

Henning Hermjakob

List of Publications by Year in descending order

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Version: 2024-02-01

258
papers

74,142
citations

5268

83
h-index

613

259
g-index

307
all docs

307
docs citations

307
times ranked

85806
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	27.8	21,074
2	2016 update of the PRIDE database and its related tools. <i>Nucleic Acids Research</i> , 2016, 44, D447-D456.	14.5	3,451
3	The Reactome pathway Knowledgebase. <i>Nucleic Acids Research</i> , 2016, 44, D481-D487.	14.5	3,319
4	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	17.5	2,505
5	The Reactome Pathway Knowledgebase. <i>Nucleic Acids Research</i> , 2018, 46, D649-D655.	14.5	2,388
6	The Proteomics Identifications (PRIDE) database and associated tools: status in 2013. <i>Nucleic Acids Research</i> , 2012, 41, D1063-D1069.	14.5	1,858
7	The MIntAct project—IntAct as a common curation platform for 11 molecular interaction databases. <i>Nucleic Acids Research</i> , 2014, 42, D358-D363.	14.5	1,634
8	On the frequency of protein glycosylation, as deduced from analysis of the SWISS-PROT database. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 1999, 1473, 4-8.	2.4	1,601
9	The reactome pathway knowledgebase. <i>Nucleic Acids Research</i> , 2020, 48, D498-D503.	14.5	1,570
10	The Reactome pathway knowledgebase. <i>Nucleic Acids Research</i> , 2014, 42, D472-D477.	14.5	1,448
11	Reactome: a database of reactions, pathways and biological processes. <i>Nucleic Acids Research</i> , 2011, 39, D691-D697.	14.5	1,391
12	Databases on transcriptional regulation: TRANSFAC, TRRD and COMPEL. <i>Nucleic Acids Research</i> , 1998, 26, 362-367.	14.5	1,345
13	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008, 26, 541-547.	17.5	1,069
14	iProX: an integrated proteome resource. <i>Nucleic Acids Research</i> , 2019, 47, D1211-D1217.	14.5	1,001
15	The IntAct molecular interaction database in 2012. <i>Nucleic Acids Research</i> , 2012, 40, D841-D846.	14.5	962
16	The InterPro database, an integrated documentation resource for protein families, domains and functional sites. <i>Nucleic Acids Research</i> , 2001, 29, 37-40.	14.5	928
17	The reactome pathway knowledgebase 2022. <i>Nucleic Acids Research</i> , 2022, 50, D687-D692.	14.5	924
18	IntAct: an open source molecular interaction database. <i>Nucleic Acids Research</i> , 2004, 32, 452D-455.	14.5	864

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19	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. <i>Nucleic Acids Research</i> , 2017, 45, D1100-D1106.	14.5	860
20	Overview of the HUPO Plasma Proteome Project: Results from the pilot phase with 35 collaborating laboratories and multiple analytical groups, generating a core dataset of 3020 proteins and a publicly available database. <i>Proteomics</i> , 2005, 5, 3226-3245.	2.2	766
21	Reactome knowledgebase of human biological pathways and processes. <i>Nucleic Acids Research</i> , 2009, 37, D619-D622.	14.5	760
22	A common open representation of mass spectrometry data and its application to proteomics research. <i>Nature Biotechnology</i> , 2004, 22, 1459-1466.	17.5	724
23	IntAct—open source resource for molecular interaction data. <i>Nucleic Acids Research</i> , 2007, 35, D561-D565.	14.5	701
24	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893.	17.5	694
25	Reactome pathway analysis: a high-performance in-memory approach. <i>BMC Bioinformatics</i> , 2017, 18, 142.	2.6	600
26	The HUPO PSI's Molecular Interaction format—a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004, 22, 177-183.	17.5	581
27	The IntAct molecular interaction database in 2010. <i>Nucleic Acids Research</i> , 2010, 38, D525-D531.	14.5	574
28	mzML—a Community Standard for Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2011, 10, R110.000133.	3.8	555
29	PRIDE: The proteomics identifications database. <i>Proteomics</i> , 2005, 5, 3537-3545.	2.2	553
30	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896.	17.5	506
31	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. <i>Nature Methods</i> , 2012, 9, 345-350.	19.0	500
32	The ProteomeXchange consortium in 2020: enabling “big data” approaches in proteomics. <i>Nucleic Acids Research</i> , 2020, 48, D1145-D1152.	14.5	491
33	Disrupted in Schizophrenia 1 Interactome: evidence for the close connectivity of risk genes and a potential synaptic basis for schizophrenia. <i>Molecular Psychiatry</i> , 2007, 12, 74-86.	7.9	386
34	Toward interoperable bioscience data. <i>Nature Genetics</i> , 2012, 44, 121-126.	21.4	362
35	Open Targets: a platform for therapeutic target identification and validation. <i>Nucleic Acids Research</i> , 2017, 45, D985-D994.	14.5	355
36	BioModels: ten-year anniversary. <i>Nucleic Acids Research</i> , 2015, 43, D542-D548.	14.5	334

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37	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	17.5	314
38	InterPro--an integrated documentation resource for protein families, domains and functional sites. <i>Bioinformatics</i> , 2000, 16, 1145-1150.	4.1	301
39	Clinical proteomics: A need to define the field and to begin to set adequate standards. <i>Proteomics - Clinical Applications</i> , 2007, 1, 148-156.	1.6	274
40	The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007, 25, 894-898.	17.5	274
41	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.	19.0	274
42	Annotating Cancer Variants and Anti-Cancer Therapeutics in Reactome. <i>Cancers</i> , 2012, 4, 1180-1211.	3.7	270
43	PRIDE: a public repository of protein and peptide identifications for the proteomics community. <i>Nucleic Acids Research</i> , 2006, 34, D659-D663.	14.5	254
44	Broadening the horizon " level 2.5 of the HUPO-PSI format for molecular interactions. <i>BMC Biology</i> , 2007, 5, 44.	3.8	237
45	ProteomeBinders: planning a European resource of affinity reagents for analysis of the human proteome. <i>Nature Methods</i> , 2007, 4, 13-17.	19.0	231
46	A guide to the Proteomics Identifications Database proteomics data repository. <i>Proteomics</i> , 2009, 9, 4276-4283.	2.2	220
47	The Proteomics Identifications database: 2010 update. <i>Nucleic Acids Research</i> , 2010, 38, D736-D742.	14.5	220
48	The implications of alternative splicing in the ENCODE protein complement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5495-5500.	7.1	206
49	Reactome graph database: Efficient access to complex pathway data. <i>PLoS Computational Biology</i> , 2018, 14, e1005968.	3.2	202
50	iProX in 2021: connecting proteomics data sharing with big data. <i>Nucleic Acids Research</i> , 2022, 50, D1522-D1527.	14.5	197
51	Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. <i>Nature Communications</i> , 2019, 10, 10.	12.8	193
52	The Proteomics Standards Initiative. <i>Proteomics</i> , 2003, 3, 1374-1376.	2.2	188
53	Making proteomics data accessible and reusable: Current state of proteomics databases and repositories. <i>Proteomics</i> , 2015, 15, 930-950.	2.2	181
54	<sc>SBML</sc> Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020, 16, e9110.	7.2	178

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55	The mzIdentML Data Standard for Mass Spectrometry-Based Proteomics Results. <i>Molecular and Cellular Proteomics</i> , 2012, 11, M111.014381-1-M111.014381-10.	3.8	175
56	BioModelsâ€™15 years of sharing computational models in life science. <i>Nucleic Acids Research</i> , 2020, 48, D407-D415.	14.5	175
57	The Ontology Lookup Service, a lightweight cross-platform tool for controlled vocabulary queries. <i>BMC Bioinformatics</i> , 2006, 7, 97.	2.6	170
58	Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , 2017, 35, 406-409.	17.5	159
59	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. <i>Journal of Proteome Research</i> , 2016, 15, 3961-3970.	3.7	158
60	PhaSepDB: a database of liquidâ€™liquid phase separation related proteins. <i>Nucleic Acids Research</i> , 2020, 48, D354-D359.	14.5	157
61	InterPro: An integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002, 3, 225-235.	6.5	155
62	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. <i>Nature Methods</i> , 2016, 13, 651-656.	19.0	147
63	Analyzing Proteinâ€™Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2012, 11, 2014-2031.	3.7	145
64	Path2Models: large-scale generation of computational models from biochemical pathway maps. <i>BMC Systems Biology</i> , 2013, 7, 116.	3.0	145
65	ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. <i>Molecular and Cellular Proteomics</i> , 2020, 19, 2115-2125.	3.8	145
66	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.	3.8	140
67	Reactome enhanced pathway visualization. <i>Bioinformatics</i> , 2017, 33, 3461-3467.	4.1	140
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, 2765-2775.	3.8	130
69	PRIDE: new developments and new datasets. <i>Nucleic Acids Research</i> , 2007, 36, D878-D883.	14.5	124
70	Reactome diagram viewer: data structures and strategies to boost performance. <i>Bioinformatics</i> , 2018, 34, 1208-1214.	4.1	121
71	A comparison of signal sequence prediction methods using a test set of signal peptides. <i>Bioinformatics</i> , 2000, 16, 741-742.	4.1	120
72	Calling on a million minds for community annotation in WikiProteins. <i>Genome Biology</i> , 2008, 9, R89.	9.6	117

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73	The Protein Identifier Cross-Reference (PICR) service: reconciling protein identifiers across multiple source databases. <i>BMC Bioinformatics</i> , 2007, 8, 401.	2.6	112
74	BioJS: an open source JavaScript framework for biological data visualization. <i>Bioinformatics</i> , 2013, 29, 1103-1104.	4.1	110
75	PRIDE Inspector: a tool to visualize and validate MS proteomics data. <i>Nature Biotechnology</i> , 2012, 30, 135-137.	17.5	109
76	The Ontology Lookup Service: bigger and better. <i>Nucleic Acids Research</i> , 2010, 38, W155-W160.	14.5	108
77	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.	3.8	105
78	Common interchange standards for proteomics data: Public availability of tools and schemaReport on the Proteomic Standards Initiative Workshop, 2nd Annual HUPO Congress, Montreal, Canada, 8th-11th October 2003. <i>Proteomics</i> , 2004, 4, 490-491.	2.2	100
79	The complex portal - an encyclopaedia of macromolecular complexes. <i>Nucleic Acids Research</i> , 2015, 43, D479-D484.	14.5	100
80	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. <i>Scientific Data</i> , 2020, 7, 136.	5.3	99
81	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data. <i>PLoS Biology</i> , 2017, 15, e2001414.	5.6	97
82	The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics. <i>Nature Biotechnology</i> , 2007, 25, 1127-1133.	17.5	96
83	A new reference implementation of the PSICQUIC web service. <i>Nucleic Acids Research</i> , 2013, 41, W601-W606.	14.5	91
84	Reactome pathway analysis to enrich biological discovery in proteomics data sets. <i>Proteomics</i> , 2011, 11, 3598-3613.	2.2	89
85	The IntAct database: efficient access to fine-grained molecular interaction data. <i>Nucleic Acids Research</i> , 2022, 50, D648-D653.	14.5	89
86	Integrating biological data – the Distributed Annotation System. <i>BMC Bioinformatics</i> , 2008, 9, S3.	2.6	87
87	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017, 16, 4288-4298.	3.7	87
88	Complex Portal 2018: extended content and enhanced visualization tools for macromolecular complexes. <i>Nucleic Acids Research</i> , 2019, 47, D550-D558.	14.5	85
89	Understudied proteins: opportunities and challenges for functional proteomics. <i>Nature Methods</i> , 2022, 19, 774-779.	19.0	83
90	The Proteomics Identifications Database (PRIDE) and the ProteomExchange Consortium: making proteomics data accessible. <i>Expert Review of Proteomics</i> , 2006, 3, 1-3.	3.0	82

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91	Minimum information about a bioactive entity (MIABE). <i>Nature Reviews Drug Discovery</i> , 2011, 10, 661-669.	46.4	80
92	BioModels: expanding horizons to include more modelling approaches and formats. <i>Nucleic Acids Research</i> , 2018, 46, D1248-D1253.	14.5	80
93	Quantifying the impact of public omics data. <i>Nature Communications</i> , 2019, 10, 3512.	12.8	79
94	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the <i>Journal of Biological Databases and Curation</i> , 2013, 2013, bat009-bat009.	3.0	76
95	Wikidata as a knowledge graph for the life sciences. <i>ELife</i> , 2020, 9, .	6.0	76
96	Recommendations from the 2008 International Summit on Proteomics Data Release and Sharing Policy: The Amsterdam Principles. <i>Journal of Proteome Research</i> , 2009, 8, 3689-3692.	3.7	75
97	The Ontology Lookup Service: more data and better tools for controlled vocabulary queries. <i>Nucleic Acids Research</i> , 2008, 36, W372-W376.	14.5	70
98	LipidHome: A Database of Theoretical Lipids Optimized for High Throughput Mass Spectrometry Lipidomics. <i>PLoS ONE</i> , 2013, 8, e61951.	2.5	69
99	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.	2.3	67
100	Reproducibility in systems biology modelling. <i>Molecular Systems Biology</i> , 2021, 17, e9982.	7.2	67
101	Submit Your Interaction Data the IMEx Way. <i>Proteomics</i> , 2007, 7, 28-34.	2.2	65
102	Integration of Cardiac Proteome Biology and Medicine by a Specialized Knowledgebase. <i>Circulation Research</i> , 2013, 113, 1043-1053.	4.5	65
103	The Work of the Human Proteome Organisation's Proteomics Standards Initiative (HUPO PSI). <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 145-151.	2.0	64
104	Integrated omics dissection of proteome dynamics during cardiac remodeling. <i>Nature Communications</i> , 2018, 9, 120.	12.8	64
105	R spider: a network-based analysis of gene lists by combining signaling and metabolic pathways from Reactome and KEGG databases. <i>Nucleic Acids Research</i> , 2010, 38, W78-W83.	14.5	62
106	PRIDE Cluster: building a consensus of proteomics data. <i>Nature Methods</i> , 2013, 10, 95-96.	19.0	62
107	Characterization, Design, and Function of the Mitochondrial Proteome: From Organs to Organisms. <i>Journal of Proteome Research</i> , 2014, 13, 433-446.	3.7	59
108	A data citation roadmap for scholarly data repositories. <i>Scientific Data</i> , 2019, 6, 28.	5.3	59

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109	Recurated protein interaction datasets. <i>Nature Methods</i> , 2009, 6, 860-861.	19.0	58
110	BioModels: Content, Features, Functionality, and Use. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2015, 4, 55-68.	2.5	56
111	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. <i>Journal of Proteomics</i> , 2017, 150, 170-182.	2.4	56
112	The PSI semantic validator: A framework to check MIAPE compliance of proteomics data. <i>Proteomics</i> , 2009, 9, 5112-5119.	2.2	55
113	Accurate estimation of isoelectric point of protein and peptide based on amino acid sequences. <i>Bioinformatics</i> , 2016, 32, 821-827.	4.1	55
114	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , 2010, 10, 3957-3969.	2.2	54
115	How to submit MS proteomics data to ProteomeXchange via the PRIDE database. <i>Proteomics</i> , 2014, 14, 2233-2241.	2.2	54
116	Harnessing the Heart of Big Data. <i>Circulation Research</i> , 2015, 116, 1115-1119.	4.5	54
117	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.	4.4	54
118	Do we want our data raw? Including binary mass spectrometry data in public proteomics data repositories. <i>Proteomics</i> , 2005, 5, 3501-3505.	2.2	53
119	Data management and preliminary data analysis in the pilot phase of the HUPO Plasma Proteome Project. <i>Proteomics</i> , 2005, 5, 3246-3261.	2.2	53
120	Merging and scoring molecular interactions utilising existing community standards: tools, use-cases and a case study. <i>Database: the Journal of Biological Databases and Curation</i> , 2015, 2015, bau131-bau131.	3.0	53
121	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	7.2	53
122	Minimum information about a protein affinity reagent (MIAPAR). <i>Nature Biotechnology</i> , 2010, 28, 650-653.	17.5	50
123	A Critical Appraisal of Techniques, Software Packages, and Standards for Quantitative Proteomic Analysis. <i>OMICS A Journal of Integrative Biology</i> , 2012, 16, 431-442.	2.0	50
124	Uniform resolution of compact identifiers for biomedical data. <i>Scientific Data</i> , 2018, 5, 180029.	5.3	50
125	Towards a unified open access dataset of molecular interactions. <i>Nature Communications</i> , 2020, 11, 6144.	12.8	49
126	Hydra: a scalable proteomic search engine which utilizes the Hadoop distributed computing framework. <i>BMC Bioinformatics</i> , 2012, 13, 324.	2.6	48

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127	AAtlas 1.0: a human autoantigen database. <i>Nucleic Acids Research</i> , 2017, 45, D769-D776.	14.5	48
128	VARSPIC: alternatively-spliced protein sequences derived from SWISS-PROT and TrEMBL. <i>Bioinformatics</i> , 2000, 16, 1048-1049.	4.1	47
129	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. <i>BMC Bioinformatics</i> , 2018, 19, 134.	2.6	47
130	The HUPO Proteomics Standards Initiative - Overcoming the Fragmentation of Proteomics Data. <i>Proteomics</i> , 2006, 6, 34-38.	2.2	46
131	Five years of progress in the Standardization of Proteomics Data 4th Annual Spring Workshop of the HUPO-Proteomics Standards Initiative April 23-25, 2007 Ecole Nationale Supérieure (ENS), Lyon, France. <i>Proteomics</i> , 2007, 7, 3436-3440.	2.2	46
132	The PSI formal document process and its implementation on the PSI website. <i>Proteomics</i> , 2007, 7, 2355-2357.	2.2	45
133	Open source libraries and frameworks for biological data visualisation: A guide for developers. <i>Proteomics</i> , 2015, 15, 1356-1374.	2.2	43
134	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	3.8	42
135	Proteomics data validation: why all must provide data. <i>Molecular BioSystems</i> , 2007, 3, 518.	2.9	41
136	Analyzing Large-Scale Proteomics Projects with Latent Semantic Indexing. <i>Journal of Proteome Research</i> , 2008, 7, 182-191.	3.7	41
137	A domain level interaction network of amyloid precursor protein and A β of Alzheimer's disease. <i>Proteomics</i> , 2010, 10, 2377-2395.	2.2	41
138	InteroPORC: automated inference of highly conserved protein interaction networks. <i>Bioinformatics</i> , 2008, 24, 1625-1631.	4.1	39
139	The HUPO proteomics standards initiative—easing communication and minimizing data loss in a changing world. <i>Briefings in Bioinformatics</i> , 2007, 9, 166-173.	6.5	38
140	A visual review of the interactome of LRRK2: Using deep-curated molecular interaction data to represent biology. <i>Proteomics</i> , 2015, 15, 1390-1404.	2.2	38
141	Pharmacometrics Markup Language (PharmML): Opening New Perspectives for Model Exchange in Drug Development. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2015, 4, 316-319.	2.5	37
142	Controlled vocabularies and ontologies in proteomics: Overview, principles and practice. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014, 1844, 98-107.	2.3	36
143	A Community Standard Format for the Representation of Protein Affinity Reagents. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1-10.	3.8	35
144	PRIDE: Quality control in a proteomics data repository. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas004-bas004.	3.0	35

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145	The evolution of standards and data management practices in systems biology. <i>Molecular Systems Biology</i> , 2015, 11, 851.	7.2	35
146	Testing and Validation of Computational Methods for Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 809-814.	3.7	34
147	The Impact of Mathematical Modeling in Understanding the Mechanisms Underlying Neurodegeneration: Evolving Dimensions and Future Directions. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2017, 6, 73-86.	2.5	34
148	HENA, heterogeneous network-based data set for Alzheimer's disease. <i>Scientific Data</i> , 2019, 6, 151.	5.3	34
149	The IMEx coronavirus interactome: an evolving map of <i>Coronaviridae</i> host molecular interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	3.0	34
150	The European Bioinformatics Institute (EMBL-EBI) in 2021. <i>Nucleic Acids Research</i> , 2022, 50, D11-D19.	14.5	34
151	Mapping Plant Interactomes Using Literature Curated and Predicted Protein-Protein Interaction Data Sets. <i>Plant Cell</i> , 2010, 22, 997-1005.	6.6	33
152	Meeting Report from the Second "Minimum Information for Biological and Biomedical Investigations" (MIBBI) workshop. <i>Standards in Genomic Sciences</i> , 2010, 3, 259-266.	1.5	32
153	The Reactome BioMart. <i>Database: the Journal of Biological Databases and Curation</i> , 2011, 2011, bar031-bar031.	3.0	32
154	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, 3026-3035.	3.8	32
155	CausalTAB: the PSI-MITAB 2.8 updated format for signalling data representation and dissemination. <i>Bioinformatics</i> , 2019, 35, 3779-3785.	4.1	32
156	A public repository for mass spectrometry imaging data. <i>Analytical and Bioanalytical Chemistry</i> , 2015, 407, 2027-2033.	3.7	31
157	jmzReader: A Java parser library to process and visualize multiple text and XML-based mass spectrometry data formats. <i>Proteomics</i> , 2012, 12, 795-798.	2.2	30
158	ms-data-core-api: an open-source, metadata-oriented library for computational proteomics. <i>Bioinformatics</i> , 2015, 31, 2903-2905.	4.1	30
159	Current status of proteomic standards development. <i>Expert Review of Proteomics</i> , 2004, 1, 179-183.	3.0	29
160	Advances in the development of common interchange standards for proteomic data. <i>Proteomics</i> , 2004, 4, 2363-2365.	2.2	29
161	jmzIdentML API: A Java interface to the mzIdentML standard for peptide and protein identification data. <i>Proteomics</i> , 2012, 12, 790-794.	2.2	29
162	Improvements in the protein identifier cross-reference service. <i>Nucleic Acids Research</i> , 2012, 40, W276-W280.	14.5	27

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163	Complex Portal 2022: new curation frontiers. <i>Nucleic Acids Research</i> , 2022, 50, D578-D586.	14.5	27
164	The HUPO Proteomics Standards Initiative Meeting: Towards Common Standards for Exchanging Proteomics Data. <i>Comparative and Functional Genomics</i> , 2003, 4, 16-19.	2.0	26
165	Dasty2, an Ajax protein DAS client. <i>Bioinformatics</i> , 2008, 24, 2119-2121.	4.1	25
166	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, 4434-4438.	2.2	25
167	An open invitation to the Understudied Proteins Initiative. <i>Nature Biotechnology</i> , 2022, 40, 815-817.	17.5	25
168	Annotating the Human Proteome. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 435-440.	3.8	24
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