Andrew R Jones

List of Publications by Year
in descending order

111 papers	8,550 citations	108046 37 h-index	56606 87 g-index
134 all docs	134 docs citations	134 times ranked	17952 citing authors

#	Article	IF	Citations
1	VEuPathDB: the eukaryotic pathogen, vector and host bioinformatics resource center. Nucleic Acids Research, 2022, 50, D898-D911.	6.5	277
2	Profiling the Human Phosphoproteome to Estimate the True Extent of Protein Phosphorylation. Journal of Proteome Research, 2022, 21, 1510-1524.	1.8	15
3	Method for Independent Estimation of the False Localization Rate for Phosphoproteomics. Journal of Proteome Research, 2022, 21, 1603-1615.	1.8	14
4	Integrated view and comparative analysis of baseline protein expression in mouse and rat tissues. PLoS Computational Biology, 2022, 18, e1010174.	1.5	11
5	A snapshot of human leukocyte antigen (HLA) diversity using data from the Allele Frequency Net Database. Human Immunology, 2021, 82, 496-504.	1.2	13
6	mzMLb: A Future-Proof Raw Mass Spectrometry Data Format Based on Standards-Compliant mzML and Optimized for Speed and Storage Requirements. Journal of Proteome Research, 2021, 20, 172-183.	1.8	12
7	An OMICs-based meta-analysis to support infection state stratification. Bioinformatics, 2021, 37, 2347-2355.	1.8	2
8	A Proteome-Wide Immunoinformatics Tool to Accelerate T-Cell Epitope Discovery and Vaccine Design in the Context of Emerging Infectious Diseases: An Ethnicity-Oriented Approach. Frontiers in Immunology, 2021, 12, 598778.	2.2	14
9	Temporal modulation of the NF-κB RelA network in response to different types of DNA damage. Biochemical Journal, 2021, 478, 533-551.	1.7	10
10	lcmsWorld: High-Performance 3D Visualization Software for Mass Spectrometry. Journal of Proteome Research, 2021, 20, 1981-1985.	1.8	1
11	MHCVision: estimation of global and local false discovery rate for MHC class I peptide binding prediction. Bioinformatics, 2021, 37, 3830-3838.	1.8	1
12	Characterising proteolysis during SARS-CoV-2 infection identifies viral cleavage sites and cellular targets with therapeutic potential. Nature Communications, 2021, 12, 5553.	5.8	76
13	Allele frequency net database (AFND) 2020 update: gold-standard data classification, open access genotype data and new query tools. Nucleic Acids Research, 2020, 48, D783-D788.	6.5	352
14	Investigating the relationship between class I HLA-specific immunoglobulin-G subclasses, Pan-IgG single antigen bead assays and complement mediated interference in sera from renal transplant recipients. Transplant Immunology, 2020, 63, 101332.	0.6	0
15	Investigating complement mediated interference in class I HLA-specific antibodies following renal transplantation. Transplant Immunology, 2020, 62, 101310.	0.6	3
16	Informatics investigations into anti-thyroid drug induced agranulocytosis associated with multiple HLA-B alleles. PLoS ONE, 2020, 15, e0220754.	1.1	3
17	Use of the Polo-like kinase 4 (PLK4) inhibitor centrinone to investigate intracellular signalling networks using SILAC-based phosphoproteomics. Biochemical Journal, 2020, 477, 2451-2475.	1.7	23
18	Proteome Bioinformatics Methods for Studying Histidine Phosphorylation. Methods in Molecular Biology, 2020, 2077, 237-250.	0.4	0

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19	Strong anion exchange–mediated phosphoproteomics reveals extensive human non–canonical phosphorylation. EMBO Journal, 2019, 38, e100847.	3.5	118
20	VAPPER: High-throughput variant antigen profiling in African trypanosomes of livestock. GigaScience, 2019, 8, .	3.3	5
21	mzTab-M: A Data Standard for Sharing Quantitative Results in Mass Spectrometry Metabolomics. Analytical Chemistry, 2019, 91, 3302-3310.	3.2	43
22	Improvements to the Rice Genome Annotation Through Large-Scale Analysis of RNA-Seq and Proteomics Data Sets. Molecular and Cellular Proteomics, 2019, 18, 86-98.	2.5	22
23	Comparative qualitative phosphoproteomics analysis identifies shared phosphorylation motifs and associated biological processes in evolutionary divergent plants. Journal of Proteomics, 2018, 181, 152-159.	1.2	20
24	phpMs: A PHP-Based Mass Spectrometry Utilities Library. Journal of Proteome Research, 2018, 17, 1309-1313.	1.8	8
25	nmrML: A Community Supported Open Data Standard for the Description, Storage, and Exchange of NMR Data. Analytical Chemistry, 2018, 90, 649-656.	3.2	50
26	The proBAM and proBed standard formats: enabling a seamless integration of genomics and proteomics data. Genome Biology, 2018, 19, 12.	3.8	21
27	Critical assessment of approaches for molecular docking to elucidate associations of HLA alleles with adverse drug reactions. Molecular Immunology, 2018, 101, 488-499.	1.0	14
28	Allele Frequency Net Database. Methods in Molecular Biology, 2018, 1802, 49-62.	0.4	38
29	Genome-wide association study of nevirapine hypersensitivity in a sub-Saharan African HIV-infected population. Journal of Antimicrobial Chemotherapy, 2017, 72, dkw545.	1.3	42
30	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. Journal of Proteome Research, 2017, 16, 4288-4298.	1.8	87
31	Evaluation of Parameters for Confident Phosphorylation Site Localization Using an Orbitrap Fusion Tribrid Mass Spectrometer. Journal of Proteome Research, 2017, 16, 3448-3459.	1.8	68
32	The mzIdentML Data Standard Version 1.2, Supporting Advances in Proteome Informatics. Molecular and Cellular Proteomics, 2017, 16, 1275-1285.	2.5	55
33	Neopeptide Analyser: A software tool for neopeptide discovery in proteomics data. Wellcome Open Research, 2017, 2, 24.	0.9	8
34	A web resource for mining HLA associations with adverse drug reactions: HLA-ADR. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw069.	1.4	24
35	Allele Frequencies Net Database: Improvements for storage of individual genotypes and analysis of existing data. Human Immunology, 2016, 77, 238-248.	1.2	107
36	Chapter 5. Protein Inference and Grouping. New Developments in Mass Spectrometry, 2016, , 93-115.	0.2	0

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37	Chapter 15. Proteogenomics: Proteomics for Genome Annotation. New Developments in Mass Spectrometry, 2016, , 365-384.	0.2	0
38	Chapter 11. Data Formats of the Proteomics Standards Initiative. New Developments in Mass Spectrometry, 2016, , 229-258.	0.2	0
39	The mzqLibrary â€" An open source Java library supporting the HUPOâ€PSI quantitative proteomics standard. Proteomics, 2015, 15, 3152-3162.	1.3	5
40	Representation of selectedâ€reaction monitoring data in the mzQuantML data standard. Proteomics, 2015, 15, 2592-2596.	1.3	7
41	Galaxy Integrated Omics: Web-based Standards-Compliant Workflows for Proteomics Informed by Transcriptomics*. Molecular and Cellular Proteomics, 2015, 14, 3087-3093.	2.5	30
42	A bioinformatics tool for epitope-based vaccine design that accounts for human ethnic diversity: Application to emerging infectious diseases. Vaccine, 2015, 33, 1267-1273.	1.7	40
43	Allele frequency net 2015 update: new features for HLA epitopes, KIR and disease and HLA adverse drug reaction associations. Nucleic Acids Research, 2015, 43, D784-D788.	6.5	693
44	A largeâ€scale proteogenomics study of apicomplexan pathogensâ€"<i>Toxoplasma gondii</i> and <i>Neospora caninum</i>. Proteomics, 2015, 15, 2618-2628.	1.3	19
45	IPeak: An open source tool to combine results from multiple MS/MS search engines. Proteomics, 2015, 15, 2916-2920.	1.3	33
46	Development of data representation standards by the human proteome organization proteomics standards initiative. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 495-506.	2.2	54
47	Embedding standards in metabolomics: the Metabolomics Society data standards task group. Metabolomics, 2015, 11, 782-783.	1.4	13
48	Computational phosphoproteomics: From identification to localization. Proteomics, 2015, 15, 950-963.	1.3	24
49	A standardized framing for reporting protein identifications in mzIdentML 1.2. Proteomics, 2014, 14, 2389-2399.	1.3	23
50	ProteoAnnotator â€" Open source proteogenomics annotation software supporting PSI standards. Proteomics, 2014, 14, 2731-2741.	1.3	38
51	The jmzQuantML programming interface and validator for the mzQuantML data standard. Proteomics, 2014, 14, 685-688.	1.3	8
52	The mzTab Data Exchange Format: Communicating Mass-spectrometry-based Proteomics and Metabolomics Experimental Results to a Wider Audience. Molecular and Cellular Proteomics, 2014, 13, 2765-2775.	2.5	130
53	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. Nature Biotechnology, 2014, 32, 223-226.	9.4	2,505
54	A tutorial for software development in quantitative proteomics using PSI standard formats. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 88-97.	1.1	4

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55	How to submit MS proteomics data to ProteomeXchange via the PRIDE database. Proteomics, 2014, 14, 2233-2241.	1.3	54
56	Numerical Compression Schemes for Proteomics Mass Spectrometry Data. Molecular and Cellular Proteomics, 2014, 13, 1537-1542.	2.5	53
57	An integrated approach to understand apicomplexan metabolism from their genomes. BMC Bioinformatics, 2014, 15, .	1.2	1
58	jmzTab: A Java interface to the mzTab data standard. Proteomics, 2014, 14, 1328-1332.	1.3	16
59	Controlled vocabularies and ontologies in proteomics: Overview, principles and practice. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 98-107.	1.1	36
60	Allele Frequencies Database. Transfusion Medicine and Hemotherapy, 2014, 41, 352-355.	0.7	31
61	Guidelines for reporting quantitative mass spectrometry based experiments in proteomics. Journal of Proteomics, 2013, 95, 84-88.	1.2	46
62	A guide for integration of proteomic data standards into laboratory workflows. Proteomics, 2013, 13, 480-492.	1.3	7
63	The mzQuantML Data Standard for Mass Spectrometry–based Quantitative Studies in Proteomics. Molecular and Cellular Proteomics, 2013, 12, 2332-2340.	2.5	66
64	Tools (Viewer, Library and Validator) that Facilitate Use of the Peptide and Protein Identification Standard Format, Termed mzIdentML. Molecular and Cellular Proteomics, 2013, 12, 3026-3035.	2.5	32
65	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat009-bat009.	1.4	76
66	A database for curating the associations between killer cell immunoglobulin-like receptors and diseases in worldwide populations. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat021.	1.4	27
67	Library of Apicomplexan Metabolic Pathways: a manually curated database for metabolic pathways of apicomplexan parasites. Nucleic Acids Research, 2013, 41, D706-D713.	6.5	61
68	FuGE. , 2013, , 762-765.		0
69	The mzIdentML Data Standard for Mass Spectrometry-Based Proteomics Results. Molecular and Cellular Proteomics, 2012, 11, M111.014381-1-M111.014381-10.	2.5	175
70	A Software Toolkit and Interface for Performing Stable Isotope Labeling and Top3 Quantification Using Progenesis LC-MS. OMICS A Journal of Integrative Biology, 2012, 16, 489-495.	1.0	47
71	Bioinformatics Challenges and Solutions in Proteomics as Quantitative Methods Mature. OMICS A Journal of Integrative Biology, 2012, 16, 429-430.	1.0	0
72	Ten Years of Standardizing Proteomic Data: A Report on the HUPO–PSI Spring Workshop. Proteomics, 2012, 12, 2767-2772.	1.3	16

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73	A Critical Appraisal of Techniques, Software Packages, and Standards for Quantitative Proteomic Analysis. OMICS A Journal of Integrative Biology, 2012, 16, 431-442.	1.0	50
74	In silico analysis of HLA associations with drug-induced liver injury: use of a HLA-genotyped DNA archive from healthy volunteers. Genome Medicine, 2012, 4, 51.	3.6	58
75	jmzIdentML API: A Java interface to the mzIdentML standard for peptide and protein identification data. Proteomics, 2012, 12, 790-794.	1.3	29
76	Software for analysing ion mobility mass spectrometry data to improve peptide identification. Proteomics, 2012, 12, 1912-1916.	1.3	3
77	FDRAnalysis: A Tool for the Integrated Analysis of Tandem Mass Spectrometry Identification Results from Multiple Search Engines. Journal of Proteome Research, 2011, 10, 2088-2094.	1.8	18
78	A DIGE study on the effects of salbutamol on the rat muscle proteome - an exemplar of best practice for data sharing in proteomics. BMC Research Notes, 2011, 4, 86.	0.6	6
79	Allele frequency net: a database and online repository for immune gene frequencies in worldwide populations. Nucleic Acids Research, 2011, 39, D913-D919.	6.5	637
80	The ProteoRed MIAPE web toolkit: A User-friendly Framework to Connect and Share Proteomics Standards. Molecular and Cellular Proteomics, 2011, 10, M111.008334.	2.5	23
81	Semi‐automatic tool to describe, store and compare proteomics experiments based on MIAPE compliant reports. Proteomics, 2010, 10, 1256-1260.	1.3	16
82	The Gel Electrophoresis Markup Language (GelML) from the Proteomics Standards Initiative. Proteomics, 2010, 10, 3073-3081.	1.3	19
83	Guidelines for reporting the use of column chromatography in proteomics. Nature Biotechnology, 2010, 28, 654-654.	9.4	24
84	Guidelines for reporting the use of gel image informatics in proteomics. Nature Biotechnology, 2010, 28, 655-656.	9.4	22
85	Managing Experimental Data Using FuGE. Methods in Molecular Biology, 2010, 604, 333-343.	0.4	4
86	An Introduction to Proteome Bioinformatics. Methods in Molecular Biology, 2010, 604, 1-5.	0.4	5
87	XGAP: a uniform and extensible data model and software platform for genotype and phenotype experiments. Genome Biology, 2010, 11, R27.	13.9	20
88	Modeling and Managing Experimental Data Using FuGE. OMICS A Journal of Integrative Biology, 2009, 13, 239-251.	1.0	8
89	FuGEFlow: data model and markup language for flow cytometry. BMC Bioinformatics, 2009, 10, 184.	1.2	6
90	Improving sensitivity in proteome studies by analysis of false discovery rates for multiple search engines. Proteomics, 2009, 9, 1220-1229.	1.3	91

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91	The PSI semantic validator: A framework to check MIAPE compliance of proteomics data. Proteomics, 2009, 9, 5112-5119.	1.3	55
92	Annual Spring Meeting of the Proteomics Standards Initiative. Proteomics, 2009, 9, 4429-4432.	1.3	9
93	Guidelines for reporting the use of gel electrophoresis in proteomics. Nature Biotechnology, 2008, 26, 863-864.	9.4	61
94	The proteome of Toxoplasma gondii: integration with the genome provides novel insights into gene expression and annotation. Genome Biology, 2008, 9, R116.	13.9	109
95	Modulation of the Host Cell Proteome by the Intracellular Apicomplexan Parasite<i>Toxoplasma gondii</i>. Infection and Immunity, 2008, 76, 828-844.	1.0	114
96	A toolkit for capturing and sharing FuGE experiments. Bioinformatics, 2008, 24, 2647-2649.	1.8	8
97	Minimum Reporting Guidelines for Proteomics Released by the Proteomics Standards Initiative. Molecular and Cellular Proteomics, 2008, 7, 2067-2068.	2.5	7
98	An informatic pipeline for the data capture and submission of quantitative proteomic data using iTRAQ. Proteome Science, 2007, 5, 4.	0.7	21
99	Capture and analysis of quantitative proteomic data. Proteomics, 2007, 7, 2787-2799.	1.3	54
100	An Update on Data Standards for Gel Electrophoresis. Proteomics, 2007, 7, 35-40.	1.3	12
101	Five years of progress in the Standardization of Proteomics Data 4th Annual Spring Workshop of the HUPO-Proteomics Standards Initiative April 23â€"25, 2007 Ecole Nationale SupÃ©rieure (ENS), Lyon, France. Proteomics, 2007, 7, 3436-3440.	1.3	46
102	The minimum information about a proteomics experiment (MIAPE). Nature Biotechnology, 2007, 25, 887-893.	9.4	694
103	The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics. Nature Biotechnology, 2007, 25, 1127-1133.	9.4	96
104	Storing, Searching, and Disseminating Experimental Proteomics Data. , 2007, , 472-483.		0
105	FuGE: Functional Genomics Experiment Object Model. OMICS A Journal of Integrative Biology, 2006, 10, 179-184.	1.0	20
106	A Strategy Capitalizing on Synergies: The Reporting Structure for Biological Investigation (RSBI) Working Group. OMICS A Journal of Integrative Biology, 2006, 10, 164-171.	1.0	33
107	Visualisation and analysis of proteomic data from the procyclic form ofTrypanosoma brucei. Proteomics, 2006, 6, 259-267.	1.3	43
108	Data Access and Integration in the ISPIDER Proteomics Grid. Lecture Notes in Computer Science, 2006, , 3-18.	1.0	14

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109	An analysis of extensible modelling for functional genomics data. BMC Bioinformatics, 2005, 6, 235.	1.2	10
110	An object model and database for functional genomics. Bioinformatics, 2004, 20, 1583-1590.	1.8	40
111	Proposal for a Standard Representation of Two-Dimensional Gel Electrophoresis Data. Comparative and Functional Genomics, 2003, 4, 492-501.	2.0	11