Amos Bairoch

List of Publications by Year in descending order

197 papers	62,210 citations	2963 93 h-index	3094 187 g-index
208 all docs	208 docs citations	208 times ranked	61830 citing authors

#	Article	IF	Citations
1	Protein Identification and Analysis Tools on the ExPASy Server. , 2005, , 571-607.		4,810
2	ExPASy: the proteomics server for in-depth protein knowledge and analysis. Nucleic Acids Research, 2003, 31, 3784-3788.	6.5	4,128
3	The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. Nucleic Acids Research, 2003, 31, 365-370.	6.5	3,096
4	UniProt: the Universal Protein knowledgebase. Nucleic Acids Research, 2004, 32, 115D-119.	6.5	2,994
5	The SWISS-PROT protein sequence database and its supplement TrEMBL in 2000. Nucleic Acids Research, 2000, 28, 45-48.	6.5	2,603
6	Protein Identification and Analysis Tools in the ExPASy Server. , 1999, 112, 531-552.		1,932
7	InterPro: the integrative protein signature database. Nucleic Acids Research, 2009, 37, D211-D215.	6.5	1,712
8	The Universal Protein Resource (UniProt). Nucleic Acids Research, 2004, 33, D154-D159.	6.5	1,681
9	The SWISS-PROT protein sequence data bank and its supplement TrEMBL in 1999. Nucleic Acids Research, 1999, 27, 49-54.	6.5	1,592
10	ScanProsite: detection of PROSITE signature matches and ProRule-associated functional and structural residues in proteins. Nucleic Acids Research, 2006, 34, W362-W365.	6.5	1,428
11	Updating the sequence-based classification of glycosyl hydrolases. Biochemical Journal, 1996, 316, 695-696.	1.7	1,293
12	The Universal Protein Resource (UniProt) in 2010. Nucleic Acids Research, 2010, 38, D142-D148.	6.5	1,131
13	The PROSITE database, its status in 1999. Nucleic Acids Research, 1999, 27, 215-219.	6.5	1,089
14	The UDP glycosyltransferase gene superfamily: recommended nomenclature update based on evolutionary divergence. Pharmacogenetics and Genomics, 1997, 7, 255-269.	5.7	1,055
15	The PROSITE database, its status in 1997. Nucleic Acids Research, 1997, 25, 217-221.	6.5	963
16	The Universal Protein Resource (UniProt): an expanding universe of protein information. Nucleic Acids Research, 2006, 34, D187-D191.	6.5	961
17	The InterPro database, an integrated documentation resource for protein families, domains and functional sites. Nucleic Acids Research, 2001, 29, 37-40.	6.5	928
18	The ENZYME database in 2000. Nucleic Acids Research, 2000, 28, 304-305.	6.5	919

#	ARTICLE	IF	CITATIONS
19	The PROSITE database, its status in 2002. Nucleic Acids Research, 2002, 30, 235-238.	6.5	908
20	IntAct: an open source molecular interaction database. Nucleic Acids Research, 2004, 32, 452D-455.	6.5	864
21	PROSITE: A documented database using patterns and profiles as motif descriptors. Briefings in Bioinformatics, 2002, 3, 265-274.	3.2	802
22	The PROSITE database. Nucleic Acids Research, 2006, 34, D227-D230.	6.5	800
23	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	9.0	789
24	Molecular basis of symbiosis between Rhizobium and legumes. Nature, 1997, 387, 394-401.	13.7	753
25	PROSITE, a protein domain database for functional characterization and annotation. Nucleic Acids Research, 2010, 38, D161-D166.	6.5	744
26	Ongoing and future developments at the Universal Protein Resource. Nucleic Acids Research, 2011, 39, D214-D219.	6.5	649
27	The InterPro Database, 2003 brings increased coverage and new features. Nucleic Acids Research, 2003, 31, 315-318.	6.5	640
28	Prosite: a dictionary of sites and patterns in proteins. Nucleic Acids Research, 1991, 19, 2241-2245.	6.5	618
29	UniProtKB/Swiss-Prot. , 2007, 406, 89-112.		569
30	A new generation of information retrieval tools for biologists: the example of the ExPASy WWW server. Trends in Biochemical Sciences, 1994, 19, 258-260.	3.7	552
31	The Universal Protein Resource (UniProt) 2009. Nucleic Acids Research, 2009, 37, D169-D174.	6.5	548
32	InterPro, progress and status in 2005. Nucleic Acids Research, 2004, 33, D201-D205.	6.5	478
33	Mass spectrometry in high-throughput proteomics: ready for the big time. Nature Methods, 2010, 7, 681-685.	9.0	465
34	The SWISS-PROT protein sequence data bank and its supplement TrEMBL. Nucleic Acids Research, 1997, 25, 31-36.	6.5	451
35	The Gene Ontology in 2010: extensions and refinements. Nucleic Acids Research, 2010, 38, D331-D335.	6.5	450
36	New developments in the InterPro database. Nucleic Acids Research, 2007, 35, D224-D228.	6.5	444

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37	The 20 years of PROSITE. Nucleic Acids Research, 2007, 36, D245-D249.	6.5	441
38	The Cellosaurus, a Cell-Line Knowledge Resource. Journal of Biomolecular Techniques, 2018, 29, 25-38.	0.8	437
39	A unique signature identifies a family of zinc-dependent metallopeptidases. FEBS Letters, 1989, 242, 211-214.	1.3	435
40	The SWISS-PROT protein sequence data bank. Nucleic Acids Research, 1991, 19, 2247-2249.	6.5	409
41	Infrastructure for the life sciences: design and implementation of the UniProt website. BMC Bioinformatics, 2009, 10, 136.	1.2	405
42	The SWISS-PROT protein sequence data bank and its new supplement TREMBL. Nucleic Acids Research, 1996, 24, 21-25.	6.5	389
43	The SWISS-PROT protein sequence data bank. Nucleic Acids Research, 1992, 20, 2019-2022.	6.5	366
44	The PROSITE dictionary of sites and patterns in proteins, its current status. Nucleic Acids Research, 1993, 21, 3097-3103.	6.5	362
45	Recent improvements to the PROSITE database. Nucleic Acids Research, 2004, 32, 134D-137.	6.5	350
46	Swiss-Prot: Juggling between evolution and stability. Briefings in Bioinformatics, 2004, 5, 39-55.	3.2	338
47	CTdatabase: a knowledge-base of high-throughput and curated data on cancer-testis antigens. Nucleic Acids Research, 2009, 37, D816-D819.	6.5	338
48	Detailed peptide characterization using PEPTIDEMASS - a World-Wide-Web-accessible tool. Electrophoresis, 1997, 18, 403-408.	1.3	334
49	GPCRDB: an information system for G protein-coupled receptors. Nucleic Acids Research, 1998, 26, 275-279.	6.5	326
50	Interleukin-1-inducible genes in endothelial cells. Cloning of a new gene related to C-reactive protein and serum amyloid P component. Journal of Biological Chemistry, 1992, 267, 22190-7.	1.6	313
51	ViralZone: a knowledge resource to understand virus diversity. Nucleic Acids Research, 2011, 39, D576-D582.	6.5	312
52	High-throughput mass spectrometric discovery of protein post-translational modifications. Journal of Molecular Biology, 1999, 289, 645-657.	2.0	296
53	The Human Proteome Project: Current State and Future Direction. Molecular and Cellular Proteomics, 2011, 10, M111.009993.	2.5	294
54	ScanProsite: a reference implementation of a PROSITE scanning tool. Applied Bioinformatics, 2002, 1, 107-8.	1.7	289

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55	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. Nature Biotechnology, 2012, 30, 221-223.	9.4	281
56	High-quality protein knowledge resource: SWISS-PROT and TrEMBL. Briefings in Bioinformatics, 2002, 3, 275-284.	3.2	273
57	The Sulfinator: predicting tyrosine sulfation sites in protein sequences. Bioinformatics, 2002, 18, 769-770.	1.8	263
58	The PROSITE database, its status in 1995. Nucleic Acids Research, 1996, 24, 189-196.	6.5	259
59	Nucleotide sequences of the Acinetobacter calcoaceticus benABC genes for benzoate 1,2-dioxygenase reveal evolutionary relationships among multicomponent oxygenases. Journal of Bacteriology, 1991, 173, 5385-5395.	1.0	244
60	Inside SWISS-2DPAGE database. Electrophoresis, 1995, 16, 1131-1151.	1.3	241
61	Complementation of the DNA repair defect in xeroderma pigmentosum group G cells by a human cDNA related to yeast RAD2. Nature, 1993, 363, 182-185.	13.7	215
62	Protein sequence databases. Current Opinion in Chemical Biology, 2004, 8, 76-80.	2.8	201
63	Two-dimensional gel electrophoresis for proteome projects: The effects of protein hydrophobicity and copy number. Electrophoresis, 1998, 19, 1501-1505.	1.3	196
64	The SWISS-PROT protein sequence data bank and its supplement TrEMBL in 1998. Nucleic Acids Research, 1998, 26, 38-42.	6.5	193
65	The ENZYME data bank. Nucleic Acids Research, 1994, 22, 3626-3627.	6.5	192
66	neXtProt: a knowledge platform for human proteins. Nucleic Acids Research, 2012, 40, D76-D83.	6.5	167
67	IntEnz, the integrated relational enzyme database. Nucleic Acids Research, 2004, 32, 434D-437.	6.5	160
68	The SWISS-PROT protein sequence data bank, recent developments. Nucleic Acids Research, 1993, 21, 3093-3096.	6.5	158
69	InterPro: An integrated documentation resource for protein families, domains and functional sites. Briefings in Bioinformatics, 2002, 3, 225-235.	3.2	155
70	A high-stringency blueprint of the human proteome. Nature Communications, 2020, 11, 5301.	5.8	152
71	Federated two-dimensional electrophoresis database: A simple means of publishing two-dimensional electrophoresis data. Electrophoresis, 1996, 17, 540-546.	1.3	149
72	A superfamily of metalloenzymes unifies phosphopentomutase and cofactor-independent phosphoglycerate mutase with alkaline phosphatases and sulfatases. Protein Science, 1998, 7, 1829-1835.	3.1	148

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73	Potential DNA slippage structures acquired during evolutionary divergence of Acinetobacter calcoaceticus chromosomal benABC and Pseudomonas putida TOL pWW0 plasmid xylXYZ, genes encoding benzoate dioxygenases. Journal of Bacteriology, 1991, 173, 7540-7548.	1.0	145
74	The neXtProt knowledgebase on human proteins: 2017 update. Nucleic Acids Research, 2017, 45, D177-D182.	6.5	145
75	Improving protein identification from peptide mass fingerprinting through a parameterized multi-level scoring algorithm and an optimized peak detection. Electrophoresis, 1999, 20, 3535-3550.	1.3	140
76	New Insulin-Like Proteins with Atypical Disulfide Bond Pattern Characterized in <i>Caenorhabditis elegans</i> by Comparative Sequence Analysis and Homology Modeling. Genome Research, 1998, 8, 348-353.	2.4	138
77	HAMAP: a database of completely sequenced microbial proteome sets and manually curated microbial protein families in UniProtKB/Swiss-Prot. Nucleic Acids Research, 2009, 37, D471-D478.	6.5	136
78	Standard Guidelines for the Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2012, 11, 2005-2013.	1.8	135
79	Human liver protein map: A reference database established by microsequencing and gel comparison. Electrophoresis, 1992, 13, 992-1001.	1.3	132
80	Plasma and red blood cell protein maps: Update 1993. Electrophoresis, 1993, 14, 1223-1226.	1.3	129
81	A Molecular Scanner To Automate Proteomic Research and To Display Proteome Images. Analytical Chemistry, 1999, 71, 4981-4988.	3.2	127
82	The Swiss-Prot variant page and the ModSNP database: A resource for sequence and structure information on human protein variants. Human Mutation, 2004, 23, 464-470.	1.1	127
83	SWISS-2DPAGE: A database of two-dimensional gel electrophoresis images. Electrophoresis, 1993, 14, 1232-1238.	1.3	126
84	Automated annotation of microbial proteomes in SWISS-PROT. Computational Biology and Chemistry, 2003, 27, 49-58.	1.1	125
85	Metrics for the Human Proteome Project 2013–2014 and Strategies for Finding Missing Proteins. Journal of Proteome Research, 2014, 13, 15-20.	1.8	124
86	The neXtProt knowledgebase in 2020: data, tools and usability improvements. Nucleic Acids Research, 2020, 48, D328-D334.	6.5	121
87	Calling on a million minds for community annotation in WikiProteins. Genome Biology, 2008, 9, R89.	13.9	117
88	neXtProt: Organizing Protein Knowledge in the Context of Human Proteome Projects. Journal of Proteome Research, 2013, 12, 293-298.	1.8	116
89	Evolutionary relationships between catabolic pathways for aromatics: Conservation of gene order and nucleotide sequences of catechol oxidation genes of pWW0 and NAH7 plasmids. Molecular Genetics and Genomics, 1987, 210, 241-247.	2.4	112
90	Protein variety and functional diversity: Swiss-Prot annotation in its biological context. Comptes Rendus - Biologies, 2005, 328, 882-899.	0.1	107

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91	Annotating single amino acid polymorphisms in the UniProt/Swiss-Prot knowledgebase. Human Mutation, 2008, 29, 361-366.	1.1	105
92	Industrial-scale proteomics: From liters of plasma to chemically synthesized proteins. Proteomics, 2004, 4, 2125-2150.	1.3	103
93	The 1999 SWISS-2DPAGE database update. Nucleic Acids Research, 2000, 28, 286-288.	6.5	100
94	FindPept, a tool to identify unmatched masses in peptide mass fingerprinting protein identification. Proteomics, 2002, 2, 1435-1444.	1.3	100
95	Annotation of post-translational modifications in the Swiss-Prot knowledge base. Proteomics, 2004, 4, 1537-1550.	1.3	99
96	Tox-Prot, the toxin protein annotation program of the Swiss-Prot protein knowledgebase. Toxicon, 2005, 45, 293-301.	0.8	97
97	Cis-diol dehydrogenases encoded by the TOL pWW0 plasmid xylL gene and the Acinetobacter calcoaceticus chromosomal benD gene are members of the short-chain alcohol dehydrogenase superfamily. FEBS Journal, 1992, 204, 113-120.	0.2	96
98	Protein identification with N and C-terminal sequence tags in proteome projects. Journal of Molecular Biology, 1998, 278, 599-608.	2.0	95
99	Go hunting in sequence databases but watch out for the traps. Trends in Genetics, 1996, 12, 425-427.	2.9	94
100	The neXtProt knowledgebase on human proteins: current status. Nucleic Acids Research, 2015, 43, D764-D770.	6.5	94
101	Kinases and Cancer. Cancers, 2018, 10, 63.	1.7	93
102	'98Escherichia coli SWISS-2DPAGE database update. Electrophoresis, 1998, 19, 1960-1971.	1.3	90
103	The human proteomics initiative (HPI). Trends in Biotechnology, 2001, 19, 178-181.	4.9	87
104	UniPathway: a resource for the exploration and annotation of metabolic pathways. Nucleic Acids Research, 2012, 40, D761-D769.	6.5	83
105	Two-dimensional gel electrophoresis ofEscherichia coli homogenates: TheEscherichia coli SWISS-2DPAGE database. Electrophoresis, 1996, 17, 547-555.	1.3	80
106	The UniProtKB/Swiss-Prot knowledgebase and its Plant Proteome Annotation Program. Journal of Proteomics, 2009, 72, 567-573.	1.2	80
107	Human liver protein map: Update 1993. Electrophoresis, 1993, 14, 1216-1218.	1.3	77
108	Biocuration: Distilling data into knowledge. PLoS Biology, 2018, 16, e2002846.	2.6	75

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109	Nâ€terminome analysis of the human mitochondrial proteome. Proteomics, 2015, 15, 2519-2524.	1.3	74
110	ProRule: a new database containing functional and structural information on PROSITE profiles. Bioinformatics, 2005, 21, 4060-4066.	1.8	73
111	The xylS gene positive regulator of TOL plasmid pWWO: Identification, sequence analysis and overproduction leading to constitutive expression of meta cleavage operon. Molecular Genetics and Genomics, 1987, 207, 349-354.	2.4	70
112	A testis-specific gene, TPTE , encodes a putative transmembrane tyrosine phosphatase and maps to the pericentromeric region of human chromosomes 21 and 13, and to chromosomes 15, 22, and Y. Human Genetics, 1999, 105, 399-409.	1.8	69
113	The Swiss-Prot protein knowledgebase and ExPASy: providing the plant community with high quality proteomic data and tools. Plant Physiology and Biochemistry, 2004, 42, 1013-1021.	2.8	69
114	The ENZYME data bank. Nucleic Acids Research, 1993, 21, 3155-3156.	6.5	66
115	Protein annotation: detective work for function prediction. Trends in Genetics, 1998, 14, 248-250.	2.9	66
116	Standards for Reporting Enzyme Data: The STRENDA Consortium: What it aims to do and why it should be helpful. Perspectives in Science, 2014, 1, 131-137.	0.6	65
117	The SIB Swiss Institute of Bioinformaticsâ€™ resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	6.5	64
118	The SWISS-PROT protein sequence database: its relevance to human molecular medical research. Journal of Molecular Medicine, 1997, 75, 312-6.	1.7	63
119	C11orf83, a Mitochondrial Cardiolipin-Binding Protein Involved in bc_1 Complex Assembly and Supercomplex Stabilization. Molecular and Cellular Biology, 2015, 35, 1139-1156.	1.1	62
120	Multiple parameter cross-species protein identification using MultiIdent - a world-wide web accessible tool. Electrophoresis, 1998, 19, 3199-3206.	1.3	60
121	Low molecular weight proteins: A challenge for post-genomic research. Electrophoresis, 1998, 19, 536-544.	1.3	58
122	Human aldehyde dehydrogenase genes: alternatively spliced transcriptional variants and their suggested nomenclature. Pharmacogenetics and Genomics, 2009, 19, 893-902.	0.7	55
123	A Standard Nomenclature for Referencing and Authentication of Pluripotent Stem Cells. Stem Cell Reports, 2018, 10, 1-6.	2.3	53
124	EF-hand motifs in inositol phospholipid-specific phospholipase C. FEBS Letters, 1990, 269, 454-456.	1.3	50
125	The ENZYME data bank in 1995. Nucleic Acids Research, 1996, 24, 221-222.	6.5	49
126	Annotation of glycoproteins in the SWISS-PROT database. Proteomics, 2001, 1, 262-268.	1.3	47

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127	The ABCD database: a repository for chemically defined antibodies. Nucleic Acids Research, 2020, 48, D261-D264.	6.5	46
128	CLASTR: The Cellosaurus STR similarity search tool â€•A precious help for cell line authentication. International Journal of Cancer, 2020, 146, 1299-1306.	2.3	45
129	Sequence patterns in protein kinases. Nature, 1988, 331, 22-22.	13.7	43
130	Plant Protein Annotation in the UniProt Knowledgebase. Plant Physiology, 2005, 138, 59-66.	2.3	42
131	The yeast SWISS-2DPAGE database. Electrophoresis, 1996, 17, 556-565.	1.3	40
132	The ENZYME data bank in 1999. Nucleic Acids Research, 1999, 27, 310-311.	6.5	39
133	OpenFluDB, a database for human and animal influenza virus. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq004-baq004.	1.4	37
134	The human proteome project: Current state and future direction. Molecular and Cellular Proteomics, 2011, , .	2.5	37
135	Proto-vav and gene expression. Nature, 1992, 358, 113-113.	13.7	36
136	NEWT, a new taxonomy portal. Nucleic Acids Research, 2003, 31, 3822-3823.	6.5	36
137	A Chromosome-centric Human Proteome Project (C-HPP) to Characterize the Sets of Proteins Encoded in Chromosome 17. Journal of Proteome Research, 2013, 12, 45-57.	1.8	35
138	Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 2011, 39, D7-D10.	6.5	32
139	Exploring the Uncharacterized Human Proteome Using neXtProt. Journal of Proteome Research, 2018, 17, 4211-4226.	1.8	32
140	Integrating two-dimensional gel databases using the melanie II software. Trends in Biochemical Sciences, 1996, 21, 496-497.	3.7	31
141	Towards BioDBcore: a community-defined information specification for biological databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq027-baq027.	1.4	30
142	A possible mechanism for metal-ion induced DNA-protein dissociation in a family of prokaryotic transcriptional regulators. Nucleic Acids Research, 1993, 21, 2515-2515.	6.5	29
143	Proposals for the naming of chloroplast genes. III. Nomenclature for open reading frames encoded in chloroplast genomes. Plant Molecular Biology Reporter, 1994, 12, S29-S30.	1.0	28
144	A diverse transketolase family that includes the RecP protein of Streptococcus pneumoniae, a protein implicated in genetic recombination. Research in Microbiology, 1993, 144, 341-347.	1.0	26

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145	DERA is the human deoxyribose phosphate aldolase and is involved in stress response. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 2913-2925.	1.9	26
146	Incidences of problematic cell lines are lower in papers that use RRIDs to identify cell lines. ELife, 2019, 8, .	2.8	26
147	Functional Identification of APIP as Human mtnB, a Key Enzyme in the Methionine Salvage Pathway. PLoS ONE, 2012, 7, e52877.	1.1	24
148	Current status of the SWISS-2DPAGE database. Nucleic Acids Research, 1998, 26, 332-333.	6.5	23
149	A large-scale protein-function database. Nature Chemical Biology, 2010, 6, 785-785.	3.9	22
150	Sequence similarities in calcium-binding proteins. Nature, 1988, 331, 491-491.	13.7	21
151	The SWISS-2DPAGE database of two-dimensional polyacrylamide gel electrophoresis, its status in 1995. Nucleic Acids Research, 1996, 24, 180-181.	6.5	21
152	Large-Scale Reanalysis of Publicly Available HeLa Cell Proteomics Data in the Context of the Human Proteome Project. Journal of Proteome Research, 2018, 17, 4160-4170.	1.8	21
153	A comprehensive web resource on RNA helicases from the baker's yeastSaccharomyces cerevisiae. Yeast, 2000, 16, 507-509.	0.8	19
154	Animal Toxins: How is Complexity Represented in Databases?. Toxins, 2010, 2, 262-282.	1.5	19
155	C2orf62 and TTC17 Are Involved in Actin Organization and Ciliogenesis in Zebrafish and Human. PLoS ONE, 2014, 9, e86476.	1.1	19
156	The SWISS-2DPAGE database: what has changed during the last year. Nucleic Acids Research, 1999, 27, 289-291.	6.5	18
157	The Feature-Viewer: a visualization tool for positional annotations on a sequence. Bioinformatics, 2020, 36, 3244-3245.	1.8	18
158	Deep Question Answering for protein annotation. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav081.	1.4	17
159	Quality control in databanks for molecular biology. BioEssays, 2000, 22, 1024-1034.	1.2	16
160	A novel zincâ€binding motif found in two ubiquitous deaminase families. Protein Science, 1994, 3, 853-856.	3.1	15
161	Missing Protein Landscape of Human Chromosomes 2 and 14: Progress and Current Status. Journal of Proteome Research, 2016, 15, 3971-3978.	1.8	15
162	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. Nucleic Acids Research, 2014, 42, W436-W441.	6.5	13

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163	Converting neXtProt into Linked Data and nanopublications. Semantic Web, 2015, 6, 147-153.	1.1	13
164	Key challenges for the creation and maintenance of specialist protein resources. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1005-1013.	1.5	13
165	Post-translational modifications: A challenge for proteomics and bioinformatics. Proteomics, 2004, 4, 1525-1526.	1.3	12
166	Querying neXtProt nanopublications and their value for insights on sequence variants and tissue expression. Web Semantics, 2014, 29, 3-11.	2.2	12
167	Annotation of functional impact of voltage-gated sodium channel mutations. Human Mutation, 2017, 38, 485-493.	1.1	12
168	Proteome Databases. Principles and Practice, 1997, , 93-148.	0.3	11
169	Triage by ranking to support the curation of protein interactions. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	1.4	10
170	A new bioinformatics tool to help assess the significance of BRCA1 variants. Human Genomics, 2018, 12, 36.	1.4	10
171	Cell Lines as Biological Models: Practical Steps for More Reliable Research. Chemical Research in Toxicology, 2019, 32, 1733-1736.	1.7	10
172	Collaborative annotation of genes and proteins between UniProtKB/Swiss-Prot and dictyBase. Database: the Journal of Biological Databases and Curation, 2009, 2009, bap016-bap016.	1.4	9
173	ICEPO: the ion channel electrophysiology ontology. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw017.	1.4	9
174	Sequences and topology predicting evolution. Current Opinion in Structural Biology, 1997, 7, 367-368.	2.6	8
175	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat: Figure 1.. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav063.	1.4	8
176	Functionathon: a manual data mining workflow to generate functional hypotheses for uncharacterized human proteins and its application by undergraduate students. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	1.4	8
177	D Databases on the World Wide Web. , 1999, 112, 383-392.		7
178	Animal Toxins: How is Complexity Represented in Databases?. Toxins, 2010, 2, 262-82.	1.5	7
179	SEQANALREF: a sequence analysis bibliographic reference databank. Bioinformatics, 1991, 7, 268-268.	1.8	6
180	LISTA, LISTA-HOP and LISTA-HON: a comprehensive compilation of protein encoding sequences and its associated homology databases from the yeast Saccharomyces. Nucleic Acids Research, 1994, 22, 3459-3461.	6.5	6

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181	LISTA, LISTA-HOP and LISTA-HON: a comprehensive compilation of protein encoding sequences and its associated homology databases from the yeast Saccharomyces. Nucleic Acids Research, 1996, 24, 50-52.	6.5	6
182	Constructing a 2-D Database for the World Wide Web. , 1999, 112, 411-416.		6
183	The future of annotation/biocuration. Nature Precedings, 2009, , .	0.1	6
184	Amino acid sequence determination by gas chromatographyâ€"mass spectrometry of permethylated peptides. Journal of Chromatography A, 1983, 268, 197-206.	1.8	4
185	Bioinformatics for Human Proteomics: Current State and Future Status. Nature Precedings, 2010, , .	0.1	2
186	Data Integration in Proteomics. , 2007, , 145-168.		2
187	Querying NeXtProt Nanopublications and Their Value for Insights on Sequence Variants and Tissue Expression. SSRN Electronic Journal, 0, , .	0.4	2
188	Review of the selected proceedings of the Fifth International Workshop on Data Integration in the Life Sciences 2008. BMC Bioinformatics, 2008, 9, S1.	1.2	1
189	UniProtKB/Swiss-Prot: New and Future Developments. Lecture Notes in Computer Science, 2008, , 204-206.	1.0	1
190	A Preliminary Study on the Prediction of Human Protein Functions. Lecture Notes in Computer Science, 2011, , 334-343.	1.0	1
191	Evidence for the existence of a mutated enkephalin sequence in preproenkephalin. FEBS Letters, 1982, 145, 121-122.	1.3	0
192	New developments in linking of biological databases and computer-generation of annotation: SWISS-PROT and its computer-annotated supplement TREMBL. Lecture Notes in Computer Science, 1996, , 44-51.	1.0	0
193	Editorial: Proteomics 10/2002. Proteomics, 2002, 2, 1363-1364.	1.3	0
194	Protein Variations: Resources and Tools. , 2004, , 389-422.		0
195	Functionally and structurally relevant residues in PROSITE motif descriptors. , 2005, , .		0
196	UniProtKB/Swiss-Prot Manual and Automated Annotation of Complete Proteomes: The <i>Dictyostelium discoideum</i> Case Study. , 2009, , 149-168.		0
197	The Impact of 3D Structures on a Protein Knowledgebase: From Proteins to Systems. , 2008, , 51-77.		0