

# Yasset Perez-Riverol

## List of Publications by Year in descending order

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Version: 2024-02-01

97  
papers

21,215  
citations

109264

35  
h-index

40954

93  
g-index

123  
all docs

123  
docs citations

123  
times ranked

38133  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	2016 update of the PRIDE database and its related tools. <i>Nucleic Acids Research</i> , 2016, 44, D447-D456.	6.5	3,451
3	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
4	The Proteomics Identifications (PRIDE) database and associated tools: status in 2013. <i>Nucleic Acids Research</i> , 2012, 41, D1063-D1069.	6.5	1,858
5	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
6	Bioconda: sustainable and comprehensive software distribution for the life sciences. <i>Nature Methods</i> , 2018, 15, 475-476.	9.0	714
7	The ProteomeXchange consortium in 2020: enabling "big data" approaches in proteomics. <i>Nucleic Acids Research</i> , 2020, 48, D1145-D1152.	6.5	491
8	A multicenter study benchmarks software tools for label-free proteome quantification. <i>Nature Biotechnology</i> , 2016, 34, 1130-1136.	9.4	321
9	BioContainers: an open-source and community-driven framework for software standardization. <i>Bioinformatics</i> , 2017, 33, 2580-2582.	1.8	205
10	Making proteomics data accessible and reusable: Current state of proteomics databases and repositories. <i>Proteomics</i> , 2015, 15, 930-950.	1.3	181
11	Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , 2017, 35, 406-409.	9.4	159
12	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. <i>Nature Methods</i> , 2016, 13, 651-656.	9.0	147
13	ThermoRawFileParser: Modular, Scalable, and Cross-Platform RAW File Conversion. <i>Journal of Proteome Research</i> , 2020, 19, 537-542.	1.8	144
14	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
15	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
16	MaxDIA enables library-based and library-free data-independent acquisition proteomics. <i>Nature Biotechnology</i> , 2021, 39, 1563-1573.	9.4	115
17	PRIDE Inspector: a tool to visualize and validate MS proteomics data. <i>Nature Biotechnology</i> , 2012, 30, 135-137.	9.4	109
18	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

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19	Ten Simple Rules for Taking Advantage of Git and GitHub. PLoS Computational Biology, 2016, 12, e1004947.	1.5	96
20	Four simple recommendations to encourage best practices in research software. F1000Research, 2017, 6, 876.	0.8	88
21	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. Journal of Proteome Research, 2017, 16, 4288-4298.	1.8	87
22	Quantifying the impact of public omics data. Nature Communications, 2019, 10, 3512.	5.8	79
23	PIA: An Intuitive Protein Inference Engine with a Web-Based User Interface. Journal of Proteome Research, 2015, 14, 2988-2997.	1.8	69
24	Open source libraries and frameworks for mass spectrometry based proteomics: A developer's perspective. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 63-76.	1.1	67
25	MassIVE.quant: a community resource of quantitative mass spectrometry-based proteomics datasets. Nature Methods, 2020, 17, 981-984.	9.0	66
26	Accurate and fast feature selection workflow for high-dimensional omics data. PLoS ONE, 2017, 12, e0189875.	1.1	60
27	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. Journal of Proteomics, 2017, 150, 170-182.	1.2	56
28	Accurate estimation of isoelectric point of protein and peptide based on amino acid sequences. Bioinformatics, 2016, 32, 821-827.	1.8	55
29	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. Molecular and Cellular Proteomics, 2017, 16, 1275-1285.	2.5	55
30	On best practices in the development of bioinformatics software. Frontiers in Genetics, 2014, 5, 199.	1.1	53
31	Expanding the Use of Spectral Libraries in Proteomics. Journal of Proteome Research, 2018, 17, 4051-4060.	1.8	47
32	Universal Spectrum Identifier for mass spectra. Nature Methods, 2021, 18, 768-770.	9.0	47
33	A proteomics sample metadata representation for multiomics integration and big data analysis. Nature Communications, 2021, 12, 5854.	5.8	45
34	Open source libraries and frameworks for biological data visualisation: A guide for developers. Proteomics, 2015, 15, 1356-1374.	1.3	43
35	mzTab-M: A Data Standard for Sharing Quantitative Results in Mass Spectrometry Metabolomics. Analytical Chemistry, 2019, 91, 3302-3310.	3.2	43
36	An integrated landscape of protein expression in human cancer. Scientific Data, 2021, 8, 115.	2.4	38

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37	Isoelectric point optimization using peptide descriptors and support vector machines. <i>Journal of Proteomics</i> , 2012, 75, 2269-2274.	1.2	36
38	Protein Inference Using PIA Workflows and PSI Standard File Formats. <i>Journal of Proteome Research</i> , 2019, 18, 741-747.	1.8	33
39	In silico analysis of accurate proteomics, complemented by selective isolation of peptides. <i>Journal of Proteomics</i> , 2011, 74, 2071-2082.	1.2	30
40	ms-data-core-api: an open-source, metadata-oriented library for computational proteomics. <i>Bioinformatics</i> , 2015, 31, 2903-2905.	1.8	30
41	Recommendations for the packaging and containerizing of bioinformatics software. <i>F1000Research</i> , 2018, 7, 742.	0.8	29
42	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
43	Recommendations for the packaging and containerizing of bioinformatics software. <i>F1000Research</i> , 2018, 7, 742.	0.8	27
44	User-friendly, scalable tools and workflows for single-cell RNA-seq analysis. <i>Nature Methods</i> , 2021, 18, 327-328.	9.0	26
45	Scalable Data Analysis in Proteomics and Metabolomics Using BioContainers and Workflows Engines. <i>Proteomics</i> , 2020, 20, e1900147.	1.3	24
46	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
47	Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , 2019, 18, 2686-2692.	1.8	22
48	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
49	Effectively addressing complex proteomic search spaces with peptide spectrum matching. <i>Bioinformatics</i> , 2013, 29, 1343-1344.	1.8	20
50	Identifying novel biomarkers through data mining—A realistic scenario?. <i>Proteomics - Clinical Applications</i> , 2015, 9, 437-443.	0.8	20
51	Toward a Sample Metadata Standard in Public Proteomics Repositories. <i>Journal of Proteome Research</i> , 2020, 19, 3906-3909.	1.8	20
52	A comprehensive LFQ benchmark dataset on modern day acquisition strategies in proteomics. <i>Scientific Data</i> , 2022, 9, 126.	2.4	20
53	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 Workshop report. <i>Journal of Proteomics</i> , 2013, 87, 134-138.	1.2	19
54	BioContainers Registry: Searching Bioinformatics and Proteomics Tools, Packages, and Containers. <i>Journal of Proteome Research</i> , 2021, 20, 2056-2061.	1.8	19

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55	Proteomics Based on Peptide Fractionation by SDS-Free PAGE. <i>Journal of Proteome Research</i> , 2008, 7, 2427-2434.	1.8	18
56	OLS Client and OLS Dialog: Open Source Tools to Annotate Public Omics Datasets. <i>Proteomics</i> , 2017, 17, 1700244.	1.3	17
57	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
58	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
59	Generation of ENSEMBL-based proteogenomics databases boosts the identification of non-canonical peptides. <i>Bioinformatics</i> , 2022, 38, 1470-1472.	1.8	16
60	Future Prospects of Spectral Clustering Approaches in Proteomics. <i>Proteomics</i> , 2018, 18, e1700454.	1.3	15
61	Bioinformatics Tools for the Functional Interpretation of Quantitative Proteomics Results. <i>Current Topics in Medicinal Chemistry</i> , 2014, 14, 435-449.	1.0	14
62	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
63	Method for Independent Estimation of the False Localization Rate for Phosphoproteomics. <i>Journal of Proteome Research</i> , 2022, 21, 1603-1615.	1.8	14
64	Peptide fractionation by acid pH SDS-free electrophoresis. <i>Electrophoresis</i> , 2011, 32, 1323-1326.	1.3	13
65	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
66	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
67	Spectral Clustering Improves Label-Free Quantification of Low-Abundant Proteins. <i>Journal of Proteome Research</i> , 2019, 18, 1477-1485.	1.8	13
68	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
69	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
70	Deep learning embedder method and tool for mass spectra similarity search. <i>Journal of Proteomics</i> , 2021, 232, 104070.	1.2	10
71	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
72	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

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73	JBioWH: an open-source Java framework for bioinformatics data integration. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat051-bat051.	1.4	8
74	Introducing an Asp-Pro Linker in the Synthesis of Random One-Bead-One-Compound Hexapeptide Libraries Compatible with ESI-MS Analysis. ACS Combinatorial Science, 2012, 14, 145-149.	3.8	7
75	A Parallel Systematic-Monte Carlo Algorithm for Exploring Conformational Space. Current Topics in Medicinal Chemistry, 2012, 12, 1790-1796.	1.0	7
76	HI-Bone: A Scoring System for Identifying Phenylisothiocyanate-Derivatized Peptides Based on Precursor Mass and High Intensity Fragment Ions. Analytical Chemistry, 2013, 85, 3515-3520.	3.2	7
77	Synthetic human proteomes for accelerating protein research. Nature Methods, 2017, 14, 240-242.	9.0	6
78	ABRF Proteome Informatics Research Group (iPRG) 2016 Study: Inferring Proteoforms from Bottom-up Proteomics Data. Journal of Biomolecular Techniques, 2018, 29, 39-45.	0.8	6
79	A Survey of Molecular Descriptors Used in Mass Spectrometry Based Proteomics. Current Topics in Medicinal Chemistry, 2014, 14, 388-397.	1.0	5
80	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. European Journal of Mass Spectrometry, 2010, 16, 693-702.	0.5	4
81	Sodium dodecyl sulfate free gel electrophoresis/electroelution sorting for peptide fractionation. Journal of Separation Science, 2019, 42, 3712-3717.	1.3	4
82	Mapping the Melanoma Plasma Proteome (MPP) Using Single-Shot Proteomics Interfaced with the WiMT Database. Cancers, 2021, 13, 6224.	1.7	4
83	A Parallel Systematic-Monte Carlo Algorithm for Exploring Conformational Space. Current Topics in Medicinal Chemistry, 2012, 12, 1790-1796.	1.0	3
84	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. Journal of Proteomics, 2019, 193, 71-84.	1.2	3
85	The European Bioinformatics Community for Mass Spectrometry (EuBICMS): an open community for bioinformatics training and research. Rapid Communications in Mass Spectrometry, 2021, , e9087.	0.7	3
86	The omics discovery REST interface. Nucleic Acids Research, 2020, 48, W380-W384.	6.5	3
87	Mass spectrometry evaluation of a neuroblastoma SH-SY5Y cell culture protocol. Analytical Biochemistry, 2018, 559, 51-54.	1.1	2
88	A parallel systematic-Monte Carlo algorithm for exploring conformational space. Current Topics in Medicinal Chemistry, 2012, 12, 1790-6.	1.0	2
89	A Comprehensive Evaluation of Consensus Spectrum Generation Methods in Proteomics. Journal of Proteome Research, 2022, 21, 1566-1574.	1.8	2
90	CHAPTER 19. Cross-platform Software Development and Distribution with Bioconda and BioContainers. New Developments in Mass Spectrometry, 2020, , 415-426.	0.2	1

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91	USEDAT: USA-Europe Data Analysis Training Worldwide Program, 2019 ed., 0, , .		1
92	Selective Isolation of Multiply Charged Peptides: A Confident Strategy for Protein Identification Using a Linear Trap Quadrupole Mass Spectrometer. European Journal of Mass Spectrometry, 2012, 18, 505-508.	0.5	0
93	Editorial (Thematic Issue: Genomics and Proteomics behind Drug Design). Current Topics in Medicinal Chemistry, 2014, 14, 343-343.	1.0	0
94	Computational proteomics: Integrating mass spectral data into a biological context. Journal of Proteomics, 2015, 129, 1-2.	1.2	0
95	Data for comparative proteomics analysis of the antitumor effect of CIGB-552 peptide in HT-29 colon adenocarcinoma cells. Data in Brief, 2015, 4, 468-473.	0.5	0
96	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. F1000Research, 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