Henning Hermjakob

List of Publications by Citations

262 papers	54,917 citations	76 h-index	234 g-index
307 ext. papers	65,429 ext. citations	11.7 avg, IF	6.77 L-index

#	Paper	IF	Citations
262	Initial sequencing and analysis of the human genome. *Nature*, **2001**, 409, 860-921	50.4	17366
261	2016 update of the PRIDE database and its related tools. *Nucleic Acids Research*, **2016**, 44, D447-56	20.1	2440
260	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. *Nature Biotechnology*, **2014**, 32, 223-6	44.5	2053
259	The PRoteomics IDEntifications (PRIDE) database and associated tools: status in 2013. *Nucleic Acids Research*, **2013**, 41, D1063-9	20.1	1587
258	The Reactome Pathway Knowledgebase. *Nucleic Acids Research*, **2018**, 46, D649-D655	20.1	1496
257	On the frequency of protein glycosylation, as deduced from analysis of the SWISS-PROT database. *Biochimica Et Biophysica Acta - General Subjects*, **1999**, 1473, 4-8	4	1365
256	Databases on transcriptional regulation: TRANSFAC, TRRD and COMPEL. *Nucleic Acids Research*, **1998**, 26, 362-7	20.1	1209
255	The Reactome pathway knowledgebase. *Nucleic Acids Research*, **2014**, 42, D472-7	20.1	1188
254	The MIntAct project--IntAct as a common curation platform for 11 molecular interaction databases. *Nucleic Acids Research*, **2014**, 42, D358-63	20.1	1111
253	Reactome: a database of reactions, pathways and biological processes. *Nucleic Acids Research*, **2011**, 39, D691-7	20.1	1090
252	The minimum information about a genome sequence (MIGS) specification. *Nature Biotechnology*, **2008**, 26, 541-7	44.5	964
251	The Reactome pathway Knowledgebase. *Nucleic Acids Research*, **2016**, 44, D481-7	20.1	920
250	The reactome pathway knowledgebase. *Nucleic Acids Research*, **2020**, 48, D498-D503	20.1	848
249	The IntAct molecular interaction database in 2012. *Nucleic Acids Research*, **2012**, 40, D841-6	20.1	779
248	The InterPro database, an integrated documentation resource for protein families, domains and functional sites. *Nucleic Acids Research*, **2001**, 29, 37-40	20.1	743
247	Reactome knowledgebase of human biological pathways and processes. *Nucleic Acids Research*, **2009**, 37, D619-22	20.1	675
246	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. *Proteomics*, **2005**, 5, 3226-45	4.8	672

245	IntAct: an open source molecular interaction database. *Nucleic Acids Research*, **2004**, 32, D452-5	20.1	670
244	A common open representation of mass spectrometry data and its application to proteomics research. *Nature Biotechnology*, **2004**, 22, 1459-66	44.5	632
243	IntAct--open source resource for molecular interaction data. *Nucleic Acids Research*, **2007**, 35, D561-5	20.1	626
242	The minimum information about a proteomics experiment (MIAPE). *Nature Biotechnology*, **2007**, 25, 887-93	44.5	583
241	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. *Nucleic Acids Research*, **2017**, 45, D1100-D1106	20.1	568
240	The IntAct molecular interaction database in 2010. *Nucleic Acids Research*, **2010**, 38, D525-31	20.1	522
239	The HUPO PSI's molecular interaction format--a community standard for the representation of protein interaction data. *Nature Biotechnology*, **2004**, 22, 177-83	44.5	504
238	PRIDE: the proteomics identifications database. *Proteomics*, **2005**, 5, 3537-45	4.8	454
237	mzML--a community standard for mass spectrometry data. *Molecular and Cellular Proteomics*, **2011**, 10, R110.000133	7.6	424
236	iProX: an integrated proteome resource. *Nucleic Acids Research*, **2019**, 47, D1211-D1217	20.1	423
235	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. *Nature Biotechnology*, **2008**, 26, 889-96	44.5	417
234	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. *Nature Methods*, **2012**, 9, 345-50	21.6	375
233	Disrupted in Schizophrenia 1 Interactome: evidence for the close connectivity of risk genes and a potential synaptic basis for schizophrenia. *Molecular Psychiatry*, **2007**, 12, 74-86	15.1	349
232	Toward interoperable bioscience data. *Nature Genetics*, **2012**, 44, 121-6	36.3	286
231	Reactome pathway analysis: a high-performance in-memory approach. *BMC Bioinformatics*, **2017**, 18, 142	3.6	285
230	Open Targets: a platform for therapeutic target identification and validation. *Nucleic Acids Research*, **2017**, 45, D985-D994	20.1	241
229	Clinical proteomics: A need to define the field and to begin to set adequate standards. *Proteomics - Clinical Applications*, **2007**, 1, 148-56	3.1	237
228	Annotating cancer variants and anti-cancer therapeutics in reactome. *Cancers*, **2012**, 4, 1180-211	6.6	232

227 — The minimum information required for reporting a molecular interaction experiment (MIMIx). *Nature Biotechnology*, **2007**, 25, 894-8 — 44.5 — 229

226 — PSICQUIC and PSISCORE: accessing and scoring molecular interactions. *Nature Methods*, **2011**, 8, 528-9 — 21.6 — 227

225 — BioModels: ten-year anniversary. *Nucleic Acids Research*, **2015**, 43, D542-8 — 20.1 — 225

224 — PRIDE: a public repository of protein and peptide identifications for the proteomics community. *Nucleic Acids Research*, **2006**, 34, D659-63 — 20.1 — 222

223 — InterPro--an integrated documentation resource for protein families, domains and functional sites. *Bioinformatics*, **2000**, 16, 1145-50 — 7.2 — 217

222 — The ProteomeXchange consortium in 2020: enabling 'big data' approaches in proteomics. *Nucleic Acids Research*, **2020**, 48, D1145-D1152 — 20.1 — 212

221 — ProteomeBinders: planning a European resource of affinity reagents for analysis of the human proteome. *Nature Methods*, **2007**, 4, 13-7 — 21.6 — 207

220 — Broadening the horizon--level 2.5 of the HUPO-PSI format for molecular interactions. *BMC Biology*, **2007**, 5, 44 — 7.3 — 204

219 — The Proteomics Identifications database: 2010 update. *Nucleic Acids Research*, **2010**, 38, D736-42 — 20.1 — 199

218 — A guide to the Proteomics Identifications Database proteomics data repository. *Proteomics*, **2009**, 9, 4276-83 — 4.8 — 198

217 — The implications of alternative splicing in the ENCODE protein complement. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 5495-500 — 11.5 — 177

216 — The proteomics standards initiative. *Proteomics*, **2003**, 3, 1374-6 — 4.8 — 159

215 — The mzIdentML data standard for mass spectrometry-based proteomics results. *Molecular and Cellular Proteomics*, **2012**, 11, M111.014381 — 7.6 — 150

214 — The Ontology Lookup Service, a lightweight cross-platform tool for controlled vocabulary queries. *BMC Bioinformatics*, **2006**, 7, 97 — 3.6 — 142

213 — Making proteomics data accessible and reusable: current state of proteomics databases and repositories. *Proteomics*, **2015**, 15, 930-49 — 4.8 — 138

212 — InterPro: an integrated documentation resource for protein families, domains and functional sites. *Briefings in Bioinformatics*, **2002**, 3, 225-35 — 13.4 — 137

211 — Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. *Journal of Proteome Research*, **2016**, 15, 3961-3970 — 5.6 — 130

210 — Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. *Nature Communications*, **2019**, 10, 10 — 17.4 — 122

209	Path2Models: large-scale generation of computational models from biochemical pathway maps. *BMC Systems Biology*, **2013**, 7, 116	3.5	122
208	MEMOTE for standardized genome-scale metabolic model testing. *Nature Biotechnology*, **2020**, 38, 272-276	44.5	121
207	Discovering and linking public omics data sets using the Omics Discovery Index. *Nature Biotechnology*, **2017**, 35, 406-409	44.5	105
206	PRIDE: new developments and new datasets. *Nucleic Acids Research*, **2008**, 36, D878-83	20.1	105
205	Analyzing protein-protein interaction networks. *Journal of Proteome Research*, **2012**, 11, 2014-31	5.6	103
204	PRIDE Inspector: a tool to visualize and validate MS proteomics data. *Nature Biotechnology*, **2012**, 30, 135-7	44.5	103
203	The Protein Identifier Cross-Referencing (PICR) service: reconciling protein identifiers across multiple source databases. *BMC Bioinformatics*, **2007**, 8, 401	3.6	102
202	A comparison of signal sequence prediction methods using a test set of signal peptides. *Bioinformatics*, **2000**, 16, 741-2	7.2	102
201	Calling on a million minds for community annotation in WikiProteins. *Genome Biology*, **2008**, 9, R89	18.3	101
200	Reactome graph database: Efficient access to complex pathway data. *PLoS Computational Biology*, **2018**, 14, e1005968	5	100
199	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. *Nature Methods*, **2016**, 13, 651-656	21.6	99
198	The mzTab data exchange format: communicating mass-spectrometry-based proteomics and metabolomics experimental results to a wider audience. *Molecular and Cellular Proteomics*, **2014**, 13, 2765-75	7.6	96
197	The PRoteomics IDEntification (PRIDE) Converter 2 framework: an improved suite of tools to facilitate data submission to the PRIDE database and the ProteomeXchange consortium. *Molecular and Cellular Proteomics*, **2012**, 11, 1682-9	7.6	96
196	PRIDE Inspector Toolsuite: Moving Toward a Universal Visualization Tool for Proteomics Data Standard Formats and Quality Assessment of ProteomeXchange Datasets. *Molecular and Cellular Proteomics*, **2016**, 15, 305-17	7.6	91
195	BioJS: an open source JavaScript framework for biological data visualization. *Bioinformatics*, **2013**, 29, 1103-4	7.2	88
194	Common interchange standards for proteomics data: Public availability of tools and schema. *Proteomics*, **2004**, 4, 490-1	4.8	88
193	The Ontology Lookup Service: bigger and better. *Nucleic Acids Research*, **2010**, 38, W155-60	20.1	82
192	BioModels-15 years of sharing computational models in life science. *Nucleic Acids Research*, **2020**, 48, D407-D415	20.1	81

191	The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics. *Nature Biotechnology*, **2007**, 25, 1127-33	44.5	81
190	New open drug activity data at EBI. *Chemistry Central Journal*, **2009**, 3,		78
189	Integrating biological data--the Distributed Annotation System. *BMC Bioinformatics*, **2008**, 9 Suppl 8, S3	3.6	77
188	Reactome enhanced pathway visualization. *Bioinformatics*, **2017**, 33, 3461-3467	7.2	76
187	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. *Scientific Data*, **2020**, 7, 136	8.2	71
186	Reactome pathway analysis to enrich biological discovery in proteomics data sets. *Proteomics*, **2011**, 11, 3598-613	4.8	71
185	A new reference implementation of the PSICQUIC web service. *Nucleic Acids Research*, **2013**, 41, W601-6	20.1	70
184	Minimum information about a bioactive entity (MIABE). *Nature Reviews Drug Discovery*, **2011**, 10, 661-9	64.1	69
183	The complex portal--an encyclopaedia of macromolecular complexes. *Nucleic Acids Research*, **2015**, 43, D479-84	20.1	68
182	PhaSepDB: a database of liquid-liquid phase separation related proteins. *Nucleic Acids Research*, **2020**, 48, D354-D359	20.1	68
181	SBML Level 3: an extensible format for the exchange and reuse of biological models. *Molecular Systems Biology*, **2020**, 16, e9110	12.2	65
180	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data. *PLoS Biology*, **2017**, 15, e2001414	9.7	63
179	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. *Journal of Proteome Research*, **2017**, 16, 4288-4298	5.6	61
178	Open source libraries and frameworks for mass spectrometry based proteomics: a developer's perspective. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2014**, 1844, 63-76	4	59
177	LipidHome: a database of theoretical lipids optimized for high throughput mass spectrometry lipidomics. *PLoS ONE*, **2013**, 8, e61951	3.7	59
176	Recommendations from the 2008 International Summit on Proteomics Data Release and Sharing Policy: the Amsterdam principles. *Journal of Proteome Research*, **2009**, 8, 3689-92	5.6	58
175	The Ontology Lookup Service: more data and better tools for controlled vocabulary queries. *Nucleic Acids Research*, **2008**, 36, W372-6	20.1	58
174	Reactome diagram viewer: data structures and strategies to boost performance. *Bioinformatics*, **2018**, 34, 1208-1214	7.2	57

173	The work of the Human Proteome Organisation's Proteomics Standards Initiative (HUPO PSI). *OMICS A Journal of Integrative Biology*, **2006**, 10, 145-51	3.8	57
172	The reactome pathway knowledgebase 2022. *Nucleic Acids Research*, **2021**,	20.1	57
171	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bat009	5	56
170	R spider: a network-based analysis of gene lists by combining signaling and metabolic pathways from Reactome and KEGG databases. *Nucleic Acids Research*, **2010**, 38, W78-83	20.1	56
169	Submit your interaction data the IMEx way: a step by step guide to trouble-free deposition. *Proteomics*, **2007**, 7 Suppl 1, 28-34	4.8	56
168	BioModels: expanding horizons to include more modelling approaches and formats. *Nucleic Acids Research*, **2018**, 46, D1248-D1253	20.1	54
167	Data management and preliminary data analysis in the pilot phase of the HUPO Plasma Proteome Project. *Proteomics*, **2005**, 5, 3246-61	4.8	51
166	Characterization, design, and function of the mitochondrial proteome: from organs to organisms. *Journal of Proteome Research*, **2014**, 13, 433-46	5.6	49
165	PRIDE Cluster: building a consensus of proteomics data. *Nature Methods*, **2013**, 10, 95-6	21.6	49
164	BioModels: Content, Features, Functionality, and Use. *CPT: Pharmacometrics and Systems Pharmacology*, **2015**, 4, e3	4.5	48
163	Recurated protein interaction datasets. *Nature Methods*, **2009**, 6, 860-1	21.6	48
162	Do we want our data raw? Including binary mass spectrometry data in public proteomics data repositories. *Proteomics*, **2005**, 5, 3501-5	4.8	48
161	Harnessing the heart of big data. *Circulation Research*, **2015**, 116, 1115-9	15.7	47
160	The PSI semantic validator: a framework to check MIAPE compliance of proteomics data. *Proteomics*, **2009**, 9, 5112-9	4.8	47
159	A critical appraisal of techniques, software packages, and standards for quantitative proteomic analysis. *OMICS A Journal of Integrative Biology*, **2012**, 16, 431-42	3.8	46
158	Integrated omics dissection of proteome dynamics during cardiac remodeling. *Nature Communications*, **2018**, 9, 120	17.4	44
157	Organelle proteomics experimental designs and analysis. *Proteomics*, **2010**, 10, 3957-69	4.8	44
156	VARSPLIC: alternatively-spliced protein sequences derived from SWISS-PROT and TrEMBL. *Bioinformatics*, **2000**, 16, 1048-9	7.2	44

155	Complex Portal 2018: extended content and enhanced visualization tools for macromolecular complexes. *Nucleic Acids Research*, **2019**, 47, D550-D558	20.1	44
154	Hydra: a scalable proteomic search engine which utilizes the Hadoop distributed computing framework. *BMC Bioinformatics*, **2012**, 13, 324	3.6	43
153	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	8.6	42
152	Quantifying the impact of public omics data. *Nature Communications*, **2019**, 10, 3512	17.4	42
151	Integration of cardiac proteome biology and medicine by a specialized knowledgebase. *Circulation Research*, **2013**, 113, 1043-53	15.7	42
150	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. *Proteomics*, **2007**, 7, 3436-40	4.8	42
149	How to submit MS proteomics data to ProteomeXchange via the PRIDE database. *Proteomics*, **2014**, 14, 2233-41	4.8	41
148	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. *Journal of Proteomics*, **2017**, 150, 170-182	3.9	39
147	Proteomics data validation: why all must provide data. *Molecular BioSystems*, **2007**, 3, 518-22		39
146	The HUPO proteomics standards initiative--overcoming the fragmentation of proteomics data. *Proteomics*, **2006**, 6 Suppl 2, 34-8	4.8	39
145	A domain level interaction network of amyloid precursor protein and Abeta of Alzheimer's disease. *Proteomics*, **2010**, 10, 2377-95	4.8	38
144	ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. *Molecular and Cellular Proteomics*, **2020**, 19, 2115-2125	7.6	38
143	Minimum information about a protein affinity reagent (MIAPAR). *Nature Biotechnology*, **2010**, 28, 650-3	44.5	37
142	Merging and scoring molecular interactions utilising existing community standards: tools, use-cases and a case study. *Database: the Journal of Biological Databases and Curation*, **2015**, 2015,	5	36
141	qcML: an exchange format for quality control metrics from mass spectrometry experiments. *Molecular and Cellular Proteomics*, **2014**, 13, 1905-13	7.6	36
140	Analyzing large-scale proteomics projects with latent semantic indexing. *Journal of Proteome Research*, **2008**, 7, 182-91	5.6	36
139	The PSI formal document process and its implementation on the PSI website. *Proteomics*, **2007**, 7, 2355-7	4.8	35
138	Open source libraries and frameworks for biological data visualisation: a guide for developers. *Proteomics*, **2015**, 15, 1356-74	4.8	34

137	Pharmacometrics Markup Language (PharmML): Opening New Perspectives for Model Exchange in Drug Development. *CPT: Pharmacometrics and Systems Pharmacology*, **2015**, 4, 316-9	4.5	34
136	A data citation roadmap for scholarly data repositories. *Scientific Data*, **2019**, 6, 28	8.2	33
135	Uniform resolution of compact identifiers for biomedical data. *Scientific Data*, **2018**, 5, 180029	8.2	33
134	AAgAtlas 1.0: a human autoantigen database. *Nucleic Acids Research*, **2017**, 45, D769-D776	20.1	33
133	A visual review of the interactome of LRRK2: Using deep-curated molecular interaction data to represent biology. *Proteomics*, **2015**, 15, 1390-404	4.8	33
132	A community standard format for the representation of protein affinity reagents. *Molecular and Cellular Proteomics*, **2010**, 9, 1-10	7.6	33
131	The HUPO proteomics standards initiative--easing communication and minimizing data loss in a changing world. *Briefings in Bioinformatics*, **2008**, 9, 166-73	13.4	33
130	Accurate estimation of isoelectric point of protein and peptide based on amino acid sequences. *Bioinformatics*, **2016**, 32, 821-7	7.2	32
129	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. *BMC Bioinformatics*, **2018**, 19, 134	3.6	31
128	PRIDE: quality control in a proteomics data repository. *Database: the Journal of Biological Databases and Curation*, **2012**, 2012, bas004	5	30
127	The evolution of standards and data management practices in systems biology. *Molecular Systems Biology*, **2015**, 11, 851	12.2	29
126	The Reactome BioMart. *Database: the Journal of Biological Databases and Curation*, **2011**, 2011, bar031	5	29
125	Tools (Viewer, Library and Validator) that facilitate use of the peptide and protein identification standard format, termed mzIdentML. *Molecular and Cellular Proteomics*, **2013**, 12, 3026-35	7.6	28
124	InteroPORC: automated inference of highly conserved protein interaction networks. *Bioinformatics*, **2008**, 24, 1625-31	7.2	28
123	A public repository for mass spectrometry imaging data. *Analytical and Bioanalytical Chemistry*, **2015**, 407, 2027-33	4.4	27
122	jmzIdentML API: A Java interface to the mzIdentML standard for peptide and protein identification data. *Proteomics*, **2012**, 12, 790-4	4.8	27
121	Improvements in the Protein Identifier Cross-Reference service. *Nucleic Acids Research*, **2012**, 40, W276-80	20.1	27
120	ms-data-core-api: an open-source, metadata-oriented library for computational proteomics. *Bioinformatics*, **2015**, 31, 2903-5	7.2	26

119	Controlled vocabularies and ontologies in proteomics: overview, principles and practice. *Biochimica Et Biophysica Acta - Proteins and Proteomics*, **2014**, 1844, 98-107	4	26
118	jmzReader: A Java parser library to process and visualize multiple text and XML-based mass spectrometry data formats. *Proteomics*, **2012**, 12, 795-8	4.8	26
117	Meeting Report from the Second "Minimum Information for Biological and Biomedical Investigations" (MIBBI) workshop. *Standards in Genomic Sciences*, **2010**, 3, 259-66		26
116	Memote: A community driven effort towards a standardized genome-scale metabolic model test suite		26
115	Towards a unified open access dataset of molecular interactions. *Nature Communications*, **2020**, 11, 6144	17.4	26
114	Mapping plant interactomes using literature curated and predicted protein-protein interaction data sets. *Plant Cell*, **2010**, 22, 997-1005	11.6	25
113	Current status of proteomic standards development. *Expert Review of Proteomics*, **2004**, 1, 179-83	4.2	25
112	Testing and Validation of Computational Methods for Mass Spectrometry. *Journal of Proteome Research*, **2016**, 15, 809-14	5.6	24
111	Consequences of the discontinuation of the International Protein Index (IPI) database and its substitution by the UniProtKB "complete proteome" sets. *Proteomics*, **2011**, 11, 4434-8	4.8	24
110	Advances in the development of common interchange standards for proteomic data. *Proteomics*, **2004**, 4, 2363-5	4.8	24
109	Wikidata as a knowledge graph for the life sciences. *ELife*, **2020**, 9,	8.9	24
108	Dasty2, an Ajax protein DAS client. *Bioinformatics*, **2008**, 24, 2119-21	7.2	23
107	The HUPO Proteomics Standards Initiative Meeting: Towards Common Standards for Exchanging Proteomics Data. *Comparative and Functional Genomics*, **2003**, 4, 16-9		22
106	Dasty and UniProt DAS: a perfect pair for protein feature visualization. *Bioinformatics*, **2005**, 21, 3198-9	7.2	22
105	Annotating the human proteome. *Molecular and Cellular Proteomics*, **2005**, 4, 435-40	7.6	22
104	Reproducibility in systems biology modelling. *Molecular Systems Biology*, **2021**, 17, e9982	12.2	22
103	The Impact of Mathematical Modeling in Understanding the Mechanisms Underlying Neurodegeneration: Evolving Dimensions and Future Directions. *CPT: Pharmacometrics and Systems Pharmacology*, **2017**, 6, 73-86	4.5	21
102	MINT and IntAct contribute to the Second BioCreative challenge: serving the text-mining community with high quality molecular interaction data. *Genome Biology*, **2008**, 9 Suppl 2, S5	18.3	21

101	Swissknife - 'lazy parsing' of SWISS-PROT entries. *Bioinformatics*, **1999**, 15, 771-2	7.2	20
100	Biomedical Informatics on the Cloud: A Treasure Hunt for Advancing Cardiovascular Medicine. *Circulation Research*, **2018**, 122, 1290-1301	15.7	19
99	BioJS: an open source standard for biological visualisation - its status in 2014. *F1000Research*, **2014**, 3, 55	3.6	19
98	The IMEx coronavirus interactome: an evolving map of Coronaviridae-host molecular interactions. *Database: the Journal of Biological Databases and Curation*, **2020**, 2020,	5	19
97	An informatic pipeline for the data capture and submission of quantitative proteomic data using iTRAQ. *Proteome Science*, **2007**, 5, 4	2.6	18
96	Analysis of the experimental detection of central nervous system-related genes in human brain and cerebrospinal fluid datasets. *Proteomics*, **2008**, 8, 1138-48	4.8	18
95	The role SWISS-PROT and TrEMBL play in the genome research environment. *Journal of Biotechnology*, **2000**, 78, 221-34	3.7	18
94	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 workshop report. *Journal of Proteomics*, **2013**, 87, 134-8	3.9	17
93	The systematic annotation of the three main GPCR families in Reactome. *Database: the Journal of Biological Databases and Curation*, **2010**, 2010, baq018	5	17
92	ISPIDER Central: an integrated database web-server for proteomics. *Nucleic Acids Research*, **2008**, 36, W485-90	20.1	17
91	CausalTAB: the PSI-MITAB 2.8 updated format for signalling data representation and dissemination. *Bioinformatics*, **2019**, 35, 3779-3785	7.2	16
90	Published and perished? The influence of the searched protein database on the long-term storage of proteomics data. *Molecular and Cellular Proteomics*, **2011**, 10, M111.008490	7.6	16
89	The gel electrophoresis markup language (GelML) from the Proteomics Standards Initiative. *Proteomics*, **2010**, 10, 3073-81	4.8	16
88	The Protein Feature Ontology: a tool for the unification of protein feature annotations. *Bioinformatics*, **2008**, 24, 2767-72	7.2	16
87	A Data Citation Roadmap for Scholarly Data Repositories		16
86	Introducing the PRIDE Archive RESTful web services. *Nucleic Acids Research*, **2015**, 43, W599-604	20.1	15
85	Ten years of standardizing proteomic data: a report on the HUPO-PSI Spring Workshop: April 12-14th, 2012, San Diego, USA. *Proteomics*, **2012**, 12, 2767-72	4.8	15
84	The IntAct database: efficient access to fine-grained molecular interaction data. *Nucleic Acids Research*, **2021**,	20.1	15

83	Identifying novel biomarkers through data mining-a realistic scenario?. *Proteomics - Clinical Applications*, **2015**, 9, 437-43	3.1	14
82	jmzTab: a java interface to the mzTab data standard. *Proteomics*, **2014**, 14, 1328-32	4.8	14
81	Progress in Establishing Common Standards for Exchanging Proteomics Data: The Second Meeting of the HUPO Proteomics Standards Initiative. *Comparative and Functional Genomics*, **2003**, 4, 203-6		14
80	A reference set of curated biomedical data and metadata from clinical case reports. *Scientific Data*, **2018**, 5, 180258	8.2	14
79	The use of common ontologies and controlled vocabularies to enable data exchange and deposition for complex proteomic experiments. *Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing*, **2005**, 186-96	1.3	14
78	SPARQL-enabled identifier conversion with Identifiers.org. *Bioinformatics*, **2015**, 31, 1875-7	7.2	13
77	The EBI enzyme portal. *Nucleic Acids Research*, **2013**, 41, D773-80	20.1	13
76	Human Proteome Organization Proteomics Standards Initiative. *Molecular and Cellular Proteomics*, **2007**, 6, 1666-1667	7.6	13
75	Expression data analysis with Reactome. *Current Protocols in Bioinformatics*, **2015**, 49, 8.20.1-8.20.9	24.2	12
74	Proteomics and Beyond: a report on the 3rd Annual Spring Workshop of the HUPO-PSI 21-23 April 2006, San Francisco, CA, USA. *Proteomics*, **2006**, 6, 4439-43	4.8	12
73	BioModels linked dataset. *BMC Systems Biology*, **2014**, 8, 91	3.5	11
72	From Peptidome to PRIDE: public proteomics data migration at a large scale. *Proteomics*, **2013**, 13, 1692-58		11
71	Charting online OMICS resources: A navigational chart for clinical researchers. *Proteomics - Clinical Applications*, **2009**, 3, 18-29	3.1	11
70	Gene regulation knowledge commons: community action takes care of DNA binding transcription factors. *Database: the Journal of Biological Databases and Curation*, **2016**, 2016,	5	10
69	Shared resources, shared costs--leveraging biocuration resources. *Database: the Journal of Biological Databases and Curation*, **2015**, 2015,	5	10
68	Towards the collaborative curation of the registry underlying Identifiers.org. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bat017	5	10
67	HENA, heterogeneous network-based data set for Alzheimer's disease. *Scientific Data*, **2019**, 6, 151	8.2	9
66	Capturing cooperative interactions with the PSI-MI format. *Database: the Journal of Biological Databases and Curation*, **2013**, 2013, bat066	5	9

65	Dasty3, a WEB framework for DAS. *Bioinformatics*, **2011**, 27, 2616-7	7.2	9
64	Rintact: enabling computational analysis of molecular interaction data from the IntAct repository. *Bioinformatics*, **2008**, 24, 1100-1	7.2	9
63	Proteomic data exchange and storage: the need for common standards and public repositories. *Methods in Molecular Biology*, **2007**, 367, 261-70	1.4	9
62	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. *Molecular Systems Biology*, **2021**, 17, e10387	12.2	9
61	ComplexViewer: visualization of curated macromolecular complexes. *Bioinformatics*, **2017**, 33, 3673-3675	7.2	8
60	Interleukins and their signaling pathways in the Reactome biological pathway database. *Journal of Allergy and Clinical Immunology*, **2018**, 141, 1411-1416	11.5	8
59	The HUPO initiative on Model Organism Proteomes, iMOP. *Proteomics*, **2012**, 12, 340-5	4.8	8
58	Annual spring meeting of the Proteomics Standards Initiative. *Proteomics*, **2009**, 9, 4429-32	4.8	8
57	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	5	7
56	iProX in 2021: connecting proteomics data sharing with big data. *Nucleic Acids Research*, **2021**,	20.1	7
55	Data standards and controlled vocabularies for proteomics. *Methods in Molecular Biology*, **2008**, 484, 279-86	1.4	7
54	Data standardization by the HUPO-PSI: how has the community benefitted?. *Methods in Molecular Biology*, **2011**, 696, 149-60	1.4	7
53	HI-bone: a scoring system for identifying phenylisothiocyanate-derivatized peptides based on precursor mass and high intensity fragment ions. *Analytical Chemistry*, **2013**, 85, 3515-20	7.8	6
52	Second Joint HUPO publication and Proteomics Standards Initiative workshop. *Proteomics*, **2009**, 9, 4426-8	4.8	6
51	ENFIN--A European network for integrative systems biology. *Comptes Rendus - Biologies*, **2009**, 332, 1050-8	1.4	6
50	The first 10 years of the international coordination network for standards in systems and synthetic biology (COMBINE). *Journal of Integrative Bioinformatics*, **2020**, 17,	3.8	6
49	Understudied proteins: opportunities and challenges for functional proteomics.. *Nature Methods*, **2022**,	21.6	6
48	The publication and database deposition of molecular interaction data. *Current Protocols in Protein Science*, **2010**, Chapter 25, Unit 25.3	3.1	5

47	Towards Coordinated International Support of Core Data Resources for the Life Sciences		5
46	IntAct App: a Cytoscape application for molecular interaction network visualisation and analysis. *Bioinformatics*, **2021**,	7.2	5
45	Reactome and ORCID-fine-grained credit attribution for community curation. *Database: the Journal of Biological Databases and Curation*, **2019**, 2019,	5	5
44	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). *Bioinformatics*, **2021**, 36, 5712-5718	7.2	5
43	Deep learning embedder method and tool for mass spectra similarity search. *Journal of Proteomics*, **2021**, 232, 104070	3.9	5
42	iAnn: an event sharing platform for the life sciences. *Bioinformatics*, **2013**, 29, 1919-21	7.2	4
41	Standardising Proteomics Data – the W ork of the HUPO Proteomics Standards Initiative. *Journal of Proteomics and Bioinformatics*, **2008**, 01, 003-005	2.1	4
40	Complex Portal 2022: new curation frontiers. *Nucleic Acids Research*, **2021**,	20.1	4
39	COVID-19 Disease Map, a computational knowledge repository of SARS-CoV-2 virus-host interaction mechanisms		4
38	HUPO 2011: The new Cardiovascular Initiative - integrating proteomics and cardiovascular biology in health and disease. *Proteomics*, **2012**, 12, 749-51	4.8	3
37	easyDAS: automatic creation of DAS servers. *BMC Bioinformatics*, **2011**, 12, 23	3.6	3
36	DAS writeback: a collaborative annotation system. *BMC Bioinformatics*, **2011**, 12, 143	3.6	3
35	TEMBLOR - Perspectives of EBI Database Services. *Comparative and Functional Genomics*, **2002**, 3, 47-50		3
34	Uniform resolution of compact identifiers for biomedical data		3
33	PathwayMatcher: proteoform-centric network construction enables fine-granularity multiomics pathway mapping. *GigaScience*, **2019**, 8,	7.6	2
32	OntoDas - a tool for facilitating the construction of complex queries to the Gene Ontology. *BMC Bioinformatics*, **2008**, 9, 437	3.6	2
31	Proteomics and data standardisation. *Drug Discovery Today Biosilico*, **2004**, 2, 91-93		2
30	The European Bioinformatics Institute (EMBL-EBI) in 2021. *Nucleic Acids Research*, **2021**,	20.1	2

29	Complex Portal - A Unifying Protein Complex Database. *Genomics and Computational Biology*, **2017**, 4, 100052		2
28	The omics discovery REST interface. *Nucleic Acids Research*, **2020**, 48, W380-W384	20.1	2
27	Omics Discovery Index - Discovering and Linking Public □Omics□Datasets		2
26	ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis		2
25	MyDas, an extensible Java DAS server. *PLoS ONE*, **2012**, 7, e44180	3.7	2
24	BioModels Parameters: a treasure trove of parameter values from published systems biology models. *Bioinformatics*, **2020**, 36, 4649-4654	7.2	2
23	Equipping Physiologists with an Informatics Tool Chest: Toward an Integerated Mitochondrial Phenome. *Handbook of Experimental Pharmacology*, **2017**, 240, 377-401	3.2	2
22	An open invitation to the Understudied Proteins Initiative.. *Nature Biotechnology*, **2022**,	44.5	2
21	Development and Implementation of the PSI MI Standard for Molecular Interaction **2006**,		1
20	The ESF Programme on Functional Genomics Workshop on 'Data Integration in Functional Genomics: Application to Biological Pathways'. *Comparative and Functional Genomics*, **2004**, 5, 148-55		1
19	Path4Drug: Data Science Workflow for Identification of Tissue-Specific Biological Pathways Modulated by Toxic Drugs. *Frontiers in Pharmacology*, **2021**, 12, 708296	5.6	1
18	CausalTab: PSI-MITAB 2.8 updated format for signaling data representation and dissemination		1
17	Preparing molecular interaction data for publication. *Methods in Molecular Biology*, **2011**, 694, 229-36	1.4	1
16	Protein-protein interactions: analysis and prediction **2008**, 353-410		1
15	Reproducibility in systems biology modelling		1
14	Capturing variation impact on molecular interactions: the IMEx Consortium mutations data set		1
13	Wikidata as a FAIR knowledge graph for the life sciences		1
12	Identifiers for the 21st century: How to design, provision, and reuse persistent identifiers to maximize utility and impact of life science data		1

11	Identifiers.org: Compact Identifier services in the cloud. *Bioinformatics*, **2021**, 37, 1781-1782	7.2	1
10	Organizational principles of the Reactome human BioPAX model using graph theory methods. *Journal of Complex Networks*, **2016**, cnw003	1.7	1
9	Analysing the yeast complexome-the Complex Portal rising to the challenge. *Nucleic Acids Research*, **2021**, 49, 3156-3167	20.1	1
8	Using Reactome to build an autophagy mechanism knowledgebase. *Autophagy*, **2021**, 17, 1543-1554	10.2	0
7	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	64.1	
6	Proteomic Data Standardization, Deposition and Exchange. *Methods and Principles in Medicinal Chemistry*, **2006**, 19-30	0.4	
5	ENFIN - An Integrative Structure for Systems Biology. *Lecture Notes in Computer Science*, **2008**, 132-143	0.9	
4	EBI Proteomics Services. *Lecture Notes in Computer Science*, **2008**, 207-207	0.9	
3	Infrastructure for distributed protein annotation **2008**, 413-426		
2	A pipeline for identifying endogenous neuropeptides from spectral archives. *International Journal of Data Mining and Bioinformatics*, **2018**, 20, 12	0.5	
1	BioModels Database: A Public Repository for Sharing Models of Biological Processes **2022**, 463-467		