

Henning Hermjakob

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Understudied proteins: opportunities and challenges for functional proteomics.. <i>Nature Methods</i> , 2022 ,	21.6	6
261	An open invitation to the Understudied Proteins Initiative.. <i>Nature Biotechnology</i> , 2022 ,	44.5	2
260	BioModels Database: A Public Repository for Sharing Models of Biological Processes 2022 , 463-467		
259	The European Bioinformatics Institute (EMBL-EBI) in 2021. <i>Nucleic Acids Research</i> , 2021 ,	20.1	2
258	Complex Portal 2022: new curation frontiers. <i>Nucleic Acids Research</i> , 2021 ,	20.1	4
257	The IntAct database: efficient access to fine-grained molecular interaction data. <i>Nucleic Acids Research</i> , 2021 ,	20.1	15
256	The reactome pathway knowledgebase 2022. <i>Nucleic Acids Research</i> , 2021 ,	20.1	57
255	iProX in 2021: connecting proteomics data sharing with big data. <i>Nucleic Acids Research</i> , 2021 ,	20.1	7
254	COVID19 Disease Map, a computational knowledge repository of virus-host interaction mechanisms. <i>Molecular Systems Biology</i> , 2021 , 17, e10387	12.2	9
253	Path4Drug: Data Science Workflow for Identification of Tissue-Specific Biological Pathways Modulated by Toxic Drugs. <i>Frontiers in Pharmacology</i> , 2021 , 12, 708296	5.6	1
252	Identifiers.org: Compact Identifier services in the cloud. <i>Bioinformatics</i> , 2021 , 37, 1781-1782	7.2	1
251	IntAct App: a Cytoscape application for molecular interaction network visualisation and analysis. <i>Bioinformatics</i> , 2021 ,	7.2	5
250	Using Reactome to build an autophagy mechanism knowledgebase. <i>Autophagy</i> , 2021 , 17, 1543-1554	10.2	0
249	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). <i>Bioinformatics</i> , 2021 , 36, 5712-5718	7.2	5
248	Deep learning embedder method and tool for mass spectra similarity search. <i>Journal of Proteomics</i> , 2021 , 232, 104070	3.9	5
247	Reproducibility in systems biology modelling. <i>Molecular Systems Biology</i> , 2021 , 17, e9982	12.2	22
246	Analysing the yeast complexome-the Complex Portal rising to the challenge. <i>Nucleic Acids Research</i> , 2021 , 49, 3156-3167	20.1	1

245	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. <i>Scientific Data</i> , 2020 , 7, 136	8.2	71
244	MEMOTE for standardized genome-scale metabolic model testing. <i>Nature Biotechnology</i> , 2020 , 38, 272-276	4.5	121
243	The ProteomeXchange consortium in 2020: enabling 'big data' approaches in proteomics. <i>Nucleic Acids Research</i> , 2020 , 48, D1145-D1152	20.1	212
242	The reactome pathway knowledgebase. <i>Nucleic Acids Research</i> , 2020 , 48, D498-D503	20.1	848
241	BioModels-15 years of sharing computational models in life science. <i>Nucleic Acids Research</i> , 2020 , 48, D407-D415	20.1	81
240	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,	3.8	6
239	SBML Level 3: an extensible format for the exchange and reuse of biological models. <i>Molecular Systems Biology</i> , 2020 , 16, e9110	12.2	65
238	Wikidata as a knowledge graph for the life sciences. <i>ELife</i> , 2020 , 9,	8.9	24
237	The omics discovery REST interface. <i>Nucleic Acids Research</i> , 2020 , 48, W380-W384	20.1	2
236	The IMEx coronavirus interactome: an evolving map of Coronaviridae-host molecular interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2020 , 2020,	5	19
235	Towards a unified open access dataset of molecular interactions. <i>Nature Communications</i> , 2020 , 11, 6144	4.4	26
234	BioModels Parameters: a treasure trove of parameter values from published systems biology models. <i>Bioinformatics</i> , 2020 , 36, 4649-4654	7.2	2
233	ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. <i>Molecular and Cellular Proteomics</i> , 2020 , 19, 2115-2125	7.6	38
232	PhaSepDB: a database of liquid-liquid phase separation related proteins. <i>Nucleic Acids Research</i> , 2020 , 48, D354-D359	20.1	68
231	Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. <i>Nature Communications</i> , 2019 , 10, 10	17.4	122
230	A data citation roadmap for scholarly data repositories. <i>Scientific Data</i> , 2019 , 6, 28	8.2	33
229	CausalTAB: the PSI-MITAB 2.8 updated format for signalling data representation and dissemination. <i>Bioinformatics</i> , 2019 , 35, 3779-3785	7.2	16
228	HENA, heterogeneous network-based data set for Alzheimer's disease. <i>Scientific Data</i> , 2019 , 6, 151	8.2	9

227	Quantifying the impact of public omics data. <i>Nature Communications</i> , 2019 , 10, 3512	17.4	42
226	PathwayMatcher: proteoform-centric network construction enables fine-granularity multiomics pathway mapping. <i>GigaScience</i> , 2019 , 8,	7.6	2
225	Reactome and ORCID-fine-grained credit attribution for community curation. <i>Database: the Journal of Biological Databases and Curation</i> , 2019 , 2019,	5	5
224	iProX: an integrated proteome resource. <i>Nucleic Acids Research</i> , 2019 , 47, D1211-D1217	20.1	423
223	Complex Portal 2018: extended content and enhanced visualization tools for macromolecular complexes. <i>Nucleic Acids Research</i> , 2019 , 47, D550-D558	20.1	44
222	BioModels: expanding horizons to include more modelling approaches and formats. <i>Nucleic Acids Research</i> , 2018 , 46, D1248-D1253	20.1	54
221	Interleukins and their signaling pathways in the Reactome biological pathway database. <i>Journal of Allergy and Clinical Immunology</i> , 2018 , 141, 1411-1416	11.5	8
220	Integrated omics dissection of proteome dynamics during cardiac remodeling. <i>Nature Communications</i> , 2018 , 9, 120	17.4	44
219	Reactome diagram viewer: data structures and strategies to boost performance. <i>Bioinformatics</i> , 2018 , 34, 1208-1214	7.2	57
218	Biomedical Informatics on the Cloud: A Treasure Hunt for Advancing Cardiovascular Medicine. <i>Circulation Research</i> , 2018 , 122, 1290-1301	15.7	19
217	Uniform resolution of compact identifiers for biomedical data. <i>Scientific Data</i> , 2018 , 5, 180029	8.2	33
216	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. <i>BMC Bioinformatics</i> , 2018 , 19, 134	3.6	31
215	Reactome graph database: Efficient access to complex pathway data. <i>PLoS Computational Biology</i> , 2018 , 14, e1005968	5	100
214	A reference set of curated biomedical data and metadata from clinical case reports. <i>Scientific Data</i> , 2018 , 5, 180258	8.2	14
213	A pipeline for identifying endogenous neuropeptides from spectral archives. <i>International Journal of Data Mining and Bioinformatics</i> , 2018 , 20, 12	0.5	
212	The Reactome Pathway Knowledgebase. <i>Nucleic Acids Research</i> , 2018 , 46, D649-D655	20.1	1496
211	Discovering and linking public omics data sets using the Omics Discovery Index. <i>Nature Biotechnology</i> , 2017 , 35, 406-409	44.5	105
210	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	4.5	21

209	Open Targets: a platform for therapeutic target identification and validation. <i>Nucleic Acids Research</i> , 2017 , 45, D985-D994	20.1	241
208	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. <i>Nucleic Acids Research</i> , 2017 , 45, D1100-D1106	20.1	568
207	ComplexViewer: visualization of curated macromolecular complexes. <i>Bioinformatics</i> , 2017 , 33, 3673-3675.	2	8
206	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. <i>Journal of Proteome Research</i> , 2017 , 16, 4288-4298	5.6	61
205	Reactome enhanced pathway visualization. <i>Bioinformatics</i> , 2017 , 33, 3461-3467	7.2	76
204	Reactome pathway analysis: a high-performance in-memory approach. <i>BMC Bioinformatics</i> , 2017 , 18, 142	3.6	285
203	AAgAtlas 1.0: a human autoantigen database. <i>Nucleic Acids Research</i> , 2017 , 45, D769-D776	20.1	33
202	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. <i>Journal of Proteomics</i> , 2017 , 150, 170-182	3.9	39
201	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	9.7	63
200	Complex Portal - A Unifying Protein Complex Database. <i>Genomics and Computational Biology</i> , 2017 , 4, 100052		2
199	Equipping Physiologists with an Informatics Tool Chest: Toward an Integrated Mitochondrial Phenome. <i>Handbook of Experimental Pharmacology</i> , 2017 , 240, 377-401	3.2	2
198	Gene regulation knowledge commons: community action takes care of DNA binding transcription factors. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	10
197	2016 update of the PRIDE database and its related tools. <i>Nucleic Acids Research</i> , 2016 , 44, D447-56	20.1	2440
196	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. <i>Nature Methods</i> , 2016 , 13, 651-656	21.6	99
195	Testing and Validation of Computational Methods for Mass Spectrometry. <i>Journal of Proteome Research</i> , 2016 , 15, 809-14	5.6	24
194	Accurate estimation of isoelectric point of protein and peptide based on amino acid sequences. <i>Bioinformatics</i> , 2016 , 32, 821-7	7.2	32
193	PRIDE Inspector Toolsuite: Moving Toward a Universal Visualization Tool for Proteomics Data Standard Formats and Quality Assessment of ProteomeXchange Datasets. <i>Molecular and Cellular Proteomics</i> , 2016 , 15, 305-17	7.6	91
192	Organizational principles of the Reactome human BioPAX model using graph theory methods. <i>Journal of Complex Networks</i> , 2016 , cnw003	1.7	1

191	The Reactome pathway Knowledgebase. <i>Nucleic Acids Research</i> , 2016 , 44, D481-7	20.1	920
190	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. <i>Journal of Proteome Research</i> , 2016 , 15, 3961-3970	5.6	130
189	A public repository for mass spectrometry imaging data. <i>Analytical and Bioanalytical Chemistry</i> , 2015 , 407, 2027-33	4.4	27
188	Expression data analysis with Reactome. <i>Current Protocols in Bioinformatics</i> , 2015 , 49, 8.20.1-8.20.9	24.2	12
187	ms-data-core-api: an open-source, metadata-oriented library for computational proteomics. <i>Bioinformatics</i> , 2015 , 31, 2903-5	7.2	26
186	Harnessing the heart of big data. <i>Circulation Research</i> , 2015 , 116, 1115-9	15.7	47
185	Development of data representation standards by the human proteome organization proteomics standards initiative. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2015 , 22, 495-506	8.6	42
184	Open source libraries and frameworks for biological data visualisation: a guide for developers. <i>Proteomics</i> , 2015 , 15, 1356-74	4.8	34
183	Identifying novel biomarkers through data mining-a realistic scenario?. <i>Proteomics - Clinical Applications</i> , 2015 , 9, 437-43	3.1	14
182	Making proteomics data accessible and reusable: current state of proteomics databases and repositories. <i>Proteomics</i> , 2015 , 15, 930-49	4.8	138
181	Introducing the PRIDE Archive RESTful web services. <i>Nucleic Acids Research</i> , 2015 , 43, W599-604	20.1	15
180	Pharmacometrics Markup Language (PharmML): Opening New Perspectives for Model Exchange in Drug Development. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2015 , 4, 316-9	4.5	34
179	The evolution of standards and data management practices in systems biology. <i>Molecular Systems Biology</i> , 2015 , 11, 851	12.2	29
178	Shared resources, shared costs--leveraging biocuration resources. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015,	5	10
177	The complex portal--an encyclopaedia of macromolecular complexes. <i>Nucleic Acids Research</i> , 2015 , 43, D479-84	20.1	68
176	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,	5	36
175	BioModels: Content, Features, Functionality, and Use. <i>CPT: Pharmacometrics and Systems Pharmacology</i> , 2015 , 4, e3	4.5	48
174	SPARQL-enabled identifier conversion with Identifiers.org. <i>Bioinformatics</i> , 2015 , 31, 1875-7	7.2	13

173	A visual review of the interactome of LRRK2: Using deep-curated molecular interaction data to represent biology. <i>Proteomics</i> , 2015 , 15, 1390-404	4.8	33
172	BioModels: ten-year anniversary. <i>Nucleic Acids Research</i> , 2015 , 43, D542-8	20.1	225
171	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014 , 32, 223-6	44.5	2053
170	How to submit MS proteomics data to ProteomeXchange via the PRIDE database. <i>Proteomics</i> , 2014 , 14, 2233-41	4.8	41
169	Characterization, design, and function of the mitochondrial proteome: from organs to organisms. <i>Journal of Proteome Research</i> , 2014 , 13, 433-46	5.6	49
168	BioModels linked dataset. <i>BMC Systems Biology</i> , 2014 , 8, 91	3.5	11
167	jmzTab: a java interface to the mzTab data standard. <i>Proteomics</i> , 2014 , 14, 1328-32	4.8	14
166	Controlled vocabularies and ontologies in proteomics: overview, principles and practice. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 98-107	4	26
165	Open source libraries and frameworks for mass spectrometry based proteomics: a developer's perspective. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2014 , 1844, 63-76	4	59
164	The Reactome pathway knowledgebase. <i>Nucleic Acids Research</i> , 2014 , 42, D472-7	20.1	1188
163	qcML: an exchange format for quality control metrics from mass spectrometry experiments. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 1905-13	7.6	36
162	The mzTab data exchange format: communicating mass-spectrometry-based proteomics and metabolomics experimental results to a wider audience. <i>Molecular and Cellular Proteomics</i> , 2014 , 13, 2765-75	7.6	96
161	The MIntAct project--IntAct as a common curation platform for 11 molecular interaction databases. <i>Nucleic Acids Research</i> , 2014 , 42, D358-63	20.1	1111
160	BioJS: an open source standard for biological visualisation - its status in 2014. <i>F1000Research</i> , 2014 , 3, 55	3.6	19
159	BioJS: an open source JavaScript framework for biological data visualization. <i>Bioinformatics</i> , 2013 , 29, 1103-4	7.2	88
158	Path2Models: large-scale generation of computational models from biochemical pathway maps. <i>BMC Systems Biology</i> , 2013 , 7, 116	3.5	122
157	PRIDE Cluster: building a consensus of proteomics data. <i>Nature Methods</i> , 2013 , 10, 95-6	21.6	49
156	The PRoteomics IDentifications (PRIDE) database and associated tools: status in 2013. <i>Nucleic Acids Research</i> , 2013 , 41, D1063-9	20.1	1587

155	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 workshop report. <i>Journal of Proteomics</i> , 2013 , 87, 134-8	3.9	17
154	HI-bone: a scoring system for identifying phenylisothiocyanate-derivatized peptides based on precursor mass and high intensity fragment ions. <i>Analytical Chemistry</i> , 2013 , 85, 3515-20	7.8	6
153	Tools (Viewer, Library and Validator) that facilitate use of the peptide and protein identification standard format, termed mzIdentML. <i>Molecular and Cellular Proteomics</i> , 2013 , 12, 3026-35	7.6	28
152	iAnn: an event sharing platform for the life sciences. <i>Bioinformatics</i> , 2013 , 29, 1919-21	7.2	4
151	Capturing cooperative interactions with the PSI-MI format. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat066	5	9
150	The EBI enzyme portal. <i>Nucleic Acids Research</i> , 2013 , 41, D773-80	20.1	13
149	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat009	5	56
148	Towards the collaborative curation of the registry underlying Identifiers.org. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bat017	5	10
147	Integration of cardiac proteome biology and medicine by a specialized knowledgebase. <i>Circulation Research</i> , 2013 , 113, 1043-53	15.7	42
146	A new reference implementation of the PSICQUIC web service. <i>Nucleic Acids Research</i> , 2013 , 41, W601-6	20.1	70
145	From Peptidome to PRIDE: public proteomics data migration at a large scale. <i>Proteomics</i> , 2013 , 13, 1692-8	4.8	11
144	LipidHome: a database of theoretical lipids optimized for high throughput mass spectrometry lipidomics. <i>PLoS ONE</i> , 2013 , 8, e61951	3.7	59
143	Shouldn't enantiomeric purity be included in the 'minimum information about a bioactive entity? Response from the MIABE group. <i>Nature Reviews Drug Discovery</i> , 2012 , 11, 730-730	64.1	
142	Ten years of standardizing proteomic data: a report on the HUPO-PSI Spring Workshop: April 12-14th, 2012, San Diego, USA. <i>Proteomics</i> , 2012 , 12, 2767-72	4.8	15
141	Hydra: a scalable proteomic search engine which utilizes the Hadoop distributed computing framework. <i>BMC Bioinformatics</i> , 2012 , 13, 324	3.6	43
140	A critical appraisal of techniques, software packages, and standards for quantitative proteomic analysis. <i>OMICS A Journal of Integrative Biology</i> , 2012 , 16, 431-42	3.8	46
139	The HUPO initiative on Model Organism Proteomes, iMOP. <i>Proteomics</i> , 2012 , 12, 340-5	4.8	8
138	jmzIdentML API: A Java interface to the mzIdentML standard for peptide and protein identification data. <i>Proteomics</i> , 2012 , 12, 790-4	4.8	27

137	jmzReader: A Java parser library to process and visualize multiple text and XML-based mass spectrometry data formats. <i>Proteomics</i> , 2012 , 12, 795-8	4.8	26
136	HUPO 2011: The new Cardiovascular Initiative - integrating proteomics and cardiovascular biology in health and disease. <i>Proteomics</i> , 2012 , 12, 749-51	4.8	3
135	Analyzing protein-protein interaction networks. <i>Journal of Proteome Research</i> , 2012 , 11, 2014-31	5.6	103
134	PRIDE Inspector: a tool to visualize and validate MS proteomics data. <i>Nature Biotechnology</i> , 2012 , 30, 135-7	44.5	103
133	The PRoteomics IDentification (PRIDE) Converter 2 framework: an improved suite of tools to facilitate data submission to the PRIDE database and the ProteomeXchange consortium. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, 1682-9	7.6	96
132	Improvements in the Protein Identifier Cross-Reference service. <i>Nucleic Acids Research</i> , 2012 , 40, W276-80.1	20.1	27
131	PRIDE: quality control in a proteomics data repository. <i>Database: the Journal of Biological Databases and Curation</i> , 2012 , 2012, bas004	5	30
130	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. <i>Nature Methods</i> , 2012 , 9, 345-50	21.6	375
129	Toward interoperable bioscience data. <i>Nature Genetics</i> , 2012 , 44, 121-6	36.3	286
128	The IntAct molecular interaction database in 2012. <i>Nucleic Acids Research</i> , 2012 , 40, D841-6	20.1	779
127	Annotating cancer variants and anti-cancer therapeutics in reactome. <i>Cancers</i> , 2012 , 4, 1180-211	6.6	232
126	The mzIdentML data standard for mass spectrometry-based proteomics results. <i>Molecular and Cellular Proteomics</i> , 2012 , 11, M111.014381	7.6	150
125	MyDas, an extensible Java DAS server. <i>PLoS ONE</i> , 2012 , 7, e44180	3.7	2
124	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. <i>Nature Methods</i> , 2011 , 8, 528-9	21.6	227
123	Reactome: a database of reactions, pathways and biological processes. <i>Nucleic Acids Research</i> , 2011 , 39, D691-7	20.1	1090
122	Minimum information about a bioactive entity (MIABE). <i>Nature Reviews Drug Discovery</i> , 2011 , 10, 661-9	64.1	69
121	easyDAS: automatic creation of DAS servers. <i>BMC Bioinformatics</i> , 2011 , 12, 23	3.6	3
120	DAS writeback: a collaborative annotation system. <i>BMC Bioinformatics</i> , 2011 , 12, 143	3.6	3

119	Reactome pathway analysis to enrich biological discovery in proteomics data sets. <i>Proteomics</i> , 2011 , 11, 3598-613	4.8	71
118	Consequences of the discontinuation of the International Protein Index (IPI) database and its substitution by the UniProtKB "complete proteome" sets. <i>Proteomics</i> , 2011 , 11, 4434-8	4.8	24
117	mzML--a community standard for mass spectrometry data. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, R110.000133	7.6	424
116	Dasty3, a WEB framework for DAS. <i>Bioinformatics</i> , 2011 , 27, 2616-7	7.2	9
115	Published and perished? The influence of the searched protein database on the long-term storage of proteomics data. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.008490	7.6	16
114	Critical amino acid residues in proteins: a BioMart integration of Reactome protein annotations with PRIDE mass spectrometry data and COSMIC somatic mutations. <i>Database: the Journal of Biological Databases and Curation</i> , 2011 , 2011, bar047	5	7
113	The Reactome BioMart. <i>Database: the Journal of Biological Databases and Curation</i> , 2011 , 2011, bar031	5	29
112	Preparing molecular interaction data for publication. <i>Methods in Molecular Biology</i> , 2011 , 694, 229-36	1.4	1
111	Data standardization by the HUPO-PSI: how has the community benefitted?. <i>Methods in Molecular Biology</i> , 2011 , 696, 149-60	1.4	7
110	Minimum information about a protein affinity reagent (MIAPAR). <i>Nature Biotechnology</i> , 2010 , 28, 650-3	44.5	37
109	A community standard format for the representation of protein affinity reagents. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 1-10	7.6	33
108	Mapping plant interactomes using literature curated and predicted protein-protein interaction data sets. <i>Plant Cell</i> , 2010 , 22, 997-1005	11.6	25
107	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, W78-83	20.1	56
106	The Ontology Lookup Service: bigger and better. <i>Nucleic Acids Research</i> , 2010 , 38, W155-60	20.1	82
105	The Proteomics Identifications database: 2010 update. <i>Nucleic Acids Research</i> , 2010 , 38, D736-42	20.1	199
104	The IntAct molecular interaction database in 2010. <i>Nucleic Acids Research</i> , 2010 , 38, D525-31	20.1	522
103	The publication and database deposition of molecular interaction data. <i>Current Protocols in Protein Science</i> , 2010 , Chapter 25, Unit 25.3	3.1	5
102	The systematic annotation of the three main GPCR families in Reactome. <i>Database: the Journal of Biological Databases and Curation</i> , 2010 , 2010, baq018	5	17

101	Meeting Report from the Second "Minimum Information for Biological and Biomedical Investigations" (MIBBI) workshop. <i>Standards in Genomic Sciences</i> , 2010 , 3, 259-66		26
100	A domain level interaction network of amyloid precursor protein and Abeta of Alzheimer's disease. <i>Proteomics</i> , 2010 , 10, 2377-95	4.8	38
99	The gel electrophoresis markup language (GelML) from the Proteomics Standards Initiative. <i>Proteomics</i> , 2010 , 10, 3073-81	4.8	16
98	Organelle proteomics experimental designs and analysis. <i>Proteomics</i> , 2010 , 10, 3957-69	4.8	44
97	The PSI semantic validator: a framework to check MIAPE compliance of proteomics data. <i>Proteomics</i> , 2009 , 9, 5112-9	4.8	47
96	A guide to the Proteomics Identifications Database proteomics data repository. <i>Proteomics</i> , 2009 , 9, 4276-83	4.8	198
95	Second Joint HUPO publication and Proteomics Standards Initiative workshop. <i>Proteomics</i> , 2009 , 9, 4426-8	4.8	6
94	Annual spring meeting of the Proteomics Standards Initiative. <i>Proteomics</i> , 2009 , 9, 4429-32	4.8	8
93	Charting online OMICS resources: A navigational chart for clinical researchers. <i>Proteomics - Clinical Applications</i> , 2009 , 3, 18-29	3.1	11
92	New open drug activity data at EBI. <i>Chemistry Central Journal</i> , 2009 , 3,		78
91	Recurated protein interaction datasets. <i>Nature Methods</i> , 2009 , 6, 860-1	21.6	48
90	Reactome knowledgebase of human biological pathways and processes. <i>Nucleic Acids Research</i> , 2009 , 37, D619-22	20.1	675
89	ENFIN--A European network for integrative systems biology. <i>Comptes Rendus - Biologies</i> , 2009 , 332, 1050-4	11.4	6
88	Recommendations from the 2008 International Summit on Proteomics Data Release and Sharing Policy: the Amsterdam principles. <i>Journal of Proteome Research</i> , 2009 , 8, 3689-92	5.6	58
87	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008 , 26, 889-96	44.5	417
86	The minimum information about a genome sequence (MIGS) specification. <i>Nature Biotechnology</i> , 2008 , 26, 541-7	44.5	964
85	OntoDas - a tool for facilitating the construction of complex queries to the Gene Ontology. <i>BMC Bioinformatics</i> , 2008 , 9, 437	3.6	2
84	Integrating biological data--the Distributed Annotation System. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 8, S3	3.6	77

83	Calling on a million minds for community annotation in WikiProteins. <i>Genome Biology</i> , 2008 , 9, R89	18.3	101
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