

# Yasset Perez-Riverol

## List of Publications by Year in Descending Order

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**Version:** 2024-04-27

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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 | A comprehensive LFQ benchmark dataset on modern day acquisition strategies in proteomics.. <i>Scientific Data</i> , <b>2022</b> , 9, 126   | 8.2  | 3         |
| 100 | Generation of ENSEMBL-based proteogenomics databases boosts the identification of non-canonical peptides.. <i>Bioinformatics</i> , <b>2021</b> ,   | 7.2  | 3         |
| 99  | 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       |
| 98  | A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , <b>2021</b> , 12, 5854  | 17.4 | 7         |
| 97  | 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         |
| 96  | An integrated landscape of protein expression in human cancer. <i>Scientific Data</i> , <b>2021</b> , 8, 115   | 8.2  | 10        |
| 95  | 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         |
| 94  | Universal Spectrum Identifier for mass spectra. <i>Nature Methods</i> , <b>2021</b> , 18, 768-770  | 21.6 | 9         |
| 93  | Deep learning embedder method and tool for mass spectra similarity search. <i>Journal of Proteomics</i> , <b>2021</b> , 232, 104070  | 3.9  | 5         |
| 92  | 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         |
| 91  | 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         |
| 90  | 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         |
| 89  | MaxDIA enables library-based and library-free data-independent acquisition proteomics. <i>Nature Biotechnology</i> , <b>2021</b> ,   | 44.5 | 24        |
| 88  | 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         |
| 87  | 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       |
| 86  | The omics discovery REST interface. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, W380-W384  | 20.1 | 2         |
| 85  | Scalable Data Analysis in Proteomics and Metabolomics Using BioContainers and Workflows Engines. <i>Proteomics</i> , <b>2020</b> , 20, e1900147  | 4.8  | 11        |

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| 84 | ThermoRawFileParser: Modular, Scalable, and Cross-Platform RAW File Conversion. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 537-542  | 5.6  | 45   |
| 83 | Toward a Sample Metadata Standard in Public Proteomics Repositories. <i>Journal of Proteome Research</i> , <b>2020</b> , 19, 3906-3909   | 5.6  | 7    |
| 82 | 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   |
| 81 | 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    |
| 80 | 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   |
| 79 | Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 2686-2692   | 5.6  | 11   |
| 78 | 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    |
| 77 | Quantifying the impact of public omics data. <i>Nature Communications</i> , <b>2019</b> , 10, 3512   | 17.4 | 42   |
| 76 | 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    |
| 75 | 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 |
| 74 | 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   |
| 73 | 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    |
| 72 | 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    |
| 71 | 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   |
| 70 | Mass spectrometry evaluation of a neuroblastoma SH-SY5Y cell culture protocol. <i>Analytical Biochemistry</i> , <b>2018</b> , 559, 51-54   | 3.1  | 1    |
| 69 | Future Prospects of Spectral Clustering Approaches in Proteomics. <i>Proteomics</i> , <b>2018</b> , 18, e1700454   | 4.8  | 10   |
| 68 | Recommendations for the packaging and containerizing of bioinformatics software. <i>F1000Research</i> , <b>2018</b> , 7,   | 3.6  | 17   |
| 67 | Recommendations for the packaging and containerizing of bioinformatics software. <i>F1000Research</i> , <b>2018</b> , 7, 742   | 3.6  | 13   |

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| 66 | Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 4051-4066   | 26        |
| 65 | 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     |
| 64 | Bioconda: sustainable and comprehensive software distribution for the life sciences. <i>Nature Methods</i> , <b>2018</b> , 15, 475-476   | 21.6 416  |
| 63 | Synthetic human proteomes for accelerating protein research. <i>Nature Methods</i> , <b>2017</b> , 14, 240-242   | 21.6 4    |
| 62 | 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  |
| 61 | BioContainers: an open-source and community-driven framework for software standardization. <i>Bioinformatics</i> , <b>2017</b> , 33, 2580-2582   | 7.2 123   |
| 60 | 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     |
| 59 | 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  |
| 58 | Four simple recommendations to encourage best practices in research software. <i>F1000Research</i> , <b>2017</b> , 6,  | 3.6 58    |
| 57 | 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    |
| 56 | OLS Client and OLS Dialog: Open Source Tools to Annotate Public Omics Datasets. <i>Proteomics</i> , <b>2017</b> , 17, 1700244  | 4.8 13    |
| 55 | 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    |
| 54 | 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    |
| 53 | Accurate and fast feature selection workflow for high-dimensional omics data. <i>PLoS ONE</i> , <b>2017</b> , 12, e0189975   | 3.7 40    |
| 52 | 2016 update of the PRIDE database and its related tools. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D447-56   | 20.1 2440 |
| 51 | 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   |
| 50 | 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    |
| 49 | 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    |

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| 48 | 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   |
| 47 | A multicenter study benchmarks software tools for label-free proteome quantification. <i>Nature Biotechnology</i> , <b>2016</b> , 34, 1130-1136  | 44.5 | 202  |
| 46 | 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  |      |
| 45 | 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   |
| 44 | 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   |
| 43 | 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   |
| 42 | Identifying novel biomarkers through data mining-a realistic scenario?. <i>Proteomics - Clinical Applications</i> , <b>2015</b> , 9, 437-43  | 3.1  | 14   |
| 41 | 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  |
| 40 | 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   |
| 39 | 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   |
| 38 | On best practices in the development of bioinformatics software. <i>Frontiers in Genetics</i> , <b>2014</b> , 5, 199   | 4.5  | 34   |
| 37 | 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   |
| 36 | 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   |
| 35 | 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    |
| 34 | 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   |
| 33 | 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 |
| 32 | Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 workshop report. <i>Journal of Proteomics</i> , <b>2013</b> , 87, 134-8   | 3.9  | 17   |
| 31 | 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   |

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| 30 | 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   |
| 29 | Effectively addressing complex proteomic search spaces with peptide spectrum matching. <i>Bioinformatics</i> , <b>2013</b> , 29, 1343-4   | 7.2  | 19  |
| 28 | 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   |
| 27 | 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  |     |
| 26 | 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   |
| 25 | Isoelectric point optimization using peptide descriptors and support vector machines. <i>Journal of Proteomics</i> , <b>2012</b> , 75, 2269-74  | 3.9  | 30  |
| 24 | 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   |
| 23 | PRIDE Inspector: a tool to visualize and validate MS proteomics data. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 135-7   | 44.5 | 103 |
| 22 | 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  |
| 21 | 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   |
| 20 | 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   |
| 19 | 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  |
| 18 | Peptide fractionation by acid pH SDS-free electrophoresis. <i>Electrophoresis</i> , <b>2011</b> , 32, 1323-6  | 3.6  | 11  |
| 17 | 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  |
| 16 | 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   |
| 15 | Proteomics based on peptide fractionation by SDS-free PAGE. <i>Journal of Proteome Research</i> , <b>2008</b> , 7, 2427-34  | 5.6  | 16  |
| 14 | A comprehensive LFQ benchmark dataset on modern day acquisition strategies in proteomics  |      | 1   |
| 13 | A protein standard that emulates homology for the characterization of protein inference algorithms  |      | 1   |

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| 12 | BioHackathon series in 2013 and 2014: improvements of semantic interoperability in life science data and services. <i>F1000Research</i> ,8, 1677 | 3.6 |
| 11 | Omics Discovery Index - Discovering and Linking Public Omics Datasets  | 2   |
| 10 | Accurate and Fast feature selection workflow for high-dimensional omics data   | 2   |
| 9  | User-friendly, scalable tools and workflows for single-cell analysis   | 4   |
| 8  | BioContainers Registry: searching for bioinformatics tools, packages and containers  | 4   |
| 7  | Universal Spectrum Explorer: A standalone (web-)application for cross-resource spectrum comparison   | 2   |
| 6  | Universal Spectrum Identifier for mass spectra   | 5   |
| 5  | Bioconda: A sustainable and comprehensive software distribution for the life sciences  | 12  |
| 4  | Galaxy-Kubernetes integration: scaling bioinformatics workflows in the cloud   | 9   |
| 3  | ThermoRawFileParser: modular, scalable and cross-platform RAW file conversion  | 3   |
| 2  | Proteomics Standards Initiative Extended FASTA Format (PEFF)   | 1   |
| 1  | An integrated landscape of protein expression in human cancer  | 2   |