

# Rolf Apweiler

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/994614/publications.pdf>

Version: 2024-02-01

178  
papers

43,625  
citations

11608

70  
h-index

3714

179  
g-index

210  
all docs

210  
docs citations

210  
times ranked

54811  
citing authors

#	ARTICLE	IF	CITATIONS
1	The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. <i>Nucleic Acids Research</i> , 2003, 31, 365-370.	6.5	3,096
2	UniProt: the Universal Protein knowledgebase. <i>Nucleic Acids Research</i> , 2004, 32, 115D-119.	6.5	2,994
3	The SWISS-PROT protein sequence database and its supplement TrEMBL in 2000. <i>Nucleic Acids Research</i> , 2000, 28, 45-48.	6.5	2,603
4	InterProScan - an integration platform for the signature-recognition methods in InterPro. <i>Bioinformatics</i> , 2001, 17, 847-848.	1.8	2,580
5	ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014, 32, 223-226.	9.4	2,505
6	Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. <i>Bioinformatics</i> , 2009, 25, 2865-2871.	1.8	1,811
7	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009, 37, D211-D215.	6.5	1,712
8	The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2004, 33, D154-D159.	6.5	1,681
9	Comparative Genomics of the Eukaryotes. <i>Science</i> , 2000, 287, 2204-2215.	6.0	1,573
10	Evaluation of methods for the prediction of membrane spanning regions. <i>Bioinformatics</i> , 2001, 17, 646-653.	1.8	1,050
11	The Universal Protein Resource (UniProt): an expanding universe of protein information. <i>Nucleic Acids Research</i> , 2006, 34, D187-D191.	6.5	961
12	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	6.5	921
13	IntAct: an open source molecular interaction database. <i>Nucleic Acids Research</i> , 2004, 32, 452D-455.	6.5	864
14	QuickGO: a web-based tool for Gene Ontology searching. <i>Bioinformatics</i> , 2009, 25, 3045-3046.	1.8	789
15	The Gene Ontology Annotation (GOA) Database: sharing knowledge in Uniprot with Gene Ontology. <i>Nucleic Acids Research</i> , 2004, 32, 262D-266.	6.5	780
16	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
17	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
18	The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007, 25, 887-893.	9.4	694

#	ARTICLE	IF	CITATIONS
19	The International Protein Index: An integrated database for proteomics experiments. <i>Proteomics</i> , 2004, 4, 1985-1988.	1.3	685
20	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003, 31, 315-318.	6.5	640
21	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
22	PRIDE: The proteomics identifications database. <i>Proteomics</i> , 2005, 5, 3537-3545.	1.3	553
23	Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008, 26, 889-896.	9.4	506
24	The GOA database in 2009—an integrated Gene Ontology Annotation resource. <i>Nucleic Acids Research</i> , 2009, 37, D396-D403.	6.5	497
25	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2004, 33, D201-D205.	6.5	478
26	The SWISS-PROT protein sequence data bank and its supplement TrEMBL. <i>Nucleic Acids Research</i> , 1997, 25, 31-36.	6.5	451
27	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007, 35, D224-D228.	6.5	444
28	The UniProt-GO Annotation database in 2011. <i>Nucleic Acids Research</i> , 2012, 40, D565-D570.	6.5	349
29	InterPro and InterProScan. <i>Methods in Molecular Biology</i> , 2007, 396, 59-70.	0.4	339
30	The Gene Ontology Annotation (GOA) Project: Implementation of GO in SWISS-PROT, TrEMBL, and InterPro. <i>Genome Research</i> , 2003, 13, 662-672.	2.4	297
31	The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2007, 36, D1028-D1033.	6.5	295
32	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	2.6	290
33	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
34	The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007, 25, 894-898.	9.4	274
35	High-quality protein knowledge resource: SWISS-PROT and TrEMBL. <i>Briefings in Bioinformatics</i> , 2002, 3, 275-284.	3.2	273
36	Recommendations for Biomarker Identification and Qualification in Clinical Proteomics. <i>Science Translational Medicine</i> , 2010, 2, 46ps42.	5.8	273

#	ARTICLE	IF	CITATIONS
37	The EMBL Nucleotide Sequence Database. <i>Nucleic Acids Research</i> , 2004, 33, D29-D33.	6.5	269
38	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
39	Prepublication data sharing. <i>Nature</i> , 2009, 461, 168-170.	13.7	243
40	Broadening the horizon – level 2.5 of the HUPO-PSI format for molecular interactions. <i>BMC Biology</i> , 2007, 5, 44.	1.7	237
41	Finding one's way in proteomics: a protein species nomenclature. <i>Chemistry Central Journal</i> , 2009, 3, 11.	2.6	229
42	Curated genome annotation of <i>Oryza sativa</i> ssp. <i>japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	2.4	218
43	Increase of functional diversity by alternative splicing. <i>Trends in Genetics</i> , 2003, 19, 124-128.	2.9	208
44	The speciation of the proteome. <i>Chemistry Central Journal</i> , 2008, 2, 16.	2.6	207
45	Protein sequence databases. <i>Current Opinion in Chemical Biology</i> , 2004, 8, 76-80.	2.8	201
46	The Proteomics Standards Initiative. <i>Proteomics</i> , 2003, 3, 1374-1376.	1.3	188
47	Systematic comparison of the human saliva and plasma proteomes. <i>Proteomics - Clinical Applications</i> , 2009, 3, 116-134.	0.8	186
48	UniProt archive. <i>Bioinformatics</i> , 2004, 20, 3236-3237.	1.8	173
49	The Ontology Lookup Service, a lightweight cross-platform tool for controlled vocabulary queries. <i>BMC Bioinformatics</i> , 2006, 7, 97.	1.2	170
50	IntEnz, the integrated relational enzyme database. <i>Nucleic Acids Research</i> , 2004, 32, 434D-437.	6.5	160
51	InterPro: An integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002, 3, 225-235.	3.2	155
52	An evaluation of GO annotation retrieval for BioCreAtIvE and GOA. <i>BMC Bioinformatics</i> , 2005, 6, S17.	1.2	141
53	EMBL Nucleotide Sequence Database in 2006. <i>Nucleic Acids Research</i> , 2007, 35, D16-D20.	6.5	136
54	The EMBL Nucleotide Sequence Database. <i>Nucleic Acids Research</i> , 2004, 32, 27D-30.	6.5	132

#	ARTICLE	IF	CITATIONS
55	Integr8 and Genome Reviews: integrated views of complete genomes and proteomes. <i>Nucleic Acids Research</i> , 2004, 33, D297-D302.	6.5	125
56	The EBI SRS server--recent developments. <i>Bioinformatics</i> , 2002, 18, 368-373.	1.8	119
57	The Protein Identifier Cross-Reference (PICR) service: reconciling protein identifiers across multiple source databases. <i>BMC Bioinformatics</i> , 2007, 8, 401.	1.2	112
58	Approaching clinical proteomics: current state and future fields of application in fluid proteomics. <i>Clinical Chemistry and Laboratory Medicine</i> , 2009, 47, 724-44.	1.4	112
59	The European Bioinformatics Institute in 2016: Data growth and integration. <i>Nucleic Acids Research</i> , 2016, 44, D20-D26.	6.5	108
60	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
61	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
62	The EBI SRS server--new features. <i>Bioinformatics</i> , 2002, 18, 1149-1150.	1.8	94
63	Systematic characterization of the murine mitochondrial proteome using functionally validated cardiac mitochondria. <i>Proteomics</i> , 2008, 8, 1564-1575.	1.3	90
64	Phosphoproteome Analysis Reveals Regulatory Sites in Major Pathways of Cardiac Mitochondria. <i>Molecular and Cellular Proteomics</i> , 2011, 10, S1-S14.	2.5	90
65	The human proteomics initiative (HPI). <i>Trends in Biotechnology</i> , 2001, 19, 178-181.	4.9	87
66	ASTD: The Alternative Splicing and Transcript Diversity database. <i>Genomics</i> , 2009, 93, 213-220.	1.3	87
67	EMBL Nucleotide Sequence Database: developments in 2005. <i>Nucleic Acids Research</i> , 2006, 34, D10-D15.	6.5	83
68	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
69	On the Importance of Comprehensible Classification Models for Protein Function Prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010, 7, 172-182.	1.9	80
70	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
71	The European Bioinformatics Institute's data resources 2014. <i>Nucleic Acids Research</i> , 2014, 42, D18-D25.	6.5	71
72	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

#	ARTICLE	IF	CITATIONS
73	The InterPro Database and Tools for Protein Domain Analysis. <i>Current Protocols in Bioinformatics</i> , 2008, 21, Unit 2.7.	25.8	69
74	LipidHome: A Database of Theoretical Lipids Optimized for High Throughput Mass Spectrometry Lipidomics. <i>PLoS ONE</i> , 2013, 8, e61951.	1.1	69
75	Integration of Cardiac Proteome Biology and Medicine by a Specialized Knowledgebase. <i>Circulation Research</i> , 2013, 113, 1043-1053.	2.0	65
76	The Proteome Analysis database: a tool for the in silico analysis of whole proteomes. <i>Nucleic Acids Research</i> , 2003, 31, 414-417.	6.5	64
77	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
78	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
79	Altered Proteome Biology of Cardiac Mitochondria Under Stress Conditions. <i>Journal of Proteome Research</i> , 2008, 7, 2204-2214.	1.8	58
80	The European Bioinformatics Institute's data resources. <i>Nucleic Acids Research</i> , 2003, 31, 43-50.	6.5	56
81	Automated reprocessing pipeline for searching heterogeneous mass spectrometric data of the HUPO Brain Proteome Project pilot phase. <i>Proteomics</i> , 2006, 6, 5015-5029.	1.3	56
82	UniProt API: a remote API for accessing UniProt data. <i>Bioinformatics</i> , 2008, 24, 1321-1322.	1.8	56
83	The European Bioinformatics Institute in 2017: data coordination and integration. <i>Nucleic Acids Research</i> , 2018, 46, D21-D29.	6.5	56
84	Applications of InterPro in protein annotation and genome analysis. <i>Briefings in Bioinformatics</i> , 2002, 3, 285-295.	3.2	54
85	In Silico Characterization of Proteins: UniProt, InterPro and Integr8. <i>Molecular Biotechnology</i> , 2008, 38, 165-177.	1.3	53
86	Missing in action: enzyme functional annotations in biological databases. <i>Nature Chemical Biology</i> , 2009, 5, 521-525.	3.9	53
87	The COVID-19 Data Portal: accelerating SARS-CoV-2 and COVID-19 research through rapid open access data sharing. <i>Nucleic Acids Research</i> , 2021, 49, W619-W623.	6.5	53
88	Approaching clinical proteomics: Current state and future fields of application in cellular proteomics. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2009, 75A, 816-832.	1.1	52
89	Identifying ELIXIR Core Data Resources. <i>F1000Research</i> , 2016, 5, 2422.	0.8	52
90	Whither systems medicine?. <i>Experimental and Molecular Medicine</i> , 2018, 50, e453-e453.	3.2	49

#	ARTICLE	IF	CITATIONS
91	Clustering and analysis of protein families. <i>Current Opinion in Structural Biology</i> , 2001, 11, 334-339.	2.6	48
92	VARSP LIC: alternatively-spliced protein sequences derived from SWISS-PROT and TrEMBL. <i>Bioinformatics</i> , 2000, 16, 1048-1049.	1.8	47
93	HUPO Brain Proteome Project: Summary of the pilot phase and introduction of a comprehensive data reprocessing strategy. <i>Proteomics</i> , 2006, 6, 4890-4898.	1.3	47
94	GOAnnotator: linking protein GO annotations to evidence text. <i>Journal of Biomedical Discovery and Collaboration</i> , 2006, 1, 19.	2.0	47
95	Data Sharing Under the General Data Protection Regulation. <i>Hypertension</i> , 2021, 77, 1029-1035.	1.3	47
96	Priorities for nucleotide trace, sequence and annotation data capture at the Ensembl Trace Archive and the EMBL Nucleotide Sequence Database. <i>Nucleic Acids Research</i> , 2007, 36, D5-D12.	6.5	46
97	Cellular resolution models for even skipped regulation in the entire <i>Drosophila</i> embryo. <i>ELife</i> , 2013, 2, e00522.	2.8	45
98	The predictive power of the CluSTr database. <i>Bioinformatics</i> , 2005, 21, 3604-3609.	1.8	43
99	Plant Protein Annotation in the UniProt Knowledgebase. <i>Plant Physiology</i> , 2005, 138, 59-66.	2.3	42
100	QuickGO: a user tutorial for the web-based Gene Ontology browser. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap010.	1.4	42
101	Analyzing Large-Scale Proteomics Projects with Latent Semantic Indexing. <i>Journal of Proteome Research</i> , 2008, 7, 182-191.	1.8	41
102	The Gene Ontology Annotation (GOA) Project – Application of GO in SWISS-PROT, TrEMBL and InterPro. <i>Comparative and Functional Genomics</i> , 2003, 4, 71-74.	2.0	36
103	Comparative Proteomics Profiling Reveals Role of Smooth Muscle Progenitors in Extracellular Matrix Production. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2010, 30, 1325-1332.	1.1	34
104	The European Bioinformatics Institute (EMBL-EBI) in 2021. <i>Nucleic Acids Research</i> , 2022, 50, D11-D19.	6.5	34
105	Linking publication, gene and protein data. <i>Nature Cell Biology</i> , 2006, 8, 1183-1189.	4.6	33
106	The European Bioinformatics Institute in 2018: tools, infrastructure and training. <i>Nucleic Acids Research</i> , 2019, 47, D15-D22.	6.5	33
107	Annotating the human proteome: Beyond establishing a parts list. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007, 1774, 175-191.	1.1	32
108	Current status of proteomic standards development. <i>Expert Review of Proteomics</i> , 2004, 1, 179-183.	1.3	29

#	ARTICLE	IF	CITATIONS
109	Advances in the development of common interchange standards for proteomic data. <i>Proteomics</i> , 2004, 4, 2363-2365.	1.3	29
110	The Gene Ontology " Providing a Functional Role in Proteomic Studies. <i>Proteomics</i> , 2008, 8, .	1.3	29
111	A posteriori quality control for the curation and reuse of public proteomics data. <i>Proteomics</i> , 2011, 11, 2182-2194.	1.3	29
112	The power of cooperative investigation: Summary and comparison of the HUPO Brain Proteome Project pilot study results. <i>Proteomics</i> , 2006, 6, 4997-5014.	1.3	28
113	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
114	Genome Reviews: Standardizing Content and Representation of Information about Complete Genomes. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 114-118.	1.0	25
115	A comparison of the HUPO Brain Proteome Project pilot with other proteomics studies. <i>Proteomics</i> , 2006, 6, 5076-5086.	1.3	25
116	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
117	The European Bioinformatics Institute in 2020: building a global infrastructure of interconnected data resources for the life sciences. <i>Nucleic Acids Research</i> , 2020, 48, D17-D23.	6.5	25
118	Annotating the Human Proteome. <i>Molecular and Cellular Proteomics</i> , 2005, 4, 435-440.	2.5	24
119	Evidence Standards in Experimental and Inferential INSDC Third Party Annotation Data. <i>OMICS A Journal of Integrative Biology</i> , 2006, 10, 105-113.	1.0	24
120	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
121	The role SWISS-PROT and TrEMBL play in the genome research environment. <i>Journal of Biotechnology</i> , 2000, 78, 221-234.	1.9	23
122	Tools and resources for identifying protein families, domains and motifs. <i>Genome Biology</i> , 2001, 3, reviews2001.1.	13.9	23
123	Towards data management of the HUPO Human Brain Proteome Project pilot phase. <i>Proteomics</i> , 2004, 4, 2361-2362.	1.3	23
124	Dasty and UniProt DAS: a perfect pair for protein feature visualization. <i>Bioinformatics</i> , 2005, 21, 3198-3199.	1.8	23
125	Functional annotation of proteins identified in human brain during the HUPO Brain Proteome Project pilot study. <i>Proteomics</i> , 2006, 6, 5059-5075.	1.3	23
126	The Impact of Focused Gene Ontology Curation of Specific Mammalian Systems. <i>PLoS ONE</i> , 2011, 6, e27541.	1.1	23



#	ARTICLE	IF	CITATIONS
127	The importance of uniformity in reporting protein-function data. Trends in Biochemical Sciences, 2005, 30, 11-12.	3.7	22
128	A large-scale protein-function database. Nature Chemical Biology, 2010, 6, 785-785.	3.9	22
129	The European Bioinformatics Institute: empowering cooperation in response to a global health crisis. Nucleic Acids Research, 2021, 49, D29-D37.	6.5	22
130	UniSave: the UniProtKB Sequence/Annotation Version database. Bioinformatics, 2006, 22, 1284-1285.	1.8	21
131	The Integr8 project—a resource for genomic and proteomic data. In Silico Biology, 2005, 5, 179-85.	0.4	21
132	Protein sequence databases. Advances in Protein Chemistry, 2000, 54, 31-71.	4.4	20
133	Human Proteome Organization Proteomics Standards Initiative. Molecular and Cellular Proteomics, 2007, 6, 1666-1667.	2.5	20
134	Analysis of the experimental detection of central nervous system-related genes in human brain and cerebrospinal fluid datasets. Proteomics, 2008, 8, 1138-1148.	1.3	18
135	Use of Gene Ontology Annotation to understand the peroxisome proteome in humans. Database: the Journal of Biological Databases and Curation, 2013, 2013, bas062.	1.4	17
136	Representing Kidney Development Using the Gene Ontology. PLoS ONE, 2014, 9, e99864.	1.1	17
137	Progress in Establishing Common Standards for Exchanging Proteomics Data: The Second Meeting of the HUPO Proteomics Standards Initiative. Comparative and Functional Genomics, 2003, 4, 203-206.	2.0	16
138	Bioinformatics database infrastructure for biotechnology research. Journal of Biotechnology, 2006, 124, 629-639.	1.9	15
139	Cardiovascular GO Annotation Initiative Year 1 Report: Why Cardiovascular GO?. Proteomics, 2008, 8, 1950-1953.	1.3	15
140	Getting a grip on proteomics data — Proteomics Data Collection (ProDaC). Proteomics, 2009, 9, 3928-3933.	1.3	15
141	A Guide to UniProt for Protein Scientists. Methods in Molecular Biology, 2011, 694, 25-35.	0.4	15
142	Gaining knowledge from previously unexplained spectra-application of the PTM-Explorer software to detect PTM in HUPO BPP MS/MS data. Proteomics, 2006, 6, 5048-5058.	1.3	14
143	The EMBL Nucleotide Sequence and Genome Reviews Databases. , 2007, 406, 1-21.		14
144	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.	0.7	14

#	ARTICLE	IF	CITATIONS
145	Proteomics and Beyond A report on the 3rd Annual Spring Workshop of the HUPO-PSI 21â€“23 April 2006, San Francisco, CA, USA. <i>Proteomics</i> , 2006, 6, 4439-4443.	1.3	13
146	The Renal Gene Ontology Annotation Initiative. <i>Organogenesis</i> , 2010, 6, 71-75.	0.4	13
147	Consistent integration of non-reliable heterogeneous information resources applied to the annotation of transmembrane proteins. <i>Computers &amp; Chemistry</i> , 2001, 26, 41-49.	1.2	11
148	Bioinformatics Resources for In Silico Proteome Analysis. <i>Journal of Biomedicine and Biotechnology</i> , 2003, 2003, 231-236.	3.0	11
149	Proteomic Data Exchange and Storage: The Need for Common Standards and Public Repositories. , 2007, 367, 261-270.		10
150	The HUPO initiative on Model Organism Proteomes, iMOP. <i>Proteomics</i> , 2012, 12, 340-345.	1.3	9
151	Biomolecular Data Resources: Bioinformatics Infrastructure for Biomedical Data Science. <i>Annual Review of Biomedical Data Science</i> , 2019, 2, 199-222.	2.8	8
152	Know your limits: Assumptions, constraints and interpretation in systems biology. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009, 1794, 1280-1287.	1.1	7
153	Do you do text?. <i>Bioinformatics</i> , 2005, 21, 4199-4200.	1.8	6
154	Application of InterPro for the functional classification of the proteins of fish origin in SWISS-PROT and TrEMBL. <i>Journal of Biosciences</i> , 2001, 26, 277-284.	0.5	5
155	Algorithms and Databases. <i>Methods in Molecular Biology</i> , 2009, 564, 245-259.	0.4	5
156	Managing core resources for genomics and proteomics. <i>Pharmacogenomics</i> , 2003, 4, 343-350.	0.6	4
157	The InterPro Database and Tools for Protein Domain Analysis. <i>Current Protocols in Bioinformatics</i> , 2003, 2, 2.7.1.	25.8	4
158	Mining Unique-m Substrings from Genomes. <i>Journal of Proteomics and Bioinformatics</i> , 2010, 03, 099-103.	0.4	4
159	TEMBLOR â€“ Perspectives of EBI Database Services. <i>Comparative and Functional Genomics</i> , 2002, 3, 47-50.	2.0	3
160	Biological Databases: Infrastructure, Content and Integration. , 2005, , 11-28.		3
161	Proteomics Data Collection â€“ 4<sup>th</sup> ProDaC Workshop 15 August 2008, Amsterdam, The Netherlands. <i>Proteomics</i> , 2009, 9, 218-222.	1.3	3
162	Proteomics and data standardisation. <i>Drug Discovery Today Biosilico</i> , 2004, 2, 91-93.	0.7	2

#	ARTICLE	IF	CITATIONS
163	â€œ4D Biology for health and diseaseâ€workshop report. <i>New Biotechnology</i> , 2011, 28, 291-293.	2.4	2
164	Organisation and standardisation of information in SWISS-PROT and TrEMBL. <i>Data Science Journal</i> , 2002, 1, 13-18.	0.6	2
165	Focus on InterPro. <i>Briefings in Bioinformatics</i> , 2002, 3, 221-223.	3.2	1
166	Databases and Resources for in silico Proteome Analysis. <i>Methods of Biochemical Analysis</i> , 2005, , 395-414.	0.2	1
167	Wiley-VCH and HUPO: A Global Effort to Advance Proteomic Science. <i>Proteomics - Clinical Applications</i> , 2008, 2, 4-6.	0.8	1
168	Building a Biological Space Based on Protein Sequence Similarities and Biological Ontologies. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2008, 11, 653-660.	0.6	1
169	New developments in linking of biological databases and computer-generation of annotation: SWISS-PROT and its computer-annotated supplement TREMBL. <i>Lecture Notes in Computer Science</i> , 1996, , 44-51.	1.0	0
170	Mus musculus in the SWISS-PROT database: Its relevance to developmental research. <i>Genesis</i> , 2000, 26, 1-4.	0.8	0
171	Computational Methods and Bioinformatic Tools. , 0, , 769-904.		0
172	Bioinformatics: Using the Molecular Biology Data. , 0, , 265-284.		0
173	Classification of proteins into families. , 2005, , .		0
174	Protein interaction databases. , 2005, , .		0
175	Data standardization and the HUPO proteomics standards initiative. , 2005, , .		0
176	Practical Applications of the Gene Ontology Resource. , 2010, , 319-339.		0
177	Protein Sequence Database Methods. , 2004, , 13-17.		0
178	Data Mining, Quality and Management in the Life Sciences. <i>Methods in Molecular Biology</i> , 2022, 2449, 3-25.	0.4	0