

Juan Antonio Vizcano

List of Publications by Year in Descending Order

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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.

139 papers	17,485 citations	49 h-index	132 g-index
163 ext. papers	23,772 ext. citations	9.2 avg, IF	6.4 L-index

#	Paper	IF	Citations
139	Expression Atlas update: gene and protein expression in multiple species. <i>Nucleic Acids Research</i> , 2021 ,	20.1	8
138	The PRIDE database resources in 2022: a hub for mass spectrometry-based proteomics evidences. <i>Nucleic Acids Research</i> , 2021 ,	20.1	200
137	A proteomics sample metadata representation for multiomics integration and big data analysis. <i>Nature Communications</i> , 2021 , 12, 5854	17.4	7
136	An integrated landscape of protein expression in human cancer. <i>Scientific Data</i> , 2021 , 8, 115	8.2	10
135	Protamine Characterization by Top-Down Proteomics: Boosting Proteoform Identification with DBSCAN. <i>Proteomes</i> , 2021 , 9,	4.6	1
134	Universal Spectrum Identifier for mass spectra. <i>Nature Methods</i> , 2021 , 18, 768-770	21.6	9
133	Data Management of Sensitive Human Proteomics Data: Current Practices, Recommendations, and Perspectives for the Future. <i>Molecular and Cellular Proteomics</i> , 2021 , 20, 100071	7.6	8
132	BioContainers Registry: Searching Bioinformatics and Proteomics Tools, Packages, and Containers. <i>Journal of Proteome Research</i> , 2021 , 20, 2056-2061	5.6	4
131	The growing need for controlled data access models in clinical proteomics and metabolomics. <i>Nature Communications</i> , 2021 , 12, 5787	17.4	1
130	The ELIXIR Core Data Resources: fundamental infrastructure for the life sciences. <i>Bioinformatics</i> , 2020 , 36, 2636-2642	7.2	29
129	Expression Atlas update: from tissues to single cells. <i>Nucleic Acids Research</i> , 2020 , 48, D77-D83	20.1	159
128	The ProteomeXchange consortium in 2020: enabling 'big data' approaches in proteomics. <i>Nucleic Acids Research</i> , 2020 , 48, D1145-D1152	20.1	212
127	Review of Issues and Solutions to Data Analysis Reproducibility and Data Quality in Clinical Proteomics. <i>Methods in Molecular Biology</i> , 2020 , 2051, 345-371	1.4	0
126	The functional landscape of the human phosphoproteome. <i>Nature Biotechnology</i> , 2020 , 38, 365-373	44.5	106
125	The Human Immunopeptidome Project: A Roadmap to Predict and Treat Immune Diseases. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 31-49	7.6	33
124	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020 , 11, 5301	17.4	59
123	Using Deep Learning to Extrapolate Protein Expression Measurements. <i>Proteomics</i> , 2020 , 20, e2000009	4.8	3

122	A five-level classification system for proteoform identifications. <i>Nature Methods</i> , 2019 , 16, 939-940	21.6	25
121	mzTab-M: A Data Standard for Sharing Quantitative Results in Mass Spectrometry Metabolomics. <i>Analytical Chemistry</i> , 2019 , 91, 3302-3310	7.8	27
120	Proteomics Standards Initiative Extended FASTA Format. <i>Journal of Proteome Research</i> , 2019 , 18, 2686-2692	5.6	11
119	First Community-Wide, Comparative Cross-Linking Mass Spectrometry Study. <i>Analytical Chemistry</i> , 2019 , 91, 6953-6961	7.8	57
118	Spectral Clustering Improves Label-Free Quantification of Low-Abundant Proteins. <i>Journal of Proteome Research</i> , 2019 , 18, 1477-1485	5.6	8
117	Quantitative Proteomics Data in the Public Domain: Challenges and Opportunities. <i>Methods in Molecular Biology</i> , 2019 , 1977, 217-235	1.4	4
116	Quantifying the impact of public omics data. <i>Nature Communications</i> , 2019 , 10, 3512	17.4	42
115	The PRIDE database and related tools and resources in 2019: improving support for quantification data. <i>Nucleic Acids Research</i> , 2019 , 47, D442-D450	20.1	3856
114	Response to "Comparison and Evaluation of Clustering Algorithms for Tandem Mass Spectra". <i>Journal of Proteome Research</i> , 2018 , 17, 1993-1996	5.6	7
113	ProForma: A Standard Proteoform Notation. <i>Journal of Proteome Research</i> , 2018 , 17, 1321-1325	5.6	27
112	Expression Atlas: gene and protein expression across multiple studies and organisms. <i>Nucleic Acids Research</i> , 2018 , 46, D246-D251	20.1	222
111	Direct Evidence of the Presence of Cross-Linked Aβ Dimers in the Brains of Alzheimer's Disease Patients. <i>Analytical Chemistry</i> , 2018 , 90, 4552-4560	7.8	28
110	The SystemMHC Atlas project. <i>Nucleic Acids Research</i> , 2018 , 46, D1237-D1247	20.1	87
109	The proBAM and proBed standard formats: enabling a seamless integration of genomics and proteomics data. <i>Genome Biology</i> , 2018 , 19, 12	18.3	16
108	Future Prospects of Spectral Clustering Approaches in Proteomics. <i>Proteomics</i> , 2018 , 18, e1700454	4.8	10
107	Expanding the Use of Spectral Libraries in Proteomics. <i>Journal of Proteome Research</i> , 2018 , 17, 4051-4060	5.6	26
106	Minimal Information About an Immuno-Peptidomics Experiment (MIAIPE). <i>Proteomics</i> , 2018 , 18, e18001108	10.3	14
105	A Golden Age for Working with Public Proteomics Data. <i>Trends in Biochemical Sciences</i> , 2017 , 42, 333-341	10.3	65

104	Synthetic human proteomes for accelerating protein research. <i>Nature Methods</i> , 2017 , 14, 240-242	21.6	4
103	Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , 2017 , 35, 406-409	44.5	105
102	Enhanced Missing Proteins Detection in NCI60 Cell Lines Using an Integrative Search Engine Approach. <i>Journal of Proteome Research</i> , 2017 , 16, 4374-4390	5.6	6
101	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. <i>Nucleic Acids Research</i> , 2017 , 45, D1100-D1106	20.1	568
100	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017 , 16, 4288-4298	5.6	61
99	Using the PRIDE Database and ProteomeXchange for Submitting and Accessing Public Proteomics Datasets. <i>Current Protocols in Bioinformatics</i> , 2017 , 59, 13.31.1-13.31.12	24.2	29
98	OLS Client and OLS Dialog: Open Source Tools to Annotate Public Omics Datasets. <i>Proteomics</i> , 2017 , 17, 1700244	4.8	13
97	Lack of Glycogenin Causes Glycogen Accumulation and Muscle Function Impairment. <i>Cell Metabolism</i> , 2017 , 26, 256-266.e4	24.6	45
96	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. <i>Molecular and Cellular Proteomics</i> , 2017 , 16, 1275-1285	7.6	37
95	A community proposal to integrate proteomics activities in ELIXIR. <i>F1000Research</i> , 2017 , 6,	3.6	10
94	Accurate and fast feature selection workflow for high-dimensional omics data. <i>PLoS ONE</i> , 2017 , 12, e0189875	39.75	40
93	2016 update of the PRIDE database and its related tools. <i>Nucleic Acids Research</i> , 2016 , 44, D447-56	20.1	2440
92	Making sense of big data in health research: Towards an EU action plan. <i>Genome Medicine</i> , 2016 , 8, 71	14.4	146
91	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. <i>Nature Methods</i> , 2016 , 13, 651-656	21.6	99
90	Exploring the potential of public proteomics data. <i>Proteomics</i> , 2016 , 16, 214-25	4.8	54
89	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, 305-17	7.6	91
88	Detection of Missing Proteins Using the PRIDE Database as a Source of Mass Spectrometry Evidence. <i>Journal of Proteome Research</i> , 2016 , 15, 4101-4115	5.6	12
87	A public repository for mass spectrometry imaging data. <i>Analytical and Bioanalytical Chemistry</i> , 2015 , 407, 2027-33	4.4	27

86	Delicate Metabolic Control and Coordinated Stress Response Critically Determine Antifungal Tolerance of <i>Candida albicans</i> Biofilm Persisters. <i>Antimicrobial Agents and Chemotherapy</i> , 2015 , 59, 6101-12	5.9	49
85	ms-data-core-api: an open-source, metadata-oriented library for computational proteomics. <i>Bioinformatics</i> , 2015 , 31, 2903-5	7.2	26
84	Quest for Missing Proteins: Update 2015 on Chromosome-Centric Human Proteome Project. <i>Journal of Proteome Research</i> , 2015 , 14, 3415-31	5.6	50
83	Development of data representation standards by the human proteome organization proteomics standards initiative. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015 , 22, 495-506	8.6	42
82	Embedding standards in metabolomics: the Metabolomics Society data standards task group. <i>Metabolomics</i> , 2015 , 11, 782-783	4.7	12
81	Open source libraries and frameworks for biological data visualisation: a guide for developers. <i>Proteomics</i> , 2015 , 15, 1356-74	4.8	34
80	Analysis of the tryptic search space in UniProt databases. <i>Proteomics</i> , 2015 , 15, 48-57	4.8	10
79	Identifying novel biomarkers through data mining-a realistic scenario?. <i>Proteomics - Clinical Applications</i> , 2015 , 9, 437-43	3.1	14
78	Making proteomics data accessible and reusable: current state of proteomics databases and repositories. <i>Proteomics</i> , 2015 , 15, 930-49	4.8	138
77	Introducing the PRIDE Archive RESTful web services. <i>Nucleic Acids Research</i> , 2015 , 43, W599-604	20.1	15
76	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014 , 32, 223-6	44.5	2053
75	How to submit MS proteomics data to ProteomeXchange via the PRIDE database. <i>Proteomics</i> , 2014 , 14, 2233-41	4.8	41
74	jmzTab: a java interface to the mzTab data standard. <i>Proteomics</i> , 2014 , 14, 1328-32	4.8	14
73	Controlled vocabularies and ontologies in proteomics: overview, principles and practice. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 98-107	4	26
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	4	59
71	A standardized framing for reporting protein identifications in mzIdentML 1.2. <i>Proteomics</i> , 2014 , 14, 2389-99	4.8	16
70	Analysis of the protein domain and domain architecture content in fungi and its application in the search of new antifungal targets. <i>PLoS Computational Biology</i> , 2014 , 10, e1003733	5	15
69	qcML: an exchange format for quality control metrics from mass spectrometry experiments. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1905-13	7.6	36

68	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, 2765-75	7.6	96
67	A survey of molecular descriptors used in mass spectrometry based proteomics. <i>Current Topics in Medicinal Chemistry</i> , 2014 , 14, 388-97	3	5
66	PRIDE Cluster: building a consensus of proteomics data. <i>Nature Methods</i> , 2013 , 10, 95-6	21.6	49
65	The PRoteomics IDentifications (PRIDE) database and associated tools: status in 2013. <i>Nucleic Acids Research</i> , 2013 , 41, D1063-9	20.1	1587
64	Pride-asap: automatic fragment ion annotation of identified PRIDE spectra. <i>Journal of Proteomics</i> , 2013 , 95, 89-92	3.9	14
63	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, 3515-20	7.8	6
62	The mzQuantML data standard for mass spectrometry-based quantitative studies in proteomics. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 2332-40	7.6	55
61	Tools (Viewer, Library and Validator) that facilitate use of the peptide and protein identification standard format, termed mzIdentML. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 3026-35	7.6	28
60	Shorthand notation for lipid structures derived from mass spectrometry. <i>Journal of Lipid Research</i> , 2013 , 54, 1523-1530	6.3	531
59	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat009	5	56
58	From Peptidome to PRIDE: public proteomics data migration at a large scale. <i>Proteomics</i> , 2013 , 13, 1692-1698	4.8	11
57	LipidHome: a database of theoretical lipids optimized for high throughput mass spectrometry lipidomics. <i>PLoS ONE</i> , 2013 , 8, e61951	3.7	59
56	Proteomics data exchange and storage: the need for common standards and public repositories. <i>Methods in Molecular Biology</i> , 2013 , 1007, 317-33	1.4	9
55	Isoelectric point optimization using peptide descriptors and support vector machines. <i>Journal of Proteomics</i> , 2012 , 75, 2269-74	3.9	30
54	Ten years of standardizing proteomic data: a report on the HUPO-PSI Spring Workshop: April 12-14th, 2012, San Diego, USA. <i>Proteomics</i> , 2012 , 12, 2767-72	4.8	15
53	jmzIdentML API: A Java interface to the mzIdentML standard for peptide and protein identification data. <i>Proteomics</i> , 2012 , 12, 790-4	4.8	27
52	jmzReader: A Java parser library to process and visualize multiple text and XML-based mass spectrometry data formats. <i>Proteomics</i> , 2012 , 12, 795-8	4.8	26
51	PRIDE Inspector: a tool to visualize and validate MS proteomics data. <i>Nature Biotechnology</i> , 2012 , 30, 135-7	44.5	103

50	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, 1682-9	7.6	96
49	Improvements in the Protein Identifier Cross-Reference service. <i>Nucleic Acids Research</i> , 2012 , 40, W276-80	10.1	27
48	PRIDE: quality control in a proteomics data repository. <i>Database: the Journal of Biological Databases and Curation</i> , 2012 , 2012, bas004	5	30
47	The mzIdentML data standard for mass spectrometry-based proteomics results. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.014381	7.6	150
46	Consequences of the discontinuation of the International Protein Index (IPI) database and its substitution by the UniProtKB "complete proteome" sets. <i>Proteomics</i> , 2011 , 11, 4434-8	4.8	24
45	Proteomic temporal profile of human brain endothelium after oxidative stress. <i>Stroke</i> , 2011 , 42, 37-43	6.7	50
44	Published and perished? The influence of the searched protein database on the long-term storage of proteomics data. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.008490	7.6	16
43	Critical amino acid residues in proteins: a BioMart integration of Reactome protein annotations with PRIDE mass spectrometry data and COSMIC somatic mutations. <i>Database: the Journal of Biological Databases and Curation</i> , 2011 , 2011, bar047	5	7
42	Submitting proteomics data to PRIDE using PRIDE Converter. <i>Methods in Molecular Biology</i> , 2011 , 694, 237-53	1.4	2
41	PRIDE and "Database on Demand" as valuable tools for computational proteomics. <i>Methods in Molecular Biology</i> , 2011 , 696, 93-105	1.4	13
40	EST analysis pipeline: use of distributed computing resources. <i>Methods in Molecular Biology</i> , 2011 , 722, 103-20	1.4	
39	The Ontology Lookup Service: bigger and better. <i>Nucleic Acids Research</i> , 2010 , 38, W155-60	20.1	82
38	The Proteomics Identifications database: 2010 update. <i>Nucleic Acids Research</i> , 2010 , 38, D736-42	20.1	199
37	PRIDE: Data submission and analysis. <i>Current Protocols in Protein Science</i> , 2010 , Chapter 25, Unit 25.4	3.1	12
36	Proteomics data repositories: providing a safe haven for your data and acting as a springboard for further research. <i>Journal of Proteomics</i> , 2010 , 73, 2136-46	3.9	49
35	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , 2010 , 10, 3957-69	4.8	44
34	A guide to the Proteomics Identifications Database proteomics data repository. <i>Proteomics</i> , 2009 , 9, 4276-83	4.8	198
33	Charting online OMICS resources: A navigational chart for clinical researchers. <i>Proteomics - Clinical Applications</i> , 2009 , 3, 18-29	3.1	11

32	PRIDE Converter: making proteomics data-sharing easy. <i>Nature Biotechnology</i> , 2009 , 27, 598-9	44.5	152
31	A HUPO test sample study reveals common problems in mass spectrometry-based proteomics. <i>Nature Methods</i> , 2009 , 6, 423-30	21.6	270
30	Gene expression analysis of the biocontrol fungus <i>Trichoderma harzianum</i> in the presence of tomato plants, chitin, or glucose using a high-density oligonucleotide microarray. <i>BMC Microbiology</i> , 2009 , 9, 217	4.5	49
29	Analyzing large-scale proteomics projects with latent semantic indexing. <i>Journal of Proteome Research</i> , 2008 , 7, 182-91	5.6	36
28	Analysis of the experimental detection of central nervous system-related genes in human brain and cerebrospinal fluid datasets. <i>Proteomics</i> , 2008 , 8, 1138-48	4.8	18
27	The PSI formal document process and its implementation on the PSI website. <i>Proteomics</i> , 2007 , 7, 2355-7	4.8	35
26	Generation, annotation, and analysis of ESTs from four different <i>Trichoderma</i> strains grown under conditions related to biocontrol. <i>Applied Microbiology and Biotechnology</i> , 2007 , 75, 853-62	5.7	38
25	Characterization of genes encoding novel peptidases in the biocontrol fungus <i>Trichoderma harzianum</i> CECT 2413 using the TrichoEST functional genomics approach. <i>Current Genetics</i> , 2007 , 51, 331-42	2.9	62
24	Partial silencing of a hydroxy-methylglutaryl-CoA reductase-encoding gene in <i>Trichoderma harzianum</i> CECT 2413 results in a lower level of resistance to lovastatin and lower antifungal activity. <i>Fungal Genetics and Biology</i> , 2007 , 44, 269-83	3.9	50
23	Detection of peptaibols and partial cloning of a putative peptaibol synthetase gene from <i>T. harzianum</i> CECT 2413. <i>Folia Microbiologica</i> , 2006 , 51, 114-20	2.8	17
22	Generation, annotation and analysis of ESTs from <i>Trichoderma harzianum</i> CECT 2413. <i>BMC Genomics</i> , 2006 , 7, 193	4.5	53
21	Cloning and characterization of the <i>erg1</i> gene of <i>Trichoderma harzianum</i> : effect of the <i>erg1</i> silencing on ergosterol biosynthesis and resistance to terbinafine. <i>Fungal Genetics and Biology</i> , 2006 , 43, 164-78	3.9	69
20	ThPTR2, a di/tri-peptide transporter gene from <i>Trichoderma harzianum</i> . <i>Fungal Genetics and Biology</i> , 2006 , 43, 234-46	3.9	34
19	A comparison of the phenotypic and genetic stability of recombinant <i>Trichoderma</i> spp. generated by protoplast- and <i>Agrobacterium</i> -mediated transformation. <i>Journal of Microbiology</i> , 2006 , 44, 383-95	3	39
18	Detection of putative peptide synthetase genes in <i>Trichoderma</i> species: application of this method to the cloning of a gene from <i>T. harzianum</i> CECT 2413. <i>FEMS Microbiology Letters</i> , 2005 , 244, 139-48	2.9	34
17	Screening of antimicrobial activities in <i>Trichoderma</i> isolates representing three trichoderma sections. <i>Mycological Research</i> , 2005 , 109, 1397-406		37
16	Genetic diversity shown in <i>Trichoderma</i> biocontrol isolates. <i>Mycological Research</i> , 2004 , 108, 897-906		63
15	Cell wall-degrading isoenzyme profiles of <i>Trichoderma</i> biocontrol strains show correlation with rDNA taxonomic species. <i>Current Genetics</i> , 2004 , 46, 277-86	2.9	46

14	Colour pigments of <i>Trichoderma harzianum</i> . Preliminary investigations with thin-layer chromatography-Fourier transform infrared spectroscopy and high-performance liquid chromatography with diode array and mass spectrometric detection. <i>Journal of Chromatography A</i> , 2000 , 896, 61-8	4.5	13
13	Microbial contamination of carcasses and equipment from an Iberian pig slaughterhouse. <i>Journal of Food Protection</i> , 2000 , 63, 1670-5	2.5	24
12	Separation and identification of volatile components in the fermentation broth of <i>Trichoderma atroviride</i> by solid-phase extraction and gas chromatography-mass spectrometry. <i>Journal of Chromatographic Science</i> , 2000 , 38, 421-4	1.4	57
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	BioContainers Registry: searching for bioinformatics tools, packages and containers		4
8	Universal Spectrum Identifier for mass spectra		5
7	Cross-linking/Mass Spectrometry: A Community-Wide, Comparative Study Towards Establishing Best Practice Guidelines		4
6	The functional landscape of the human phosphoproteome		3
5	Proteomics Standards Initiative Extended FASTA Format (PEFF)		1
4	An integrated landscape of protein expression in human cancer		2
3	Implementing the re-use of public DIA proteomics datasets: from the PRIDE database to Expression Atlas		5
2	An integrated view of baseline protein expression in human tissues		2
1	Integrated view and comparative analysis of baseline protein expression in mouse and rat tissues		1