

# Nuno Bandeira

## List of Publications by Year in descending order

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Version: 2024-02-01

89  
papers

14,272  
citations

57681

46  
h-index

51423

90  
g-index

99  
all docs

99  
docs citations

99  
times ranked

22474  
citing authors

#	ARTICLE	IF	CITATIONS
1	GNPS Dashboard: collaborative exploration of mass spectrometry data in the web browser. <i>Nature Methods</i> , 2022, 19, 134-136.	9.0	35
2	Proteomics Standards Initiative's ProForma 2.0: Unifying the Encoding of Proteoforms and Peptidoforms. <i>Journal of Proteome Research</i> , 2022, 21, 1189-1195.	1.8	14
3	Index-based, High-dimensional, Cosine Threshold Querying with Optimality Guarantees. <i>Theory of Computing Systems</i> , 2021, 65, 42-83.	0.7	2
4	Data Management of Sensitive Human Proteomics Data: Current Practices, Recommendations, and Perspectives for the Future. <i>Molecular and Cellular Proteomics</i> , 2021, 20, 100071.	2.5	25
5	A Multi-Omics Characterization of the Natural Product Potential of Tropical Filamentous Marine Cyanobacteria. <i>Marine Drugs</i> , 2021, 19, 20.	2.2	19
6	Open Science Resources for the Mass Spectrometry-Based Analysis of SARS-CoV-2. <i>Journal of Proteome Research</i> , 2021, 20, 1464-1475.	1.8	11
7	Universal Spectrum Identifier for mass spectra. <i>Nature Methods</i> , 2021, 18, 768-770.	9.0	47
8	Quick-start infrastructure for untargeted metabolomics analysis in GNPS. <i>Nature Metabolism</i> , 2021, 3, 880-882.	5.1	11
9	A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , 2021, 12, 5854.	5.8	45
10	Progress Identifying and Analyzing the Human Proteome: 2021 Metrics from the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2021, 20, 5227-5240.	1.8	30
11	The ProteomeXchange consortium in 2020: enabling "big data" approaches in proteomics. <i>Nucleic Acids Research</i> , 2020, 48, D1145-D1152.	6.5	491
12	Untargeted mass spectrometry-based metabolomics approach unveils molecular changes in raw and processed foods and beverages. <i>Food Chemistry</i> , 2020, 302, 125290.	4.2	52
13	Mass spectrometry searches using MASST. <i>Nature Biotechnology</i> , 2020, 38, 23-26.	9.4	160
14	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020, 11, 5301.	5.8	152
15	Feature-based molecular networking in the GNPS analysis environment. <i>Nature Methods</i> , 2020, 17, 905-908.	9.0	650
16	MassIVE.quant: a community resource of quantitative mass spectrometry-based proteomics datasets. <i>Nature Methods</i> , 2020, 17, 981-984.	9.0	66
17	Research on the Human Proteome Reaches a Major Milestone: >90% of Predicted Human Proteins Now Credibly Detected, According to the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2020, 19, 4735-4746.	1.8	38
18	ReDU: a framework to find and reanalyze public mass spectrometry data. <i>Nature Methods</i> , 2020, 17, 901-904.	9.0	79

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19	Insights from the First Phosphopeptide Challenge of the MS Resource Pillar of the HUPO Human Proteome Project. <i>Journal of Proteome Research</i> , 2020, 19, 4754-4765.	1.8	7
20	Reproducible molecular networking of untargeted mass spectrometry data using GNPS. <i>Nature Protocols</i> , 2020, 15, 1954-1991.	5.5	344
21	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 3.0. <i>Journal of Proteome Research</i> , 2019, 18, 4108-4116.	1.8	82
22	Molecular and Microbial Microenvironments in Chronically Diseased Lungs Associated with Cystic Fibrosis. <i>MSystems</i> , 2019, 4, .	1.7	23
23	Neutrophilic proteolysis in the cystic fibrosis lung correlates with a pathogenic microbiome. <i>Microbiome</i> , 2019, 7, 23.	4.9	53
24	Interactome Rewiring Following Pharmacological Targeting of BET Bromodomains. <i>Molecular Cell</i> , 2019, 73, 621-638.e17.	4.5	135
25	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	1.8	47
26	ProteinExplorer: A Repository-Scale Resource for Exploration of Protein Detection in Public Mass Spectrometry Data Sets. <i>Journal of Proteome Research</i> , 2018, 17, 4227-4234.	1.8	17
27	Assembling the Community-Scale Discoverable Human Proteome. <i>Cell Systems</i> , 2018, 7, 412-421.e5.	2.9	136
28	Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , 2017, 35, 406-409.	9.4	159
29	Three-Dimensional Microbiome and Metabolome Cartography of a Diseased Human Lung. <i>Cell Host and Microbe</i> , 2017, 22, 705-716.e4.	5.1	111
30	Significance estimation for large scale metabolomics annotations by spectral matching. <i>Nature Communications</i> , 2017, 8, 1494.	5.8	128
31	De Novo MS/MS Sequencing of Native Human Antibodies. <i>Journal of Proteome Research</i> , 2017, 16, 45-54.	1.8	41
32	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. <i>Nucleic Acids Research</i> , 2017, 45, D1100-D1106.	6.5	860
33	Digitizing mass spectrometry data to explore the chemical diversity and distribution of marine cyanobacteria and algae. <i>ELife</i> , 2017, 6, .	2.8	33
34	SweetNET: A Bioinformatics Workflow for Glycopeptide MS/MS Spectral Analysis. <i>Journal of Proteome Research</i> , 2016, 15, 2826-2840.	1.8	49
35	Identifying Urinary and Serum Exosome Biomarkers for Radiation Exposure Using a Data Dependent Acquisition and SWATH-MS Combined Workflow. <i>International Journal of Radiation Oncology Biology Physics</i> , 2016, 96, 566-577.	0.4	29
36	Multi-species Identification of Polymorphic Peptide Variants via Propagation in Spectral Networks. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 3501-3512.	2.5	6

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37	Data Independent Acquisition analysis in ProHits 4.0. <i>Journal of Proteomics</i> , 2016, 149, 64-68.	1.2	66
38	Mass Spectrometry-Based Visualization of Molecules Associated with Human Habitats. <i>Analytical Chemistry</i> , 2016, 88, 10775-10784.	3.2	44
39	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. <i>Nature Biotechnology</i> , 2016, 34, 828-837.	9.4	2,802
40	Lifestyle chemistries from phones for individual profiling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7645-E7654.	3.3	55
41	SPLASH, a hashed identifier for mass spectra. <i>Nature Biotechnology</i> , 2016, 34, 1099-1101.	9.4	61
42	On the privacy risks of sharing clinical proteomics data. <i>AMIA Summits on Translational Science Proceedings</i> , 2016, 2016, 122-31.	0.4	3
43	Neuropeptidomics Mass Spectrometry Reveals Signaling Networks Generated by Distinct Protease Pathways in Human Systems. <i>Journal of the American Society for Mass Spectrometry</i> , 2015, 26, 1970-1980.	1.2	23
44	The Generating Function Approach for Peptide Identification in Spectral Networks. <i>Journal of Computational Biology</i> , 2015, 22, 353-366.	0.8	5
45	Molecular cartography of the human skin surface in 3D. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2120-9.	3.3	288
46	Molecular Networking and Pattern-Based Genome Mining Improves Discovery of Biosynthetic Gene Clusters and their Products from <i>Salinispora</i> Species. <i>Chemistry and Biology</i> , 2015, 22, 460-471.	6.2	150
47	MSPLIT-DIA: sensitive peptide identification for data-independent acquisition. <i>Nature Methods</i> , 2015, 12, 1106-1108.	9.0	113
48	MixGF: Spectral Probabilities for Mixture Spectra from more than One Peptide. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 3688-3697.	2.5	17
49	The mzTab Data Exchange Format: Communicating Mass-spectrometry-based Proteomics and Metabolomics Experimental Results to a Wider Audience. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 2765-2775.	2.5	130
50	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	9.4	2,505
51	Proteome Informatics Research Group (iPRG)_2012: A Study on Detecting Modified Peptides in a Complex Mixture. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 360-371.	2.5	20
52	Automated Genome Mining of Ribosomal Peptide Natural Products. <i>ACS Chemical Biology</i> , 2014, 9, 1545-1551.	1.6	133
53	Combinatorial Approach for Large-scale Identification of Linked Peptides from Tandem Mass Spectrometry Spectra. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1128-1136.	2.5	19
54	Expanding Proteome Coverage with Orthogonal-specificity $\hat{\pm}$ -Lytic Proteases. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 823-835.	2.5	54

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55	A Turn-Key Approach for Large-Scale Identification of Complex Posttranslational Modifications. <i>Journal of Proteome Research</i> , 2014, 13, 1190-1199.	1.8	7
56	Sequencing-Grade <i>De novo</i> Analysis of MS/MS Triplets (CID/HCD/ETD) From Overlapping Peptides. <i>Journal of Proteome Research</i> , 2013, 12, 2846-2857.	1.8	63
57	Spectral Library Generating Function for Assessing Spectrum-Spectrum Match Significance. <i>Journal of Proteome Research</i> , 2013, 12, 3944-3951.	1.8	23
58	Neutron-encoded Signatures Enable Product Ion Annotation From Tandem Mass Spectra. <i>Molecular and Cellular Proteomics</i> , 2013, 12, 3812-3823.	2.5	20
59	MS/MS networking guided analysis of molecule and gene cluster families. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E2611-20.	3.3	250
60	Accurate Mass Spectrometry Based Protein Quantification via Shared Peptides. <i>Journal of Computational Biology</i> , 2012, 19, 337-348.	0.8	40
61	Shotgun Protein Sequencing with Meta-contig Assembly. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1084-1096.	2.5	25
62	Fast Multi-blind Modification Search through Tandem Mass Spectrometry. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.010199.	2.5	143
63	Interkingdom metabolic transformations captured by microbial imaging mass spectrometry. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 13811-13816.	3.3	220
64	The spectral networks paradigm in high throughput mass spectrometry. <i>Molecular BioSystems</i> , 2012, 8, 2535.	2.9	79
65	Quantitative Proteomics Reveal ATM Kinase-dependent Exchange in DNA Damage Response Complexes. <i>Journal of Proteome Research</i> , 2012, 11, 4983-4991.	1.8	24
66	Peptide Identification by Tandem Mass Spectrometry with Alternate Fragmentation Modes. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 550-557.	2.5	63
67	False discovery rates in spectral identification. <i>BMC Bioinformatics</i> , 2012, 13, S2.	1.2	118
68	Mass spectral molecular networking of living microbial colonies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, E1743-52.	3.3	804
69	Advancing Next-Generation Proteomics through Computational Research. <i>Journal of Proteome Research</i> , 2011, 10, 2895-2895.	1.8	4
70	Peptide Identification by Database Search of Mixture Tandem Mass Spectra. <i>Molecular and Cellular Proteomics</i> , 2011, 10, M111.010017.	2.5	25
71	Spectral archives: extending spectral libraries to analyze both identified and unidentified spectra. <i>Nature Methods</i> , 2011, 8, 587-591.	9.0	86
72	Target-Decoy Approach and False Discovery Rate: When Things May Go Wrong. <i>Journal of the American Society for Mass Spectrometry</i> , 2011, 22, 1111-1120.	1.2	134

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73	Connecting Chemotypes and Phenotypes of Cultured Marine Microbial Assemblages by Imaging Mass Spectrometry. <i>Angewandte Chemie - International Edition</i> , 2011, 50, 5839-5842.	7.2	53
74	Cover Picture: Connecting Chemotypes and Phenotypes of Cultured Marine Microbial Assemblages by Imaging Mass Spectrometry ( <i>Angew. Chem. Int. Ed.</i> 26/2011). <i>Angewandte Chemie - International Edition</i> , 2011, 50, 5773-5773.	7.2	0
75	Protein Identification by Spectral Networks Analysis. <i>Methods in Molecular Biology</i> , 2011, 694, 151-168.	0.4	8
76	Neuropeptidomic Components Generated by Proteomic Functions in Secretory Vesicles for Cell-Cell Communication. <i>AAPS Journal</i> , 2010, 12, 635-645.	2.2	23
77	Peptide Identification from Mixture Tandem Mass Spectra. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1476-1485.	2.5	67
78	Clostridiolysin S, a Post-translationally Modified Biotxin from <i>Clostridium botulinum</i> . <i>Journal of Biological Chemistry</i> , 2010, 285, 28220-28228.	1.6	56
79	The Generating Function of CID, ETD, and CID/ETD Pairs of Tandem Mass Spectra: Applications to Database Search. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 2840-2852.	2.5	226
80	Spectral Profiles, a Novel Representation of Tandem Mass Spectra and Their Applications for de Novo Peptide Sequencing and Identification. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 1391-1400.	2.5	37
81	Spectral Dictionaries. <i>Molecular and Cellular Proteomics</i> , 2009, 8, 53-69.	2.5	87
82	Dereplication and de novo sequencing of nonribosomal peptides. <i>Nature Methods</i> , 2009, 6, 596-599.	9.0	81
83	Interpretation of Tandem Mass Spectra Obtained from Cyclic Nonribosomal Peptides. <i>Analytical Chemistry</i> , 2009, 81, 4200-4209.	3.2	83
84	Automated de novo protein sequencing of monoclonal antibodies. <i>Nature Biotechnology</i> , 2008, 26, 1336-1338.	9.4	114
85	Clustering Millions of Tandem Mass Spectra. <i>Journal of Proteome Research</i> , 2008, 7, 113-122.	1.8	230
86	Multi-spectra peptide sequencing and its applications to multistage mass spectrometry. <i>Bioinformatics</i> , 2008, 24, i416-i423.	1.8	25
87	Protein identification by spectral networks analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 6140-6145.	3.3	157
88	Shotgun Protein Sequencing. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1123-1134.	2.5	80
89	Shotgun Protein Sequencing by Tandem Mass Spectra Assembly. <i>Analytical Chemistry</i> , 2004, 76, 7221-7233.	3.2	47