

Yasset Perez-Riverol

List of Publications by Year in descending order

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Version: 2024-02-01

97
papers

21,215
citations

109137

35
h-index

40881

93
g-index

123
all docs

123
docs citations

123
times ranked

38133
citing authors

#	ARTICLE	IF	CITATIONS
1	The PRIDE database resources in 2022: a hub for mass spectrometry-based proteomics evidences. <i>Nucleic Acids Research</i> , 2022, 50, D543-D552.	6.5	2,766
2	Generation of ENSEMBL-based proteogenomics databases boosts the identification of non-canonical peptides. <i>Bioinformatics</i> , 2022, 38, 1470-1472.	1.8	16
3	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
4	A comprehensive LFQ benchmark dataset on modern day acquisition strategies in proteomics. <i>Scientific Data</i> , 2022, 9, 126.	2.4	20
5	A Comprehensive Evaluation of Consensus Spectrum Generation Methods in Proteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1566-1574.	1.8	2
6	Method for Independent Estimation of the False Localization Rate for Phosphoproteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1603-1615.	1.8	14
7	Deep learning embedder method and tool for mass spectra similarity search. <i>Journal of Proteomics</i> , 2021, 232, 104070.	1.2	10
8	BioContainers Registry: Searching Bioinformatics and Proteomics Tools, Packages, and Containers. <i>Journal of Proteome Research</i> , 2021, 20, 2056-2061.	1.8	19
9	User-friendly, scalable tools and workflows for single-cell RNA-seq analysis. <i>Nature Methods</i> , 2021, 18, 327-328.	9.0	26
10	The European Bioinformatics Community for Mass Spectrometry (EuBICâ€MS): an open community for bioinformatics training and research. <i>Rapid Communications in Mass Spectrometry</i> , 2021, , e9087.	0.7	3
11	An integrated landscape of protein expression in human cancer. <i>Scientific Data</i> , 2021, 8, 115.	2.4	38
12	Universal Spectrum Explorer: A Standalone (Web-)Application for Cross-Resource Spectrum Comparison. <i>Journal of Proteome Research</i> , 2021, 20, 3388-3394.	1.8	22
13	Universal Spectrum Identifier for mass spectra. <i>Nature Methods</i> , 2021, 18, 768-770.	9.0	47
14	Integrative analysis of genomic variants reveals new associations of candidate haploinsufficient genes with congenital heart disease. <i>PLoS Genetics</i> , 2021, 17, e1009679.	1.5	17
15	MaxDIA enables library-based and library-free data-independent acquisition proteomics. <i>Nature Biotechnology</i> , 2021, 39, 1563-1573.	9.4	115
16	A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , 2021, 12, 5854.	5.8	45
17	Mapping the Melanoma Plasma Proteome (MPP) Using Single-Shot Proteomics Interfaced with the WiMT Database. <i>Cancers</i> , 2021, 13, 6224.	1.7	4
18	The ProteomeXchange consortium in 2020: enabling â€big dataâ€ approaches in proteomics. <i>Nucleic Acids Research</i> , 2020, 48, D1145-D1152.	6.5	491

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19	Novel functional proteins coded by the human genome discovered in metastases of melanoma patients. <i>Cell Biology and Toxicology</i> , 2020, 36, 261-272.	2.4	9
20	Scalable Data Analysis in Proteomics and Metabolomics Using BioContainers and Workflows Engines. <i>Proteomics</i> , 2020, 20, e1900147.	1.3	24
21	ThermoRawFileParser: Modular, Scalable, and Cross-Platform RAW File Conversion. <i>Journal of Proteome Research</i> , 2020, 19, 537-542.	1.8	144
22	Toward a Sample Metadata Standard in Public Proteomics Repositories. <i>Journal of Proteome Research</i> , 2020, 19, 3906-3909.	1.8	20
23	MassIVE.quant: a community resource of quantitative mass spectrometry-based proteomics datasets. <i>Nature Methods</i> , 2020, 17, 981-984.	9.0	66
24	CHAPTER 19. Cross-platform Software Development and Distribution with Bioconda and BioContainers. <i>New Developments in Mass Spectrometry</i> , 2020, , 415-426.	0.2	1
25	The omics discovery REST interface. <i>Nucleic Acids Research</i> , 2020, 48, W380-W384.	6.5	3
26	Quantifying the impact of public omics data. <i>Nature Communications</i> , 2019, 10, 3512.	5.8	79
27	Sodium dodecyl sulfate free gel electrophoresis/electroelution sorting for peptide fractionation. <i>Journal of Separation Science</i> , 2019, 42, 3712-3717.	1.3	4
28	mzTab-M: A Data Standard for Sharing Quantitative Results in Mass Spectrometry Metabolomics. <i>Analytical Chemistry</i> , 2019, 91, 3302-3310.	3.2	43
29	Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , 2019, 18, 2686-2692.	1.8	22
30	Spectral Clustering Improves Label-Free Quantification of Low-Abundant Proteins. <i>Journal of Proteome Research</i> , 2019, 18, 1477-1485.	1.8	13
31	The PRIDE database and related tools and resources in 2019: improving support for quantification data. <i>Nucleic Acids Research</i> , 2019, 47, D442-D450.	6.5	6,449
32	Protein Inference Using PIA Workflows and PSI Standard File Formats. <i>Journal of Proteome Research</i> , 2019, 18, 741-747.	1.8	33
33	An "on-matrix" digestion procedure for AP-MS experiments dissects the interplay between complex-conserved and serotype-specific reactivities in Dengue virus-human plasma interactome. <i>Journal of Proteomics</i> , 2019, 193, 71-84.	1.2	3
34	Response to "Comparison and Evaluation of Clustering Algorithms for Tandem Mass Spectra". <i>Journal of Proteome Research</i> , 2018, 17, 1993-1996.	1.8	9
35	A Protein Standard That Emulates Homology for the Characterization of Protein Inference Algorithms. <i>Journal of Proteome Research</i> , 2018, 17, 1879-1886.	1.8	22
36	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018, 17, 4051-4060.	1.8	47

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37	ABRF Proteome Informatics Research Group (iPRG) 2016 Study: Inferring Proteoforms from Bottom-up Proteomics Data. <i>Journal of Biomolecular Techniques</i> , 2018, 29, 39-45.	0.8	6
38	Bioconda: sustainable and comprehensive software distribution for the life sciences. <i>Nature Methods</i> , 2018, 15, 475-476.	9.0	714
39	Mass spectrometry evaluation of a neuroblastoma SH-SY5Y cell culture protocol. <i>Analytical Biochemistry</i> , 2018, 559, 51-54.	1.1	2
40	Future Prospects of Spectral Clustering Approaches in Proteomics. <i>Proteomics</i> , 2018, 18, e1700454.	1.3	15
41	Recommendations for the packaging and containerizing of bioinformatics software. <i>F1000Research</i> , 2018, 7, 742.	0.8	27
42	Recommendations for the packaging and containerizing of bioinformatics software. <i>F1000Research</i> , 2018, 7, 742.	0.8	29
43	Synthetic human proteomes for accelerating protein research. <i>Nature Methods</i> , 2017, 14, 240-242.	9.0	6
44	Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , 2017, 35, 406-409.	9.4	159
45	BioContainers: an open-source and community-driven framework for software standardization. <i>Bioinformatics</i> , 2017, 33, 2580-2582.	1.8	205
46	Enhanced Missing Proteins Detection in NCI60 Cell Lines Using an Integrative Search Engine Approach. <i>Journal of Proteome Research</i> , 2017, 16, 4374-4390.	1.8	13
47	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017, 16, 4288-4298.	1.8	87
48	OLS Client and OLS Dialog: Open Source Tools to Annotate Public Omics Datasets. <i>Proteomics</i> , 2017, 17, 1700244.	1.3	17
49	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. <i>Molecular and Cellular Proteomics</i> , 2017, 16, 1275-1285.	2.5	55
50	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. <i>Journal of Proteomics</i> , 2017, 150, 170-182.	1.2	56
51	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
52	Four simple recommendations to encourage best practices in research software. <i>F1000Research</i> , 2017, 6, 876.	0.8	88
53	Accurate and fast feature selection workflow for high-dimensional omics data. <i>PLoS ONE</i> , 2017, 12, e0189875.	1.1	60
54	A multicenter study benchmarks software tools for label-free proteome quantification. <i>Nature Biotechnology</i> , 2016, 34, 1130-1136.	9.4	321

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55	2016 update of the PRIDE database and its related tools. <i>Nucleic Acids Research</i> , 2016, 44, D447-D456.	6.5	3,451
56	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. <i>Nature Methods</i> , 2016, 13, 651-656.	9.0	147
57	Accurate estimation of isoelectric point of protein and peptide based on amino acid sequences. <i>Bioinformatics</i> , 2016, 32, 821-827.	1.8	55
58	PRIDE Inspector Toolsuite: Moving Toward a Universal Visualization Tool for Proteomics Data Standard Formats and Quality Assessment of ProteomeXchange Datasets. <i>Molecular and Cellular Proteomics</i> , 2016, 15, 305-317.	2.5	140
59	Novel interactions of domain III from the envelope glycoprotein of dengue 2 virus with human plasma proteins. <i>Journal of Proteomics</i> , 2016, 131, 205-213.	1.2	16
60	Ten Simple Rules for Taking Advantage of Git and GitHub. <i>PLoS Computational Biology</i> , 2016, 12, e1004947.	1.5	96
61	Comparative proteomics analysis of the antitumor effect of CIGB-552 peptide in HT-29 colon adenocarcinoma cells. <i>Journal of Proteomics</i> , 2015, 126, 163-171.	1.2	13
62	Computational proteomics: Integrating mass spectral data into a biological context. <i>Journal of Proteomics</i> , 2015, 129, 1-2.	1.2	0
63	Data for comparative proteomics analysis of the antitumor effect of CIGB-552 peptide in HT-29 colon adenocarcinoma cells. <i>Data in Brief</i> , 2015, 4, 468-473.	0.5	0
64	ms-data-core-api: an open-source, metadata-oriented library for computational proteomics. <i>Bioinformatics</i> , 2015, 31, 2903-2905.	1.8	30
65	PIA: An Intuitive Protein Inference Engine with a Web-Based User Interface. <i>Journal of Proteome Research</i> , 2015, 14, 2988-2997.	1.8	69
66	Open source libraries and frameworks for biological data visualisation: A guide for developers. <i>Proteomics</i> , 2015, 15, 1356-1374.	1.3	43
67	Identifying novel biomarkers through data mining – A realistic scenario?. <i>Proteomics - Clinical Applications</i> , 2015, 9, 437-443.	0.8	20
68	Making proteomics data accessible and reusable: Current state of proteomics databases and repositories. <i>Proteomics</i> , 2015, 15, 930-950.	1.3	181
69	On best practices in the development of bioinformatics software. <i>Frontiers in Genetics</i> , 2014, 5, 199.	1.1	53
70	Editorial (Thematic Issue: Genomics and Proteomics behind Drug Design). <i>Current Topics in Medicinal Chemistry</i> , 2014, 14, 343-343.	1.0	0
71	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
72	Open source libraries and frameworks for mass spectrometry based proteomics: A developer's perspective. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 63-76.	1.1	67

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73	Bioinformatics Tools for the Functional Interpretation of Quantitative Proteomics Results. <i>Current Topics in Medicinal Chemistry</i> , 2014, 14, 435-449.	1.0	14
74	A Survey of Molecular Descriptors Used in Mass Spectrometry Based Proteomics. <i>Current Topics in Medicinal Chemistry</i> , 2014, 14, 388-397.	1.0	5
75	SCX charge state selective separation of tryptic peptides combined with 2D-RP-HPLC allows for detailed proteome mapping. <i>Journal of Proteomics</i> , 2013, 91, 164-171.	1.2	27
76	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 Workshop report. <i>Journal of Proteomics</i> , 2013, 87, 134-138.	1.2	19
77	Pinpointing differentially expressed domains in complex protein mixtures with the cloud service of PatternLab for Proteomics. <i>Journal of Proteomics</i> , 2013, 89, 179-182.	1.2	11
78	HI-Bone: A Scoring System for Identifying Phenylisothiocyanate-Derivatized Peptides Based on Precursor Mass and High Intensity Fragment Ions. <i>Analytical Chemistry</i> , 2013, 85, 3515-3520.	3.2	7
79	Effectively addressing complex proteomic search spaces with peptide spectrum matching. <i>Bioinformatics</i> , 2013, 29, 1343-1344.	1.8	20
80	JBioWH: an open-source Java framework for bioinformatics data integration. <i>Database: the Journal of Biological Databases and Curation</i> , 2013, 2013, bat051-bat051.	1.4	8
81	The PRoteomics IDentification (PRIDE) Converter 2 Framework: An Improved Suite of Tools to Facilitate Data Submission to the PRIDE Database and the ProteomeXchange Consortium. <i>Molecular and Cellular Proteomics</i> , 2012, 11, 1682-1689.	2.5	105
82	A Parallel Systematic-Monte Carlo Algorithm for Exploring Conformational Space. <i>Current Topics in Medicinal Chemistry</i> , 2012, 12, 1790-1796.	1.0	3
83	Selective Isolation of Multiply Charged Peptides: A Confident Strategy for Protein Identification Using a Linear Trap Quadrupole Mass Spectrometer. <i>European Journal of Mass Spectrometry</i> , 2012, 18, 505-508.	0.5	0
84	Introducing an Asp-Pro Linker in the Synthesis of Random One-Bead-One-Compound Hexapeptide Libraries Compatible with ESI-MS Analysis. <i>ACS Combinatorial Science</i> , 2012, 14, 145-149.	3.8	7
85	The Proteomics Identifications (PRIDE) database and associated tools: status in 2013. <i>Nucleic Acids Research</i> , 2012, 41, D1063-D1069.	6.5	1,858
86	Isoelectric point optimization using peptide descriptors and support vector machines. <i>Journal of Proteomics</i> , 2012, 75, 2269-2274.	1.2	36
87	A Parallel Systematic-Monte Carlo Algorithm for Exploring Conformational Space. <i>Current Topics in Medicinal Chemistry</i> , 2012, 12, 1790-1796.	1.0	7
88	PRIDE Inspector: a tool to visualize and validate MS proteomics data. <i>Nature Biotechnology</i> , 2012, 30, 135-137.	9.4	109
89	A parallel systematic-Monte Carlo algorithm for exploring conformational space. <i>Current Topics in Medicinal Chemistry</i> , 2012, 12, 1790-6.	1.0	2
90	In silico analysis of accurate proteomics, complemented by selective isolation of peptides. <i>Journal of Proteomics</i> , 2011, 74, 2071-2082.	1.2	30

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91	Peptide fractionation by acid pH SDS-free electrophoresis. <i>Electrophoresis</i> , 2011, 32, 1323-1326.	1.3	13
92	Selective Isolation and Detection of Two Different Positively Charged Peptides Groups by Strong Cation Exchange Chromatography and Matrix-Assisted Laser Desorption/Ionization Mass Spectrometry: Application to Proteomics Studies. <i>European Journal of Mass Spectrometry</i> , 2010, 16, 693-702.	0.5	4
93	Evaluation of Phenylthiocarbamoyl-Derivatized Peptides by Electrospray Ionization Mass Spectrometry: Selective Isolation and Analysis of Modified Multiply Charged Peptides for Liquid Chromatography-Tandem Mass Spectrometry Experiments. <i>Analytical Chemistry</i> , 2010, 82, 8492-8501.	3.2	10
94	Proteomics Based on Peptide Fractionation by SDS-Free PAGE. <i>Journal of Proteome Research</i> , 2008, 7, 2427-2434.	1.8	18
95	USEDAT: USA-Europe Data Analysis Training Worldwide Program, 2019 ed., 0, , .		1
96	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> , 0, 8, 1677.	0.8	0
97	MOL2NET-07, Conference on Molecular, Biomedical, and Computational Sciences and Engineering, ISSN: 2624-5078, MDPI SciForum, Basel, Switzerland, 2021, 7th ed., 0, , .		0