics, 2005, 5, 2381-2384.	2.2	139
42	Gold coating of non-conductive membranes before matrix-assisted laser desorption/ionization tandem mass spectrometric analysis prevents charging effect. Rapid Communications in Mass Spectrometry, 2005, 19, 605-610.	1.5	35
43	The ESF Programme on Functional Genomics Workshop on 'Data Integration in Functional Genomics: Application to Biological Pathways'. Comparative and Functional Genomics, 2004, 5, 148-155.	2.0	1
44	The molecular scanner: concept and developments. Current Opinion in Biotechnology, 2004, 15, 17-23.	6.6	28
45	Data mining for mass-spectra based diagnosis and biomarker discovery. Drug Discovery Today Biosilico, 2004, 2, 214-222.	0.7	10
46	Mass Spectrometry-Based Proteomics: Current Status and Potential Use in Clinical Chemistry. Clinical Chemistry and Laboratory Medicine, 2003, 41, 1540-51.	2.3	33
47	Peptide mass fingerprinting peak intensity prediction: Extracting knowledge from spectra. Proteomics, 2002, 2, 1374-1391.	2.2	54
48	Molecular scanner experiment with human plasma: Improving protein identification by using intensity distributions of matching peptide masses. Proteomics, 2002, 2, 1413-1425.	2.2	16
49	Conference Report: The ESF Programme on Integrated Approaches for Functional Genomics. Workshop on 'Data Integration in Functional Genomics and Proteomics'. Comparative and Functional Genomics, 2002, 3, 16-21.	2.0	2
50	The mouse SWISS-2D PAGE database: a tool for proteomics study of diabetes and obesity. Proteomics, 2001, 1, 136-163.	2.2	155
51	Modeling peptide mass fingerprinting data using the atomic composition of peptides. Electrophoresis, 1999, 20, 3527-3534.	2.4	79
52	Improving protein identification from peptide mass fingerprinting through a parameterized multi-level scoring algorithm and an optimized peak detection. Electrophoresis, 1999, 20, 3535-3550.	2.4	140
53	A Molecular Scanner To Automate Proteomic Research and To Display Proteome Images. Analytical Chemistry, 1999, 71, 4981-4988.	6.5	127
54	Toward a Clinical Molecular Scanner for Proteome Research: Parallel Protein Chemical Processing before and during Western Blot. Analytical Chemistry, 1999, 71, 4800-4807.	6.5	128

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55	High-throughput mass spectrometric discovery of protein post-translational modifications. Journal of Molecular Biology, 1999, 289, 645-657.	4.2	296
56	Modeling peptide mass fingerprinting data using the atomic composition of peptides. Electrophoresis, 1999, 20, 3527-3534.	2.4	2