

Henning Hermjakob

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1666908/publications.pdf>

Version: 2024-02-01

258
papers

74,142
citations

5248

83
h-index

609

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.	13.7	21,074
2	2016 update of the PRIDE database and its related tools. <i>Nucleic Acids Research</i> , 2016, 44, D447-D456.	6.5	3,451
3	The Reactome pathway Knowledgebase. <i>Nucleic Acids Research</i> , 2016, 44, D481-D487.	6.5	3,319
4	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	9.4	2,505
5	The Reactome Pathway Knowledgebase. <i>Nucleic Acids Research</i> , 2018, 46, D649-D655.	6.5	2,388
6	The Proteomics Identifications (PRIDE) database and associated tools: status in 2013. <i>Nucleic Acids Research</i> , 2012, 41, D1063-D1069.	6.5	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.	6.5	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.	1.1	1,601
9	The reactome pathway knowledgebase. <i>Nucleic Acids Research</i> , 2020, 48, D498-D503.	6.5	1,570
10	The Reactome pathway knowledgebase. <i>Nucleic Acids Research</i> , 2014, 42, D472-D477.	6.5	1,448
11	Reactome: a database of reactions, pathways and biological processes. <i>Nucleic Acids Research</i> , 2011, 39, D691-D697.	6.5	1,391
12	Databases on transcriptional regulation: TRANSFAC, TRRD and COMPEL. <i>Nucleic Acids Research</i> , 1998, 26, 362-367.	6.5	1,345
13	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008, 26, 541-547.	9.4	1,069
14	iProX: an integrated proteome resource. <i>Nucleic Acids Research</i> , 2019, 47, D1211-D1217.	6.5	1,001
15	The IntAct molecular interaction database in 2012. <i>Nucleic Acids Research</i> , 2012, 40, D841-D846.	6.5	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.	6.5	928
17	The reactome pathway knowledgebase 2022. <i>Nucleic Acids Research</i> , 2022, 50, D687-D692.	6.5	924
18	IntAct: an open source molecular interaction database. <i>Nucleic Acids Research</i> , 2004, 32, 452D-455.	6.5	864

#	ARTICLE	IF	CITATIONS
19	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. <i>Nucleic Acids Research</i> , 2017, 45, D1100-D1106.	6.5	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.	1.3	766
21	Reactome knowledgebase of human biological pathways and processes. <i>Nucleic Acids Research</i> , 2009, 37, D619-D622.	6.5	760
22	A common open representation of mass spectrometry data and its application to proteomics research. <i>Nature Biotechnology</i> , 2004, 22, 1459-1466.	9.4	724
23	IntAct—open source resource for molecular interaction data. <i>Nucleic Acids Research</i> , 2007, 35, D561-D565.	6.5	701
24	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893.	9.4	694
25	Reactome pathway analysis: a high-performance in-memory approach. <i>BMC Bioinformatics</i> , 2017, 18, 142.	1.2	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.	9.4	581
27	The IntAct molecular interaction database in 2010. <i>Nucleic Acids Research</i> , 2010, 38, D525-D531.	6.5	574
28	mzML—a Community Standard for Mass Spectrometry Data. <i>Molecular and Cellular Proteomics</i> , 2011, 10, R110.000133.	2.5	555
29	PRIDE: The proteomics identifications database. <i>Proteomics</i> , 2005, 5, 3537-3545.	1.3	553
30	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896.	9.4	506
31	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. <i>Nature Methods</i> , 2012, 9, 345-350.	9.0	500
32	The ProteomeXchange consortium in 2020: enabling “big data” approaches in proteomics. <i>Nucleic Acids Research</i> , 2020, 48, D1145-D1152.	6.5	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.	4.1	386
34	Toward interoperable bioscience data. <i>Nature Genetics</i> , 2012, 44, 121-126.	9.4	362
35	Open Targets: a platform for therapeutic target identification and validation. <i>Nucleic Acids Research</i> , 2017, 45, D985-D994.	6.5	355
36	BioModels: ten-year anniversary. <i>Nucleic Acids Research</i> , 2015, 43, D542-D548.	6.5	334

#	ARTICLE	IF	CITATIONS
37	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020, 38, 272-276.	9.4	314
38	InterPro--an integrated documentation resource for protein families, domains and functional sites. <i>Bioinformatics</i> , 2000, 16, 1145-1150.	1.8	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.	0.8	274
40	The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007, 25, 894-898.	9.4	274
41	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011, 8, 528-529.	9.0	274
42	Annotating Cancer Variants and Anti-Cancer Therapeutics in Reactome. <i>Cancers</i> , 2012, 4, 1180-1211.	1.7	270
43	PRIDE: a public repository of protein and peptide identifications for the proteomics community. <i>Nucleic Acids Research</i> , 2006, 34, D659-D663.	6.5	254
44	Broadening the horizon " level 2.5 of the HUPO-PSI format for molecular interactions. <i>BMC Biology</i> , 2007, 5, 44.	1.7	237
45	ProteomeBinders: planning a European resource of affinity reagents for analysis of the human proteome. <i>Nature Methods</i> , 2007, 4, 13-17.	9.0	231
46	A guide to the Proteomics Identifications Database proteomics data repository. <i>Proteomics</i> , 2009, 9, 4276-4283.	1.3	220
47	The Proteomics Identifications database: 2010 update. <i>Nucleic Acids Research</i> , 2010, 38, D736-D742.	6.5	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.	3.3	206
49	Reactome graph database: Efficient access to complex pathway data. <i>PLoS Computational Biology</i> , 2018, 14, e1005968.	1.5	202
50	iProX in 2021: connecting proteomics data sharing with big data. <i>Nucleic Acids Research</i> , 2022, 50, D1522-D1527.	6.5	197
51	Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. <i>Nature Communications</i> , 2019, 10, 10.	5.8	193
52	The Proteomics Standards Initiative. <i>Proteomics</i> , 2003, 3, 1374-1376.	1.3	188
53	Making proteomics data accessible and reusable: Current state of proteomics databases and repositories. <i>Proteomics</i> , 2015, 15, 930-950.	1.3	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.	3.2	178

#	ARTICLE	IF	CITATIONS
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.	2.5	175
56	BioModelsâ€™15 years of sharing computational models in life science. <i>Nucleic Acids Research</i> , 2020, 48, D407-D415.	6.5	175
57	The Ontology Lookup Service, a lightweight cross-platform tool for controlled vocabulary queries. <i>BMC Bioinformatics</i> , 2006, 7, 97.	1.2	170
58	Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , 2017, 35, 406-409.	9.4	159
59	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. <i>Journal of Proteome Research</i> , 2016, 15, 3961-3970.	1.8	158
60	PhaSepDB: a database of liquidâ€™liquid phase separation related proteins. <i>Nucleic Acids Research</i> , 2020, 48, D354-D359.	6.5	157
61	InterPro: An integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002, 3, 225-235.	3.2	155
62	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. <i>Nature Methods</i> , 2016, 13, 651-656.	9.0	147
63	Analyzing Proteinâ€™Protein Interaction Networks. <i>Journal of Proteome Research</i> , 2012, 11, 2014-2031.	1.8	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.	2.5	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.	2.5	140
67	Reactome enhanced pathway visualization. <i>Bioinformatics</i> , 2017, 33, 3461-3467.	1.8	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.	2.5	130
69	PRIDE: new developments and new datasets. <i>Nucleic Acids Research</i> , 2007, 36, D878-D883.	6.5	124
70	Reactome diagram viewer: data structures and strategies to boost performance. <i>Bioinformatics</i> , 2018, 34, 1208-1214.	1.8	121
71	A comparison of signal sequence prediction methods using a test set of signal peptides. <i>Bioinformatics</i> , 2000, 16, 741-742.	1.8	120
72	Calling on a million minds for community annotation in WikiProteins. <i>Genome Biology</i> , 2008, 9, R89.	13.9	117

#	ARTICLE	IF	CITATIONS
73	The Protein Identifier Cross-Reference (PICR) service: reconciling protein identifiers across multiple source databases. <i>BMC Bioinformatics</i> , 2007, 8, 401.	1.2	112
74	BioJS: an open source JavaScript framework for biological data visualization. <i>Bioinformatics</i> , 2013, 29, 1103-1104.	1.8	110
75	PRIDE Inspector: a tool to visualize and validate MS proteomics data. <i>Nature Biotechnology</i> , 2012, 30, 135-137.	9.4	109
76	The Ontology Lookup Service: bigger and better. <i>Nucleic Acids Research</i> , 2010, 38, W155-W160.	6.5	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.	2.5	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.	1.3	100
79	The complex portal - an encyclopaedia of macromolecular complexes. <i>Nucleic Acids Research</i> , 2015, 43, D479-D484.	6.5	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.	2.4	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.	2.6	97
82	The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics. <i>Nature Biotechnology</i> , 2007, 25, 1127-1133.	9.4	96
83	A new reference implementation of the PSICQUIC web service. <i>Nucleic Acids Research</i> , 2013, 41, W601-W606.	6.5	91
84	Reactome pathway analysis to enrich biological discovery in proteomics data sets. <i>Proteomics</i> , 2011, 11, 3598-3613.	1.3	89
85	The IntAct database: efficient access to fine-grained molecular interaction data. <i>Nucleic Acids Research</i> , 2022, 50, D648-D653.	6.5	89
86	Integrating biological data – the Distributed Annotation System. <i>BMC Bioinformatics</i> , 2008, 9, S3.	1.2	87
87	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017, 16, 4288-4298.	1.8	87
88	Complex Portal 2018: extended content and enhanced visualization tools for macromolecular complexes. <i>Nucleic Acids Research</i> , 2019, 47, D550-D558.	6.5	85
89	Understudied proteins: opportunities and challenges for functional proteomics. <i>Nature Methods</i> , 2022, 19, 774-779.	9.0	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.	1.3	82

#	ARTICLE	IF	CITATIONS
91	Minimum information about a bioactive entity (MIABE). <i>Nature Reviews Drug Discovery</i> , 2011, 10, 661-669.	21.5	80
92	BioModels: expanding horizons to include more modelling approaches and formats. <i>Nucleic Acids Research</i> , 2018, 46, D1248-D1253.	6.5	80
93	Quantifying the impact of public omics data. <i>Nature Communications</i> , 2019, 10, 3512.	5.8	79
94	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat009-bat009.	1.4	76
95	Wikidata as a knowledge graph for the life sciences. <i>ELife</i> , 2020, 9, .	2.8	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.	1.8	75
97	The Ontology Lookup Service: more data and better tools for controlled vocabulary queries. <i>Nucleic Acids Research</i> , 2008, 36, W372-W376.	6.5	70
98	LipidHome: A Database of Theoretical Lipids Optimized for High Throughput Mass Spectrometry Lipidomics. <i>PLoS ONE</i> , 2013, 8, e61951.	1.1	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.	1.1	67
100	Reproducibility in systems biology modelling. <i>Molecular Systems Biology</i> , 2021, 17, e9982.	3.2	67
101	Submit Your Interaction Data the IMEx Way. <i>Proteomics</i> , 2007, 7, 28-34.	1.3	65
102	Integration of Cardiac Proteome Biology and Medicine by a Specialized Knowledgebase. <i>Circulation Research</i> , 2013, 113, 1043-1053.	2.0	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.	1.0	64
104	Integrated omics dissection of proteome dynamics during cardiac remodeling. <i>Nature Communications</i> , 2018, 9, 120.	5.8	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.	6.5	62
106	PRIDE Cluster: building a consensus of proteomics data. <i>Nature Methods</i> , 2013, 10, 95-96.	9.0	62
107	Characterization, Design, and Function of the Mitochondrial Proteome: From Organs to Organisms. <i>Journal of Proteome Research</i> , 2014, 13, 433-446.	1.8	59
108	A data citation roadmap for scholarly data repositories. <i>Scientific Data</i> , 2019, 6, 28.	2.4	59

#	ARTICLE	IF	CITATIONS
109	Recurated protein interaction datasets. <i>Nature Methods</i> , 2009, 6, 860-861.	9.0	58
110	BioModels: Content, Features, Functionality, and Use. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2015, 4, 55-68.	1.3	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.	1.2	56
112	The PSI semantic validator: A framework to check MIAPE compliance of proteomics data. <i>Proteomics</i> , 2009, 9, 5112-5119.	1.3	55
113	Accurate estimation of isoelectric point of protein and peptide based on amino acid sequences. <i>Bioinformatics</i> , 2016, 32, 821-827.	1.8	55
114	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , 2010, 10, 3957-3969.	1.3	54
115	How to submit MS proteomics data to ProteomeXchange via the PRIDE database. <i>Proteomics</i> , 2014, 14, 2233-2241.	1.3	54
116	Harnessing the Heart of Big Data. <i>Circulation Research</i> , 2015, 116, 1115-1119.	2.0	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.	2.2	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.	1.3	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.	1.3	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.	1.4	53
121	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021, 17, e10387.	3.2	53
122	Minimum information about a protein affinity reagent (MIAPAR). <i>Nature Biotechnology</i> , 2010, 28, 650-653.	9.4	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.	1.0	50
124	Uniform resolution of compact identifiers for biomedical data. <i>Scientific Data</i> , 2018, 5, 180029.	2.4	50
125	Towards a unified open access dataset of molecular interactions. <i>Nature Communications</i> , 2020, 11, 6144.	5.8	49
126	Hydra: a scalable proteomic search engine which utilizes the Hadoop distributed computing framework. <i>BMC Bioinformatics</i> , 2012, 13, 324.	1.2	48

#	ARTICLE	IF	CITATIONS
127	AAtlas 1.0: a human autoantigen database. <i>Nucleic Acids Research</i> , 2017, 45, D769-D776.	6.5	48
128	VARSPIC: alternatively-spliced protein sequences derived from SWISS-PROT and TrEMBL. <i>Bioinformatics</i> , 2000, 16, 1048-1049.	1.8	47
129	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. <i>BMC Bioinformatics</i> , 2018, 19, 134.	1.2	47
130	The HUPO Proteomics Standards Initiative - Overcoming the Fragmentation of Proteomics Data. <i>Proteomics</i> , 2006, 6, 34-38.	1.3	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.	1.3	46
132	The PSI formal document process and its implementation on the PSI website. <i>Proteomics</i> , 2007, 7, 2355-2357.	1.3	45
133	Open source libraries and frameworks for biological data visualisation: A guide for developers. <i>Proteomics</i> , 2015, 15, 1356-1374.	1.3	43
134	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1905-1913.	2.5	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.	1.8	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.	1.3	41
138	InteroPORC: automated inference of highly conserved protein interaction networks. <i>Bioinformatics</i> , 2008, 24, 1625-1631.	1.8	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.	3.2	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.	1.3	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.	1.3	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.	1.1	36
143	A Community Standard Format for the Representation of Protein Affinity Reagents. <i>Molecular and Cellular Proteomics</i> , 2010, 9, 1-10.	2.5	35
144	PRIDE: Quality control in a proteomics data repository. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bas004-bas004.	1.4	35

#	ARTICLE	IF	CITATIONS
145	The evolution of standards and data management practices in systems biology. <i>Molecular Systems Biology</i> , 2015, 11, 851.	3.2	35
146	Testing and Validation of Computational Methods for Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016, 15, 809-814.	1.8	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.	1.3	34
148	HENA, heterogeneous network-based data set for Alzheimer's disease. <i>Scientific Data</i> , 2019, 6, 151.	2.4	34
149	The IMEx coronavirus interactome: an evolving map of coronavirus host molecular interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	34
150	The European Bioinformatics Institute (EMBL-EBI) in 2021. <i>Nucleic Acids Research</i> , 2022, 50, D11-D19.	6.5	34
151	Mapping Plant Interactomes Using Literature Curated and Predicted Protein-Protein Interaction Data Sets. <i>Plant Cell</i> , 2010, 22, 997-1005.	3.1	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.	1.4	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.	2.5	32
155	CausalTAB: the PSI-MITAB 2.8 updated format for signalling data representation and dissemination. <i>Bioinformatics</i> , 2019, 35, 3779-3785.	1.8	32
156	A public repository for mass spectrometry imaging data. <i>Analytical and Bioanalytical Chemistry</i> , 2015, 407, 2027-2033.	1.9	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.	1.3	30
158	ms-data-core-api: an open-source, metadata-oriented library for computational proteomics. <i>Bioinformatics</i> , 2015, 31, 2903-2905.	1.8	30
159	Current status of proteomic standards development. <i>Expert Review of Proteomics</i> , 2004, 1, 179-183.	1.3	29
160	Advances in the development of common interchange standards for proteomic data. <i>Proteomics</i> , 2004, 4, 2363-2365.	1.3	29
161	jmzIdentML API: A Java interface to the mzIdentML standard for peptide and protein identification data. <i>Proteomics</i> , 2012, 12, 790-794.	1.3	29
162	Improvements in the protein identifier cross-reference service. <i>Nucleic Acids Research</i> , 2012, 40, W276-W280.	6.5	27

#	ARTICLE	IF	CITATIONS
163	Complex Portal 2022: new curation frontiers. <i>Nucleic Acids Research</i> , 2022, 50, D578-D586.	6.5	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.	1.8	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.	1.3	25
167	An open invitation to the Understudied Proteins Initiative. <i>Nature Biotechnology</i> , 2022, 40, 815-817.	9.4	25
168	Annotating the Human Proteome. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 435-440.	2.5	24
169	MINT and IntAct contribute to the Second BioCreative challenge: serving the text-mining community with high quality molecular interaction data. <i>Genome Biology</i> , 2008, 9, S5.	13.9	24
170	The systematic annotation of the three main GPCR families in Reactome. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq018-baq018.	1.4	24
171	The role SWISS-PROT and TrEMBL play in the genome research environment. <i>Journal of Biotechnology</i> , 2000, 78, 221-234.	1.9	23
172	Dasty and UniProt DAS: a perfect pair for protein feature visualization. <i>Bioinformatics</i> , 2005, 21, 3198-3199.	1.8	23
173	Swissknife - 'lazy parsing' of SWISS-PROT entries. <i>Bioinformatics</i> , 1999, 15, 771-772.	1.8	22
174	Biomedical Informatics on the Cloud. <i>Circulation Research</i> , 2018, 122, 1290-1301.	2.0	22
175	A reference set of curated biomedical data and metadata from clinical case reports. <i>Scientific Data</i> , 2018, 5, 180258.	2.4	22
176	BioJS: an open source standard for biological visualisation " its status in 2014. <i>F1000Research</i> , 2014, 3, 55.	0.8	22
177	An informatic pipeline for the data capture and submission of quantitative proteomic data using iTRAQ. <i>Proteome Science</i> , 2007, 5, 4.	0.7	21
178	IntAct App: a Cytoscape application for molecular interaction network visualization and analysis. <i>Bioinformatics</i> , 2021, 37, 3684-3685.	1.8	21
179	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.	2.5	20
180	Identifying novel biomarkers through data mining "A realistic scenario?. <i>Proteomics - Clinical Applications</i> , 2015, 9, 437-443.	0.8	20

#	ARTICLE	IF	CITATIONS
181	Human Proteome Organization Proteomics Standards Initiative. <i>Molecular and Cellular Proteomics</i> , 2007, 6, 1666-1667.	2.5	20
182	The Protein Feature Ontology: a tool for the unification of protein feature annotations. <i>Bioinformatics</i> , 2008, 24, 2767-2772.	1.8	19
183	The Gel Electrophoresis Markup Language (GelML) from the Proteomics Standards Initiative. <i>Proteomics</i> , 2010, 10, 3073-3081.	1.3	19
184	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 Workshop report. <i>Journal of Proteomics</i> , 2013, 87, 134-138.	1.2	19
185	The EBI enzyme portal. <i>Nucleic Acids Research</i> , 2013, 41, D773-D780.	6.5	19
186	Analysis of the experimental detection of central nervous system-related genes in human brain and cerebrospinal fluid datasets. <i>Proteomics</i> , 2008, 8, 1138-1148.	1.3	18
187	ISPIDER Central: an integrated database web-server for proteomics. <i>Nucleic Acids Research</i> , 2008, 36, W485-W490.	6.5	18
188	Introducing the PRIDE Archive RESTful web services. <i>Nucleic Acids Research</i> , 2015, 43, W599-W604.	6.5	18
189	The first 10 years of the international coordination network for standards in systems and synthetic biology (COMBINE). <i>Journal of Integrative Bioinformatics</i> , 2020, 17, .	1.0	18
190	Progress in Establishing Common Standards for Exchanging Proteomics Data: The Second Meeting of the HUPO Proteomics Standards Initiative. <i>Comparative and Functional Genomics</i> , 2003, 4, 203-206.	2.0	16
191	Ten Years of Standardizing Proteomic Data: A Report on the HUPO-PSI Spring Workshop. <i>Proteomics</i> , 2012, 12, 2767-2772.	1.3	16
192	jmzTab: A Java interface to the mzTab data standard. <i>Proteomics</i> , 2014, 14, 1328-1332.	1.3	16
193	Expression Data Analysis with Reactome. <i>Current Protocols in Bioinformatics</i> , 2015, 49, 8.20.1-8.20.9.	25.8	15
194	Dasty3, a WEB framework for DAS. <i>Bioinformatics</i> , 2011, 27, 2616-2617.	1.8	14
195	SPARQL-enabled identifier conversion with Identifiers.org. <i>Bioinformatics</i> , 2015, 31, 1875-1877.	1.8	14
196	The Minimum Information about a Molecular Interaction CAusal STATEment (MI2CAST). <i>Bioinformatics</i> , 2021, 36, 5712-5718.	1.8	14
197	The use of common ontologies and controlled vocabularies to enable data exchange and deposition for complex proteomic experiments. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2005, , 186-96.	0.7	14
198	Proteomics and Beyond A report on the 3rd Annual Spring Workshop of the HUPO-PSI 21-23 April 2006, San Francisco, CA, USA. <i>Proteomics</i> , 2006, 6, 4439-4443.	1.3	13

#	ARTICLE	IF	CITATIONS
199	Towards the Collaborative Curation of the Registry underlying identifiers.org. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat017.	1.4	13
200	Shared resources, shared costs – leveraging biocuration resources. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	1.4	13
201	Charting online OMICS resources: A navigational chart for clinical researchers. Proteomics - Clinical Applications, 2009, 3, 18-29.	0.8	12
202	From Peptidome to PRIDE : Public proteomics data migration at a large scale. Proteomics, 2013, 13, 1692-1695.	1.3	12
203	Gene regulation knowledge commons: community action takes care of DNA binding transcription factors. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw088.	1.4	12
204	Reactome and ORCID – fine-grained credit attribution for community curation. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	12
205	BioModels linked dataset. BMC Systems Biology, 2014, 8, 91.	3.0	11
206	Interleukins and their signaling pathways in the Reactome biological pathway database. Journal of Allergy and Clinical Immunology, 2018, 141, 1411-1416.	1.5	11
207	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	6.5	11
208	Proteomic Data Exchange and Storage: The Need for Common Standards and Public Repositories. , 2007, 367, 261-270.		10
209	Capturing cooperative interactions with the PSI-MI format. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat066.	1.4	10
210	ComplexViewer: visualization of curated macromolecular complexes. Bioinformatics, 2017, 33, 3673-3675.	1.8	10
211	Deep learning embedder method and tool for mass spectra similarity search. Journal of Proteomics, 2021, 232, 104070.	1.2	10
212	Addressing <i>barriers in comprehensiveness, accessibility, reusability, interoperability and reproducibility of computational models in systems biology</i>. Briefings in Bioinformatics, 2022, 23, .	3.2	10
213	Rintact: enabling computational analysis of molecular interaction data from the IntAct repository. Bioinformatics, 2008, 24, 1100-1101.	1.8	9
214	Annual Spring Meeting of the Proteomics Standards Initiative. Proteomics, 2009, 9, 4429-4432.	1.3	9
215	The HUPO initiative on Model Organism Proteomes, iMOP. Proteomics, 2012, 12, 340-345.	1.3	9
216	Data Standardization by the HUPO-PSI: How has the Community Benefitted?. Methods in Molecular Biology, 2011, 696, 149-160.	0.4	9

#	ARTICLE	IF	CITATIONS
217	Critical amino acid residues in proteins: a BioMart integration of Reactome protein annotations with PRIDE mass spectrometry data and COSMIC somatic mutations. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar047.	1.4	8
218	HI-Bone: A Scoring System for Identifying Phenylisothiocyanate-Derivatized Peptides Based on Precursor Mass and High Intensity Fragment Ions. Analytical Chemistry, 2013, 85, 3515-3520.	3.2	7
219	Data Standards and Controlled Vocabularies for Proteomics. Methods in Molecular Biology, 2008, 484, 279-286.	0.4	7
220	Second Joint HUPO Publication and Proteomics Standards Initiative Workshop. Proteomics, 2009, 9, 4426-4428.	1.3	6
221	ENFIN " A European network for integrative systems biology. Comptes Rendus - Biologies, 2009, 332, 1050-1058.	0.1	6
222	easyDAS: Automatic creation of DAS servers. BMC Bioinformatics, 2011, 12, 23.	1.2	6
223	iAnn: an event sharing platform for the life sciences. Bioinformatics, 2013, 29, 1919-1921.	1.8	6
224	The Publication and Database Deposition of Molecular Interaction Data. Current Protocols in Protein Science, 2010, 60, Unit 25.3.	2.8	5
225	Identifiers.org: Compact Identifier services in the cloud. Bioinformatics, 2021, 37, 1781-1782.	1.8	5
226	BioModels Parameters: a treasure trove of parameter values from published systems biology models. Bioinformatics, 2020, 36, 4649-4654.	1.8	5
227	Using Reactome to build an autophagy mechanism knowledgebase. Autophagy, 2021, 17, 1543-1554.	4.3	5
228	Analysing the yeast complexome"the Complex Portal rising to the challenge. Nucleic Acids Research, 2021, 49, 3156-3167.	6.5	5
229	Standardising Proteomics Data " the W ork of the HUPO Proteomics Standards Initiative. Journal of Proteomics and Bioinformatics, 2008, 01, 003-005.	0.4	5
230	Path4Drug: Data Science Workflow for Identification of Tissue-Specific Biological Pathways Modulated by Toxic Drugs. Frontiers in Pharmacology, 2021, 12, 708296.	1.6	5
231	OntoDas " a tool for facilitating the construction of complex queries to the Gene Ontology. BMC Bioinformatics, 2008, 9, 437.	1.2	4
232	DAS Writeback: A Collaborative Annotation System. BMC Bioinformatics, 2011, 12, 143.	1.2	4
233	HUPO 2011: The New Cardiovascular Initiative "Integrating Proteomics and Cardiovascular Biology in Health and Disease. Proteomics, 2012, 12, 749-751.	1.3	4
234	PathwayMatcher: proteoform-centric network construction enables fine-granularity multiomics pathway mapping. GigaScience, 2019, 8, .	3.3	4

#	ARTICLE	IF	CITATIONS
235	TEMBLOR " Perspectives of EBI Database Services. Comparative and Functional Genomics, 2002, 3, 47-50.	2.0	3
236	The omics discovery REST interface. Nucleic Acids Research, 2020, 48, W380-W384.	6.5	3
237	Proteomics and data standardisation. Drug Discovery Today Biosilico, 2004, 2, 91-93.	0.7	2
238	Equipping Physiologists with an Informatics Tool Chest: Toward an Integrated Mitochondrial Phenome. Handbook of Experimental Pharmacology, 2016, 240, 377-401.	0.9	2
239	MyDas, an Extensible Java DAS Server. PLoS ONE, 2012, 7, e44180.	1.1	2
240	Complex Portal - A Unifying Protein Complex Database. Genomics and Computational Biology, 2017, 4, 100052.	0.7	2
241	The ESF Programme on Functional Genomics Workshop on "Data Integration in Functional Genomics: Application to Biological Pathways"™. Comparative and Functional Genomics, 2004, 5, 148-155.	2.0	1
242	Development and Implementation of the PSI MI Standard for Molecular Interaction. , 2006, , .		1
243	Organizational principles of the Reactome human BioPAX model using graph theory methods. Journal of Complex Networks, 2016, , cnw003.	1.1	1
244	Preparing Molecular Interaction Data for Publication. Methods in Molecular Biology, 2011, 694, 229-236.	0.4	1
245	Protein-protein interactions: analysis and prediction. , 2008, , 353-410.		1
246	KNIME workflow for retrieving causal drug and protein interactions, building networks, and performing topological enrichment analysis demonstrated by a DILI case study. Journal of Cheminformatics, 2022, 14, .	2.8	1
247	Protein interaction databases. , 2005, , .		0
248	Data standardization and the HUPO proteomics standards initiative. , 2005, , .		0
249	New open drug activity data at EBI. Chemistry Central Journal, 2009, 3, .	2.6	0
250	Shouldn't enantiomeric purity be included in the 'minimum information about a bioactive entity? Response from the MIABE group. Nature Reviews Drug Discovery, 2012, 11, 730-730.	21.5	0
251	The cardiovascular gene annotation initiative: current and future aims. Atherosclerosis, 2014, 237, e10.	0.4	0
252	A pipeline for identifying endogenous neuropeptides from spectral archives. International Journal of Data Mining and Bioinformatics, 2018, 20, 12.	0.1	0

#	ARTICLE	IF	CITATIONS
253	A decoupled, modular and scriptable architecture for tools to curate data platforms. <i>Bioinformatics</i> , 2021, 37, 3693-3694.	1.8	0
254	Infrastructure for distributed protein annotation. , 2008, , 413-426.		0
255	BioModels Database: a public repository for sharing models of biological processes. , 2013, , 1-5.		0
256	ENFIN - An Integrative Structure for Systems Biology. <i>Lecture Notes in Computer Science</i> , 2008, , 132-143.	1.0	0
257	EBI Proteomics Services. <i>Lecture Notes in Computer Science</i> , 2008, , 207-207.	1.0	0
258	BioModels Database: A Public Repository for Sharing Models of Biological Processes. , 2022, , 463-467.		0