Henning Hermjakob

List of Publications by Year
in descending order

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258	74,142	5261	611
papers	citations	83 h-index	259 g-index

307	307	307	85806
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Complex Portal 2022: new curation frontiers. Nucleic Acids Research, 2022, 50, D578-D586.	6.5	27
2	The IntAct database: efficient access to fine-grained molecular interaction data. Nucleic Acids Research, 2022, 50, D648-D653.	6.5	89
3	The reactome pathway knowledgebase 2022. Nucleic Acids Research, 2022, 50, D687-D692.	6.5	924
4	iProX in 2021: connecting proteomics data sharing with big data. Nucleic Acids Research, 2022, 50, D1522-D1527.	6.5	197
5	The European Bioinformatics Institute (EMBL-EBI) in 2021. Nucleic Acids Research, 2022, 50, D11-D19.	6.5	34
6	BioSimulators: a central registry of simulation engines and services for recommending specific tools. Nucleic Acids Research, 2022, 50, W108-W114.	6.5	11
7	Understudied proteins: opportunities and challenges for functional proteomics. Nature Methods, 2022, 19, 774-779.	9.0	83
8	An open invitation to the Understudied Proteins Initiative. Nature Biotechnology, 2022, 40, 815-817.	9.4	25
9	Addressing barriers in comprehensiveness, accessibility, reusability, interoperability and reproducibility of computational models in systems biology. Briefings in Bioinformatics, 2022, 23, .	3.2	10
10	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
11	BioModels Database: A Public Repository for Sharing Models of Biological Processes. , 2022, , 463-467.		0
12	Identifiers.org: Compact Identifier services in the cloud. Bioinformatics, 2021, 37, 1781-1782.	1.8	5
13	Using Reactome to build an autophagy mechanism knowledgebase. Autophagy, 2021, 17, 1543-1554.	4.3	5
14	The Minimum Information about a Molecular Interaction CAusal STatement (MI2CAST). Bioinformatics, 2021, 36, 5712-5718.	1.8	14
15	Deep learning embedder method and tool for mass spectra similarity search. Journal of Proteomics, 2021, 232, 104070.	1.2	10
16	Reproducibility in systems biology modelling. Molecular Systems Biology, 2021, 17, e9982.	3.2	67
17	Analysing the yeast complexomeâ€"the Complex Portal rising to the challenge. Nucleic Acids Research, 2021, 49, 3156-3167.	6.5	5
18	A decoupled, modular and scriptable architecture for tools to curate data platforms. Bioinformatics, 2021, 37, 3693-3694.	1.8	0

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19	IntAct App: a Cytoscape application for molecular interaction network visualization and analysis. Bioinformatics, 2021, 37, 3684-3685.	1.8	21
20	COVID19 Disease Map, a computational knowledge repository of virusâ€“host interaction mechanisms. Molecular Systems Biology, 2021, 17, e10387.	3.2	53
21	Path4Drug: Data Science Workflow for Identification of Tissue-Specific Biological Pathways Modulated by Toxic Drugs. Frontiers in Pharmacology, 2021, 12, 708296.	1.6	5
22	The ProteomeXchange consortium in 2020: enabling â€˜big dataâ€™ approaches in proteomics. Nucleic Acids Research, 2020, 48, D1145-D1152.	6.5	491
23	The reactome pathway knowledgebase. Nucleic Acids Research, 2020, 48, D498-D503.	6.5	1,570
24	BioModelsâ€”15 years of sharing computational models in life science. Nucleic Acids Research, 2020, 48, D407-D415.	6.5	175
25	PhaSepDB: a database of liquidâ€“liquid phase separation related proteins. Nucleic Acids Research, 2020, 48, D354-D359.	6.5	157
26	Towards a unified open access dataset of molecular interactions. Nature Communications, 2020, 11, 6144.	5.8	49
27	BioModels Parameters: a treasure trove of parameter values from published systems biology models. Bioinformatics, 2020, 36, 4649-4654.	1.8	5
28	ReactomeGSA - Efficient Multi-Omics Comparative Pathway Analysis. Molecular and Cellular Proteomics, 2020, 19, 2115-2125.	2.5	145
29	COVID-19 Disease Map, building a computational repository of SARS-CoV-2 virus-host interaction mechanisms. Scientific Data, 2020, 7, 136.	2.4	99
30	MEMOTE for standardized genome-scale metabolic model testing. Nature Biotechnology, 2020, 38, 272-276.	9.4	314
31	The IMEx coronavirus interactome: an evolving map ofCoronaviridaeâ€“host molecular interactions. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	34
32	The first 10 years of the international coordination network for standards in systems and synthetic biology (COMBINE). Journal of Integrative Bioinformatics, 2020, 17, .	1.0	18
33	<scp>SBML</scp> Level 3: an extensible format for the exchange and reuse of biological models. Molecular Systems Biology, 2020, 16, e9110.	3.2	178
34	Wikidata as a knowledge graph for the life sciences. ELife, 2020, 9, .	2.8	76
35	The omics discovery REST interface. Nucleic Acids Research, 2020, 48, W380-W384.	6.5	3
36	HENA, heterogeneous network-based data set for Alzheimerâ€™s disease. Scientific Data, 2019, 6, 151.	2.4	34

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37	Quantifying the impact of public omics data. Nature Communications, 2019, 10, 3512.	5.8	79
38	PathwayMatcher: proteoform-centric network construction enables fine-granularity multiomics pathway mapping. GigaScience, 2019, 8, .	3.3	4
39	Capturing variation impact on molecular interactions in the IMEx Consortium mutations data set. Nature Communications, 2019, 10, 10.	5.8	193
40	A data citation roadmap for scholarly data repositories. Scientific Data, 2019, 6, 28.	2.4	59
41	CausalTAB: the PSI-MITAB 2.8 updated format for signalling data representation and dissemination. Bioinformatics, 2019, 35, 3779-3785.	1.8	32
42	Reactome and ORCIDâ€"fine-grained credit attribution for community curation. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	12
43	iProX: an integrated proteome resource. Nucleic Acids Research, 2019, 47, D1211-D1217.	6.5	1,001
44	Complex Portal 2018: extended content and enhanced visualization tools for macromolecular complexes. Nucleic Acids Research, 2019, 47, D550-D558.	6.5	85
45	BioModels: expanding horizons to include more modelling approaches and formats. Nucleic Acids Research, 2018, 46, D1248-D1253.	6.5	80
46	Interleukins and their signaling pathways in the Reactome biological pathway database. Journal of Allergy and Clinical Immunology, 2018, 141, 1411-1416.	1.5	11
47	Integrated omics dissection of proteome dynamics during cardiac remodeling. Nature Communications, 2018, 9, 120.	5.8	64
48	Reactome diagram viewer: data structures and strategies to boost performance. Bioinformatics, 2018, 34, 1208-1214.	1.8	121
49	Biomedical Informatics on the Cloud. Circulation Research, 2018, 122, 1290-1301.	2.0	22
50	A pipeline for identifying endogenous neuropeptides from spectral archives. International Journal of Data Mining and Bioinformatics, 2018, 20, 12.	0.1	0
51	The Reactome Pathway Knowledgebase. Nucleic Acids Research, 2018, 46, D649-D655.	6.5	2,388
52	Uniform resolution of compact identifiers for biomedical data. Scientific Data, 2018, 5, 180029.	2.4	50
53	Encompassing new use cases - level 3.0 of the HUPO-PSI format for molecular interactions. BMC Bioinformatics, 2018, 19, 134.	1.2	47
54	A reference set of curated biomedical data and metadata from clinical case reports. Scientific Data, 2018, 5, 180258.	2.4	22

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55	Reactome graph database: Efficient access to complex pathway data. PLoS Computational Biology, 2018, 14, e1005968.	1.5	202
56	Discovering and linking public omics data sets using the Omics Discovery Index. Nature Biotechnology, 2017, 35, 406-409.	9.4	159
57	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.	1.3	34
58	Open Targets: a platform for therapeutic target identification and validation. Nucleic Acids Research, 2017, 45, D985-D994.	6.5	355
59	Proteomics Standards Initiative: Fifteen Years of Progress and Future Work. Journal of Proteome Research, 2017, 16, 4288-4298.	1.8	87
60	Reactome enhanced pathway visualization. Bioinformatics, 2017, 33, 3461-3467.	1.8	140
61	Reactome pathway analysis: a high-performance in-memory approach. BMC Bioinformatics, 2017, 18, 142.	1.2	600
62	AAgAtlas 1.0: a human autoantigen database. Nucleic Acids Research, 2017, 45, D769-D776.	6.5	48
63	In-depth analysis of protein inference algorithms using multiple search engines and well-defined metrics. Journal of Proteomics, 2017, 150, 170-182.	1.2	56
64	The ProteomeXchange consortium in 2017: supporting the cultural change in proteomics public data deposition. Nucleic Acids Research, 2017, 45, D1100-D1106.	6.5	860
65	ComplexViewer: visualization of curated macromolecular complexes. Bioinformatics, 2017, 33, 3673-3675.	1.8	10
66	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.	2.6	97
67	Complex Portal - A Unifying Protein Complex Database. Genomics and Computational Biology, 2017, 4, 100052.	0.7	2
68	Organizational principles of the Reactome human BioPAX model using graph theory methods. Journal of Complex Networks, 2016, , cnw003.	1.1	1
69	Equipping Physiologists with an Informatics Tool Chest: Toward an Integerated Mitochondrial Phenome. Handbook of Experimental Pharmacology, 2016, 240, 377-401.	0.9	2
70	The Reactome pathway Knowledgebase. Nucleic Acids Research, 2016, 44, D481-D487.	6.5	3,319
71	Human Proteome Project Mass Spectrometry Data Interpretation Guidelines 2.1. Journal of Proteome Research, 2016, 15, 3961-3970.	1.8	158
72	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

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73	2016 update of the PRIDE database and its related tools. Nucleic Acids Research, 2016, 44, D447-D456.	6.5	3,451
74	Recognizing millions of consistently unidentified spectra across hundreds of shotgun proteomics datasets. Nature Methods, 2016, 13, 651-656.	9.0	147
75	Testing and Validation of Computational Methods for Mass Spectrometry. Journal of Proteome Research, 2016, 15, 809-814.	1.8	34
76	Accurate estimation of isoelectric point of protein and peptide based on amino acid sequences. Bioinformatics, 2016, 32, 821-827.	1.8	55
77	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, 305-317.	2.5	140
78	Introducing the PRIDE Archive RESTful web services. Nucleic Acids Research, 2015, 43, W599-W604.	6.5	18
79	Pharmacometrics Markup Language (PharmML): Opening New Perspectives for Model Exchange in Drug Development. CPT: Pharmacometrics and Systems Pharmacology, 2015, 4, 316-319.	1.3	37
80	The evolution of standards and data management practices in systems biology. Molecular Systems Biology, 2015, 11, 851.	3.2	35
81	Shared resources, shared costsâ€"leveraging biocuration resources. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	1.4	13
82	The complex portal - an encyclopaedia of macromolecular complexes. Nucleic Acids Research, 2015, 43, D479-D484.	6.5	100
83	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, bau131-bau131.	1.4	53
84	BioModels: Content, Features, Functionality, and Use. CPT: Pharmacometrics and Systems Pharmacology, 2015, 4, 55-68.	1.3	56
85	SPARQL-enabled identifier conversion with Identifiers.org. Bioinformatics, 2015, 31, 1875-1877.	1.8	14
86	A visual review of the interactome of LRRK2: Using deepâ€curated molecular interaction data to represent biology. Proteomics, 2015, 15, 1390-1404.	1.3	38
87	BioModels: ten-year anniversary. Nucleic Acids Research, 2015, 43, D542-D548.	6.5	334
88	A public repository for mass spectrometry imaging data. Analytical and Bioanalytical Chemistry, 2015, 407, 2027-2033.	1.9	31
89	Expression Data Analysis with Reactome. Current Protocols in Bioinformatics, 2015, 49, 8.20.1-8.20.9.	25.8	15
90	ms-data-core-api: an open-source, metadata-oriented library for computational proteomics. Bioinformatics, 2015, 31, 2903-2905.	1.8	30

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91	Harnessing the Heart of Big Data. Circulation Research, 2015, 116, 1115-1119.	2.0	54
92	Development of data representation standards by the human proteome organization proteomics standards initiative. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 495-506.	2.2	54
93	Open source libraries and frameworks for biological data visualisation: A guide for developers. Proteomics, 2015, 15, 1356-1374.	1.3	43
94	Identifying novel biomarkers through data miningâ€"A realistic scenario?. Proteomics - Clinical Applications, 2015, 9, 437-443.	0.8	20
95	Making proteomics data accessible and reusable: Current state of proteomics databases and repositories. Proteomics, 2015, 15, 930-950.	1.3	181
96	The Reactome pathway knowledgebase. Nucleic Acids Research, 2014, 42, D472-D477.	6.5	1,448
97	qcML: An Exchange Format for Quality Control Metrics from Mass Spectrometry Experiments. Molecular and Cellular Proteomics, 2014, 13, 1905-1913.	2.5	42
98	The mzTab Data Exchange Format: Communicating Mass-spectrometry-based Proteomics and Metabolomics Experimental Results to a Wider Audience. Molecular and Cellular Proteomics, 2014, 13, 2765-2775.	2.5	130
99	The MIntAct projectâ€"IntAct as a common curation platform for 11 molecular interaction databases. Nucleic Acids Research, 2014, 42, D358-D363.	6.5	1,634
100	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. Nature Biotechnology, 2014, 32, 223-226.	9.4	2,505
101	How to submit MS proteomics data to ProteomeXchange via the PRIDE database. Proteomics, 2014, 14, 2233-2241.	1.3	54
102	Characterization, Design, and Function of the Mitochondrial Proteome: From Organs to Organisms. Journal of Proteome Research, 2014, 13, 433-446.	1.8	59
103	BioModels linked dataset. BMC Systems Biology, 2014, 8, 91.	3.0	11
104	jmzTab: A Java interface to the mzTab data standard. Proteomics, 2014, 14, 1328-1332.	1.3	16
105	Controlled vocabularies and ontologies in proteomics: Overview, principles and practice. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 98-107.	1.1	36
106	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.	1.1	67
107	The cardiovascular gene annotation initiative: current and future aims. Atherosclerosis, 2014, 237, e10.	0.4	0
108	BioJS: an open source standard for biological visualisation â€“ its status in 2014. F1000Research, 2014, 3, 55.	0.8	22

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109	BioJS: an open source JavaScript framework for biological data visualization. Bioinformatics, 2013, 29, 1103-1104.	1.8	110
110	Path2Models: large-scale generation of computational models from biochemical pathway maps. BMC Systems Biology, 2013, 7, 116.	3.0	145
111	PRIDE Cluster: building a consensus of proteomics data. Nature Methods, 2013, 10, 95-96.	9.0	62
112	Computational proteomics pitfalls and challenges: HavanaBioinfo 2012 Workshop report. Journal of Proteomics, 2013, 87, 134-138.	1.2	19
113	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
114	Tools (Viewer, Library and Validator) that Facilitate Use of the Peptide and Protein Identification Standard Format, Termed mzIdentML. Molecular and Cellular Proteomics, 2013, 12, 3026-3035.	2.5	32
115	iAnn: an event sharing platform for the life sciences. Bioinformatics, 2013, 29, 1919-1921.	1.8	6
116	Capturing cooperative interactions with the PSI-MI format. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat066.	1.4	10
117	The EBI enzyme portal. Nucleic Acids Research, 2013, 41, D773-D780.	6.5	19
118	The HUPO proteomics standards initiative- mass spectrometry controlled vocabulary. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat009-bat009.	1.4	76
119	Towards the Collaborative Curation of the Registry underlying identifiers.org. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat017.	1.4	13
120	Integration of Cardiac Proteome Biology and Medicine by a Specialized Knowledgebase. Circulation Research, 2013, 113, 1043-1053.	2.0	65
121	A new reference implementation of the PSICQUIC web service. Nucleic Acids Research, 2013, 41, W601-W606.	6.5	91
122	From Peptidome to PRIDE : P ublic proteomics data migration at a large scale. Proteomics, 2013, 13, 1692-1695.	1.3	12
123	LipidHome: A Database of Theoretical Lipids Optimized for High Throughput Mass Spectrometry Lipidomics. PLoS ONE, 2013, 8, e61951.	1.1	69
124	BioModels Database: a public repository for sharing models of biological processes. , 2013, , 1-5.		0
125	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, 1682-1689.	2.5	105
126	Improvements in the protein identifier cross-reference service. Nucleic Acids Research, 2012, 40, W276-W280.	6.5	27

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127	PRIDE: Quality control in a proteomics data repository. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas004-bas004.	1.4	35
128	Protein interaction data curation: the International Molecular Exchange (IMEx) consortium. Nature Methods, 2012, 9, 345-350.	9.0	500
129	Toward interoperable bioscience data. Nature Genetics, 2012, 44, 121-126.	9.4	362
130	The IntAct molecular interaction database in 2012. Nucleic Acids Research, 2012, 40, D841-D846.	6.5	962
131	Annotating Cancer Variants and Anti-Cancer Therapeutics in Reactome. Cancers, 2012, 4, 1180-1211.	1.7	270
132	The mzIdentML Data Standard for Mass Spectrometry-Based Proteomics Results. Molecular and Cellular Proteomics, 2012, 11, M111.014381-1-M111.014381-10.	2.5	175
133	The Proteomics Identifications (PRIDE) database and associated tools: status in 2013. Nucleic Acids Research, 2012, 41, D1063-D1069.	6.5	1,858
134	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
135	Ten Years of Standardizing Proteomic Data: A Report on the HUPOâ€PSI Spring Workshop. Proteomics, 2012, 12, 2767-2772.	1.3	16
136	Hydra: a scalable proteomic search engine which utilizes the Hadoop distributed computing framework. BMC Bioinformatics, 2012, 13, 324.	1.2	48
137	A Critical Appraisal of Techniques, Software Packages, and Standards for Quantitative Proteomic Analysis. OMICS A Journal of Integrative Biology, 2012, 16, 431-442.	1.0	50
138	The HUPO initiative on Model Organism Proteomes, iMOP. Proteomics, 2012, 12, 340-345.	1.3	9
139	jmz<scp>I</scp>dent<scp>ML API</scp>: A <scp>J</scp>ava interface to the mz<scp>I</scp>dent<scp>ML</scp> standard for peptide and protein identification data. Proteomics, 2012, 12, 790-794.	1.3	29
140	jmzReader: A Java parser library to process and visualize multiple text and XMLâ€based mass spectrometry data formats. Proteomics, 2012, 12, 795-798.	1.3	30
141	HUPO 2011: The New Cardiovascular Initiative â€•Integrating Proteomics and Cardiovascular Biology in Health and Disease. Proteomics, 2012, 12, 749-751.	1.3	4
142	Analyzing Proteinâ€“Protein Interaction Networks. Journal of Proteome Research, 2012, 11, 2014-2031.	1.8	145
143	PRIDE Inspector: a tool to visualize and validate MS proteomics data. Nature Biotechnology, 2012, 30, 135-137.	9.4	109
144	MyDas, an Extensible Java DAS Server. PLoS ONE, 2012, 7, e44180.	1.1	2

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145	PSICQUIC and PSISCORE: accessing and scoring molecular interactions. Nature Methods, 2011, 8, 528-529.	9.0	274
146	Reactome: a database of reactions, pathways and biological processes. Nucleic Acids Research, 2011, 39, D691-D697.	6.5	1,391
147	Minimum information about a bioactive entity (MIABE). Nature Reviews Drug Discovery, 2011, 10, 661-669.	21.5	80
148	easyDAS: Automatic creation of DAS servers. BMC Bioinformatics, 2011, 12, 23.	1.2	6
149	DAS Writeback: A Collaborative Annotation System. BMC Bioinformatics, 2011, 12, 143.	1.2	4
150	Reactome pathway analysis to enrich biological discovery in proteomics data sets. Proteomics, 2011, 11, 3598-3613.	1.3	89
151	Consequences of the discontinuation of the International Protein Index (IPI) database and its substitution by the UniProtKB â€œcomplete proteomeâ€•sets. Proteomics, 2011, 11, 4434-4438.	1.3	25
152	mzMLâ€”a Community Standard for Mass Spectrometry Data. Molecular and Cellular Proteomics, 2011, 10, R110.000133.	2.5	555
153	Dasty3, a WEB framework for DAS. Bioinformatics, 2011, 27, 2616-2617.	1.8	14
154	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.	2.5	20
155	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
156	The Reactome BioMart. Database: the Journal of Biological Databases and Curation, 2011, 2011, bar031-bar031.	1.4	32
157	Preparing Molecular Interaction Data for Publication. Methods in Molecular Biology, 2011, 694, 229-236.	0.4	1
158	Data Standardization by the HUPO-PSI: How has the Community Benefitted?. Methods in Molecular Biology, 2011, 696, 149-160.	0.4	9
159	Meeting Report from the Second â€œMinimum Information for Biological and Biomedical Investigationsâ€• (MIBBI) workshop. Standards in Genomic Sciences, 2010, 3, 259-266.	1.5	32
160	A domain level interaction network of amyloid precursor protein and AÎ² of Alzheimer's disease. Proteomics, 2010, 10, 2377-2395.	1.3	41
161	The Gel Electrophoresis Markup Language (GelML) from the Proteomics Standards Initiative. Proteomics, 2010, 10, 3073-3081.	1.3	19
162	Organelle proteomics experimental designs and analysis. Proteomics, 2010, 10, 3957-3969.	1.3	54

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163	Minimum information about a protein affinity reagent (MIAPAR). Nature Biotechnology, 2010, 28, 650-653.	9.4	50
164	A Community Standard Format for the Representation of Protein Affinity Reagents. Molecular and Cellular Proteomics, 2010, 9, 1-10.	2.5	35
165	Mapping Plant Interactomes Using Literature Curated and Predicted Proteinâ€“Protein Interaction Data Sets. Plant Cell, 2010, 22, 997-1005.	3.1	33
166	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-W83.	6.5	62
167	The Ontology Lookup Service: bigger and better. Nucleic Acids Research, 2010, 38, W155-W160.	6.5	108
168	The Proteomics Identifications database: 2010 update. Nucleic Acids Research, 2010, 38, D736-D742.	6.5	220
169	The IntAct molecular interaction database in 2010. Nucleic Acids Research, 2010, 38, D525-D531.	6.5	574
170	The Publication and Database Deposition of Molecular Interaction Data. Current Protocols in Protein Science, 2010, 60, Unit 25.3.	2.8	5
171	The systematic annotation of the three main GPCR families in Reactome. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq018-baq018.	1.4	24
172	The PSI semantic validator: A framework to check MIAPE compliance of proteomics data. Proteomics, 2009, 9, 5112-5119.	1.3	55
173	A guide to the Proteomics Identifications Database proteomics data repository. Proteomics, 2009, 9, 4276-4283.	1.3	220
174	Second Joint HUPO Publication and Proteomics Standards Initiative Workshop. Proteomics, 2009, 9, 4426-4428.	1.3	6
175	Annual Spring Meeting of the Proteomics Standards Initiative. Proteomics, 2009, 9, 4429-4432.	1.3	9
176	Charting online OMICS resources: A navigational chart for clinical researchers. Proteomics - Clinical Applications, 2009, 3, 18-29.	0.8	12
177	New open drug activity data at EBI. Chemistry Central Journal, 2009, 3, .	2.6	0
178	Recurated protein interaction datasets. Nature Methods, 2009, 6, 860-861.	9.0	58
179	Reactome knowledgebase of human biological pathways and processes. Nucleic Acids Research, 2009, 37, D619-D622.	6.5	760
180	ENFIN â€“ A European network for integrative systems biology. Comptes Rendus - Biologies, 2009, 332, 1050-1058.	0.1	6

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181	Recommendations from the 2008 International Summit on Proteomics Data Release and Sharing Policy: The Amsterdam Principles. Journal of Proteome Research, 2009, 8, 3689-3692.	1.8	75
182	Analysis of the experimental detection of central nervous systemâ€related genes in human brain and cerebrospinal fluid datasets. Proteomics, 2008, 8, 1138-1148.	1.3	18
183	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. Nature Biotechnology, 2008, 26, 889-896.	9.4	506
184	The minimum information about a genome sequence (MIGS) specification. Nature Biotechnology, 2008, 26, 541-547.	9.4	1,069
185	OntoDas â€“ a tool for facilitating the construction of complex queries to the Gene Ontology. BMC Bioinformatics, 2008, 9, 437.	1.2	4
186	Integrating biological data â€“ the Distributed Annotation System. BMC Bioinformatics, 2008, 9, S3.	1.2	87
187	Calling on a million minds for community annotation in WikiProteins. Genome Biology, 2008, 9, R89.	13.9	117
188	MINT and IntAct contribute to the Second BioCreative challenge: serving the text-mining community with high quality molecular interaction data. Genome Biology, 2008, 9, S5.	13.9	24
189	Analyzing Large-Scale Proteomics Projects with Latent Semantic Indexing. Journal of Proteome Research, 2008, 7, 182-191.	1.8	41
190	ISPIDER Central: an integrated database web-server for proteomics. Nucleic Acids Research, 2008, 36, W485-W490.	6.5	18
191	The Protein Feature Ontology: a tool for the unification of protein feature annotations. Bioinformatics, 2008, 24, 2767-2772.	1.8	19
192	The Ontology Lookup Service: more data and better tools for controlled vocabulary queries. Nucleic Acids Research, 2008, 36, W372-W376.	6.5	70
193	Dasty2, an Ajax protein DAS client. Bioinformatics, 2008, 24, 2119-2121.	1.8	25
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