

# Yasset Perez-Riverol

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/755882/yasset-perez-riverol-publications-by-citations.pdf>

**Version:** 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

101  
papers

12,153  
citations

30  
h-index

110  
g-index

123  
ext. papers

17,737  
ext. citations

8.6  
avg, IF

6.16  
L-index

#	Paper	IF	Citations
101	The PRIDE database and related tools and resources in 2019: improving support for quantification data. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D442-D450	20.1	3856
100	2016 update of the PRIDE database and its related tools. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D447-56	20.1	2440
99	The PRoteomics IDentifications (PRIDE) database and associated tools: status in 2013. <i>Nucleic Acids Research</i> , <b>2013</b> , 41, D1063-9	20.1	1587
98	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D1100-D1106	20.1	568
97	Bioconda: sustainable and comprehensive software distribution for the life sciences. <i>Nature Methods</i> , <b>2018</b> , 15, 475-476	21.6	416
96	The ProteomeXchange consortium in 2020: enabling 'big data' approaches in proteomics. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D1145-D1152	20.1	212
95	A multicenter study benchmarks software tools for label-free proteome quantification. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 1130-1136	44.5	202
94	The PRIDE database resources in 2022: a hub for mass spectrometry-based proteomics evidences. <i>Nucleic Acids Research</i> , <b>2021</b> ,	20.1	200
93	Making proteomics data accessible and reusable: current state of proteomics databases and repositories. <i>Proteomics</i> , <b>2015</b> , 15, 930-49	4.8	138
92	BioContainers: an open-source and community-driven framework for software standardization. <i>Bioinformatics</i> , <b>2017</b> , 33, 2580-2582	7.2	123
91	Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , <b>2017</b> , 35, 406-409	44.5	105
90	PRIDE Inspector: a tool to visualize and validate MS proteomics data. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 135-7	44.5	103
89	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. <i>Nature Methods</i> , <b>2016</b> , 13, 651-656	21.6	99
88	The mzTab data exchange format: communicating mass-spectrometry-based proteomics and metabolomics experimental results to a wider audience. <i>Molecular and Cellular Proteomics</i> , <b>2014</b> , 13, 2765-75	7.6	96
87	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> , <b>2012</b> , 11, 1682-9	7.6	96
86	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> , <b>2016</b> , 15, 305-17	7.6	91
85	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 4288-4298	5.6	61

84	Open source libraries and frameworks for mass spectrometry based proteomics: a developer's perspective. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2014</b> , 1844, 63-76	4	59
83	Four simple recommendations to encourage best practices in research software. <i>F1000Research</i> , <b>2017</b> , 6,	3.6	58
82	PIA: An Intuitive Protein Inference Engine with a Web-Based User Interface. <i>Journal of Proteome Research</i> , <b>2015</b> , 14, 2988-97	5.6	51
81	ThermoRawFileParser: Modular, Scalable, and Cross-Platform RAW File Conversion. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 537-542	5.6	45
80	Quantifying the impact of public omics data. <i>Nature Communications</i> , <b>2019</b> , 10, 3512	17.4	42
79	Accurate and fast feature selection workflow for high-dimensional omics data. <i>PLoS ONE</i> , <b>2017</b> , 12, e0189975	3.7	40
78	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. <i>Journal of Proteomics</i> , <b>2017</b> , 150, 170-182	3.9	39
77	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. <i>Molecular and Cellular Proteomics</i> , <b>2017</b> , 16, 1275-1285	7.6	37
76	Open source libraries and frameworks for biological data visualisation: a guide for developers. <i>Proteomics</i> , <b>2015</b> , 15, 1356-74	4.8	34
75	On best practices in the development of bioinformatics software. <i>Frontiers in Genetics</i> , <b>2014</b> , 5, 199	4.5	34
74	Accurate estimation of isoelectric point of protein and peptide based on amino acid sequences. <i>Bioinformatics</i> , <b>2016</b> , 32, 821-7	7.2	32
73	Isoelectric point optimization using peptide descriptors and support vector machines. <i>Journal of Proteomics</i> , <b>2012</b> , 75, 2269-74	3.9	30
72	mzTab-M: A Data Standard for Sharing Quantitative Results in Mass Spectrometry Metabolomics. <i>Analytical Chemistry</i> , <b>2019</b> , 91, 3302-3310	7.8	27
71	In silico analysis of accurate proteomics, complemented by selective isolation of peptides. <i>Journal of Proteomics</i> , <b>2011</b> , 74, 2071-82	3.9	27
70	ms-data-core-api: an open-source, metadata-oriented library for computational proteomics. <i>Bioinformatics</i> , <b>2015</b> , 31, 2903-5	7.2	26
69	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 4051-4066	9.6	26
68	MaxDIA enables library-based and library-free data-independent acquisition proteomics. <i>Nature Biotechnology</i> , <b>2021</b> ,	44.5	24
67	SCX charge state selective separation of tryptic peptides combined with 2D-RP-HPLC allows for detailed proteome mapping. <i>Journal of Proteomics</i> , <b>2013</b> , 91, 164-71	3.9	21

66	Protein Inference Using PIA Workflows and PSI Standard File Formats. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 741-747	5.6	21
65	MassIVE.quant: a community resource of quantitative mass spectrometry-based proteomics datasets. <i>Nature Methods</i> , <b>2020</b> , 17, 981-984	21.6	20
64	Effectively addressing complex proteomic search spaces with peptide spectrum matching. <i>Bioinformatics</i> , <b>2013</b> , 29, 1343-4	7.2	19
63	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 workshop report. <i>Journal of Proteomics</i> , <b>2013</b> , 87, 134-8	3.9	17
62	Recommendations for the packaging and containerizing of bioinformatics software. <i>F1000Research</i> , <b>2018</b> , 7,	3.6	17
61	Proteomics based on peptide fractionation by SDS-free PAGE. <i>Journal of Proteome Research</i> , <b>2008</b> , 7, 2427-34	5.6	16
60	Identifying novel biomarkers through data mining-a realistic scenario?. <i>Proteomics - Clinical Applications</i> , <b>2015</b> , 9, 437-43	3.1	14
59	OLS Client and OLS Dialog: Open Source Tools to Annotate Public Omics Datasets. <i>Proteomics</i> , <b>2017</b> , 17, 1700244	4.8	13
58	Recommendations for the packaging and containerizing of bioinformatics software. <i>F1000Research</i> , <b>2018</b> , 7, 742	3.6	13
57	Bioinformatics tools for the functional interpretation of quantitative proteomics results. <i>Current Topics in Medicinal Chemistry</i> , <b>2014</b> , 14, 435-49	3	13
56	A Protein Standard That Emulates Homology for the Characterization of Protein Inference Algorithms. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 1879-1886	5.6	12
55	Bioconda: A sustainable and comprehensive software distribution for the life sciences		12
54	Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 2686-2692	5.6	11
53	Novel interactions of domain III from the envelope glycoprotein of dengue 2 virus with human plasma proteins. <i>Journal of Proteomics</i> , <b>2016</b> , 131, 205-213	3.9	11
52	Comparative proteomics analysis of the antitumor effect of CIGB-552 peptide in HT-29 colon adenocarcinoma cells. <i>Journal of Proteomics</i> , <b>2015</b> , 126, 163-71	3.9	11
51	Pinpointing differentially expressed domains in complex protein mixtures with the cloud service of PatternLab for Proteomics. <i>Journal of Proteomics</i> , <b>2013</b> , 89, 179-82	3.9	11
50	Peptide fractionation by acid pH SDS-free electrophoresis. <i>Electrophoresis</i> , <b>2011</b> , 32, 1323-6	3.6	11
49	Scalable Data Analysis in Proteomics and Metabolomics Using BioContainers and Workflows Engines. <i>Proteomics</i> , <b>2020</b> , 20, e1900147	4.8	11

48	Future Prospects of Spectral Clustering Approaches in Proteomics. <i>Proteomics</i> , <b>2018</b> , 18, e1700454	4.8	10
47	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> , <b>2010</b> , 82, 8492-501	7.8	10
46	An integrated landscape of protein expression in human cancer. <i>Scientific Data</i> , <b>2021</b> , 8, 115	8.2	10
45	Galaxy-Kubernetes integration: scaling bioinformatics workflows in the cloud		9
44	Universal Spectrum Identifier for mass spectra. <i>Nature Methods</i> , <b>2021</b> , 18, 768-770	21.6	9
43	Novel functional proteins coded by the human genome discovered in metastases of melanoma patients. <i>Cell Biology and Toxicology</i> , <b>2020</b> , 36, 261-272	7.4	9
42	User-friendly, scalable tools and workflows for single-cell RNA-seq analysis. <i>Nature Methods</i> , <b>2021</b> , 18, 327-328	21.6	9
41	Spectral Clustering Improves Label-Free Quantification of Low-Abundant Proteins. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 1477-1485	5.6	8
40	JBioWH: an open-source Java framework for bioinformatics data integration. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2013</b> , 2013, bat051	5	8
39	Response to "Comparison and Evaluation of Clustering Algorithms for Tandem Mass Spectra". <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 1993-1996	5.6	7
38	A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , <b>2021</b> , 12, 5854	17.4	7
37	Toward a Sample Metadata Standard in Public Proteomics Repositories. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 3906-3909	5.6	7
36	Enhanced Missing Proteins Detection in NCI60 Cell Lines Using an Integrative Search Engine Approach. <i>Journal of Proteome Research</i> , <b>2017</b> , 16, 4374-4390	5.6	6
35	HI-bone: a scoring system for identifying phenylisothiocyanate-derivatized peptides based on precursor mass and high intensity fragment ions. <i>Analytical Chemistry</i> , <b>2013</b> , 85, 3515-20	7.8	6
34	Universal Spectrum Explorer: A Standalone (Web-)Application for Cross-Resource Spectrum Comparison. <i>Journal of Proteome Research</i> , <b>2021</b> , 20, 3388-3394	5.6	6
33	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> , <b>2012</b> , 14, 145-9	3.9	5
32	A survey of molecular descriptors used in mass spectrometry based proteomics. <i>Current Topics in Medicinal Chemistry</i> , <b>2014</b> , 14, 388-97	3	5
31	Universal Spectrum Identifier for mass spectra		5

30	Deep learning embedder method and tool for mass spectra similarity search. <i>Journal of Proteomics</i> , <b>2021</b> , 232, 104070	3.9	5
29	Synthetic human proteomes for accelerating protein research. <i>Nature Methods</i> , <b>2017</b> , 14, 240-242	21.6	4
28	Selective isolation-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> , <b>2010</b> , 16, 693-702	1.1	4
27	User-friendly, scalable tools and workflows for single-cell analysis		4
26	BioContainers Registry: searching for bioinformatics tools, packages and containers		4
25	BioContainers Registry: Searching Bioinformatics and Proteomics Tools, Packages, and Containers. <i>Journal of Proteome Research</i> , <b>2021</b> , 20, 2056-2061	5.6	4
24	ABRF Proteome Informatics Research Group (iPRG) 2016 Study: Inferring Proteoforms from Bottom-up Proteomics Data. <i>Journal of Biomolecular Techniques</i> , <b>2018</b> , 29, 39-45	1.1	4
23	A Parallel Systematic-Monte Carlo Algorithm for Exploring Conformational Space. <i>Current Topics in Medicinal Chemistry</i> , <b>2012</b> , 12, 1790-1796	3	3
22	Generation of ENSEMBL-based proteogenomics databases boosts the identification of non-canonical peptides.. <i>Bioinformatics</i> , <b>2021</b> ,	7.2	3
21	ThermoRawFileParser: modular, scalable and cross-platform RAW file conversion		3
20	A comprehensive LFQ benchmark dataset on modern day acquisition strategies in proteomics.. <i>Scientific Data</i> , <b>2022</b> , 9, 126	8.2	3
19	The omics discovery REST interface. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, W380-W384	20.1	2
18	Omics Discovery Index - Discovering and Linking Public Omics Datasets		2
17	Accurate and Fast feature selection workflow for high-dimensional omics data		2
16	Universal Spectrum Explorer: A standalone (web-)application for cross-resource spectrum comparison		2
15	An integrated landscape of protein expression in human cancer		2
14	The European Bioinformatics Community for Mass Spectrometry (EuBIC-MS): an open community for bioinformatics training and research. <i>Rapid Communications in Mass Spectrometry</i> , <b>2021</b> , e9087	2.2	2
13	A parallel systematic-Monte Carlo algorithm for exploring conformational space. <i>Current Topics in Medicinal Chemistry</i> , <b>2012</b> , 12, 1790-6	3	2

12	Mapping the Melanoma Plasma Proteome (MPP) Using Single-Shot Proteomics Interfaced with the WiMT Database.. <i>Cancers</i> , <b>2021</b> , 13,	6.6	2
11	Mass spectrometry evaluation of a neuroblastoma SH-SY5Y cell culture protocol. <i>Analytical Biochemistry</i> , <b>2018</b> , 559, 51-54	3.1	1
10	Sodium dodecyl sulfate free gel electrophoresis/electroelution sorting for peptide fractionation. <i>Journal of Separation Science</i> , <b>2019</b> , 42, 3712-3717	3.4	1
9	A Parallel Systematic-Monte Carlo Algorithm for Exploring Conformational Space. <i>Current Topics in Medicinal Chemistry</i> , <b>2012</b> , 12, 1790-1796	3	1
8	A comprehensive LFQ benchmark dataset on modern day acquisition strategies in proteomics		1
7	A protein standard that emulates homology for the characterization of protein inference algorithms		1
6	Proteomics Standards Initiative Extended FASTA Format (PEFF)		1
5	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> , <b>2019</b> , 193, 71-84	3.9	1
4	Integrative analysis of genomic variants reveals new associations of candidate haploinsufficient genes with congenital heart disease. <i>PLoS Genetics</i> , <b>2021</b> , 17, e1009679	6	1
3	Data for comparative proteomics analysis of the antitumor effect of CIGB-552 peptide in HT-29 colon adenocarcinoma cells. <i>Data in Brief</i> , <b>2015</b> , 4, 468-73	1.2	
2	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> , <b>2012</b> , 18, 505-8	1.1	
1	BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> , <b>2014</b> , 8, 1677	3.6	