

# Amos Bairoch

## List of Publications by Year in descending order

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199  
papers

62,210  
citations

2975

93  
h-index

3034

188  
g-index

208  
all docs

208  
docs citations

208  
times ranked

61830  
citing authors

#	ARTICLE	IF	CITATIONS
1	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, .	3.0	8
2	The neXtProt knowledgebase in 2020: data, tools and usability improvements. Nucleic Acids Research, 2020, 48, D328-D334.	14.5	121
3	The ABCD database: a repository for chemically defined antibodies. Nucleic Acids Research, 2020, 48, D261-D264.	14.5	46
4	CLASTR: The Cellosaurus STR similarity search tool – A precious help for cell line authentication. International Journal of Cancer, 2020, 146, 1299-1306.	5.1	45
5	A high-stringency blueprint of the human proteome. Nature Communications, 2020, 11, 5301.	12.8	152
6	The Feature-Viewer: a visualization tool for positional annotations on a sequence. Bioinformatics, 2020, 36, 3244-3245.	4.1	18
7	Cell Lines as Biological Models: Practical Steps for More Reliable Research. Chemical Research in Toxicology, 2019, 32, 1733-1736.	3.3	10
8	Incidences of problematic cell lines are lower in papers that use RRIDs to identify cell lines. ELife, 2019, 8, .	6.0	26
9	A Standard Nomenclature for Referencing and Authentication of Pluripotent Stem Cells. Stem Cell Reports, 2018, 10, 1-6.	4.8	53
10	The Cellosaurus, a Cell-Line Knowledge Resource. Journal of Biomolecular Techniques, 2018, 29, 25-38.	1.5	437
11	Exploring the Uncharacterized Human Proteome Using neXtProt. Journal of Proteome Research, 2018, 17, 4211-4226.	3.7	32
12	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.	3.7	21
13	A new bioinformatics tool to help assess the significance of BRCA1 variants. Human Genomics, 2018, 12, 36.	2.9	10
14	Kinases and Cancer. Cancers, 2018, 10, 63.	3.7	93
15	Biocuration: Distilling data into knowledge. PLoS Biology, 2018, 16, e2002846.	5.6	75
16	Annotation of functional impact of voltage-gated sodium channel mutations. Human Mutation, 2017, 38, 485-493.	2.5	12
17	Triage by ranking to support the curation of protein interactions. Database: the Journal of Biological Databases and Curation, 2017, 2017, .	3.0	10
18	The neXtProt knowledgebase on human proteins: 2017 update. Nucleic Acids Research, 2017, 45, D177-D182.	14.5	145

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19	ICEPO: the ion channel electrophysiology ontology. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw017.	3.0	9
20	Missing Protein Landscape of Human Chromosomes 2 and 14: Progress and Current Status. Journal of Proteome Research, 2016, 15, 3971-3978.	3.7	15
21	The SIB Swiss Institute of Bioinformatics's resources: focus on curated databases. Nucleic Acids Research, 2016, 44, D27-D37.	14.5	64
22	Converting neXtProt into Linked Data and nanopublications. Semantic Web, 2015, 6, 147-153.	1.9	13
23	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.	3.0	8
24	N-terminome analysis of the human mitochondrial proteome. Proteomics, 2015, 15, 2519-2524.	2.2	74
25	Deep Question Answering for protein annotation. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav081.	3.0	17
26	The neXtProt knowledgebase on human proteins: current status. Nucleic Acids Research, 2015, 43, D764-D770.	14.5	94
27	C11orf83, a Mitochondrial Cardiolipin-Binding Protein Involved in $\text{bc}_1\text{Complex}$ Assembly and Supercomplex Stabilization. Molecular and Cellular Biology, 2015, 35, 1139-1156.	2.3	62
28	Key challenges for the creation and maintenance of specialist protein resources. Proteins: Structure, Function and Bioinformatics, 2015, 83, 1005-1013.	2.6	13
29	C2orf62 and TTC17 Are Involved in Actin Organization and Ciliogenesis in Zebrafish and Human. PLoS ONE, 2014, 9, e86476.	2.5	19
30	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. Nucleic Acids Research, 2014, 42, W436-W441.	14.5	13
31	Metrics for the Human Proteome Project 2013-2014 and Strategies for Finding Missing Proteins. Journal of Proteome Research, 2014, 13, 15-20.	3.7	124
32	Querying neXtProt nanopublications and their value for insights on sequence variants and tissue expression. Web Semantics, 2014, 29, 3-11.	2.9	12
33	DERA is the human deoxyribose phosphate aldolase and is involved in stress response. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 2913-2925.	4.1	26
34	Standards for Reporting Enzyme Data: The STREND Consortium: What it aims to do and why it should be helpful. Perspectives in Science, 2014, 1, 131-137.	0.6	65
35	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.	3.7	35
36	neXtProt: Organizing Protein Knowledge in the Context of Human Proteome Projects. Journal of Proteome Research, 2013, 12, 293-298.	3.7	116

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37	A large-scale evaluation of computational protein function prediction. Nature Methods, 2013, 10, 221-227.	19.0	789
38	UniPathway: a resource for the exploration and annotation of metabolic pathways. Nucleic Acids Research, 2012, 40, D761-D769.	14.5	83
39	neXtProt: a knowledge platform for human proteins. Nucleic Acids Research, 2012, 40, D76-D83.	14.5	167
40	Standard Guidelines for the Chromosome-Centric Human Proteome Project. Journal of Proteome Research, 2012, 11, 2005-2013.	3.7	135
41	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. Nature Biotechnology, 2012, 30, 221-223.	17.5	281
42	Functional Identification of APIP as Human mtnB, a Key Enzyme in the Methionine Salvage Pathway. PLoS ONE, 2012, 7, e52877.	2.5	24
43	The Human Proteome Project: Current State and Future Direction. Molecular and Cellular Proteomics, 2011, 10, M111.009993.	3.8	294
44	ViralZone: a knowledge resource to understand virus diversity. Nucleic Acids Research, 2011, 39, D576-D582.	14.5	312
45	Towards BioDBcore: a community-defined information specification for biological databases. Database: the Journal of Biological Databases and Curation, 2011, 2011, baq027-baq027.	3.0	30
46	Ongoing and future developments at the Universal Protein Resource. Nucleic Acids Research, 2011, 39, D214-D219.	14.5	649
47	Towards BioDBcore: a community-defined information specification for biological databases. Nucleic Acids Research, 2011, 39, D7-D10.	14.5	32
48	The human proteome project: Current state and future direction. Molecular and Cellular Proteomics, 2011, , .	3.8	37
49	A Preliminary Study on the Prediction of Human Protein Functions. Lecture Notes in Computer Science, 2011, , 334-343.	1.3	1
50	A large-scale protein-function database. Nature Chemical Biology, 2010, 6, 785-785.	8.0	22
51	Mass spectrometry in high-throughput proteomics: ready for the big time. Nature Methods, 2010, 7, 681-685.	19.0	465
52	Bioinformatics for Human Proteomics: Current State and Future Status. Nature Precedings, 2010, , .	0.1	2
53	Animal Toxins: How is Complexity Represented in Databases?. Toxins, 2010, 2, 262-282.	3.4	19
54	PROSITE, a protein domain database for functional characterization and annotation. Nucleic Acids Research, 2010, 38, D161-D166.	14.5	744

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55	The Gene Ontology in 2010: extensions and refinements. <i>Nucleic Acids Research</i> , 2010, 38, D331-D335.	14.5	450
56	OpenFluDB, a database for human and animal influenza virus. <i>Database: the Journal of Biological Databases and Curation</i> , 2010, 2010, baq004-baq004.	3.0	37
57	The Universal Protein Resource (UniProt) in 2010. <i>Nucleic Acids Research</i> , 2010, 38, D142-D148.	14.5	1,131
58	Animal Toxins: How is Complexity Represented in Databases?. <i>Toxins</i> , 2010, 2, 262-82.	3.4	7
59	CTdatabase: a knowledge-base of high-throughput and curated data on cancer-testis antigens. <i>Nucleic Acids Research</i> , 2009, 37, D816-D819.	14.5	338
60	HAMAP: a database of completely sequenced microbial proteome sets and manually curated microbial protein families in UniProtKB/Swiss-Prot. <i>Nucleic Acids Research</i> , 2009, 37, D471-D478.	14.5	136
61	The Universal Protein Resource (UniProt) 2009. <i>Nucleic Acids Research</i> , 2009, 37, D169-D174.	14.5	548
62	The future of annotation/biocuration. <i>Nature Precedings</i> , 2009, , .	0.1	6
63	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009, 37, D211-D215.	14.5	1,712
64	Collaborative annotation of genes and proteins between UniProtKB/Swiss-Prot and dictyBase. <i>Database: the Journal of Biological Databases and Curation</i> , 2009, 2009, bap016-bap016.	3.0	9
65	Infrastructure for the life sciences: design and implementation of the UniProt website. <i>BMC Bioinformatics</i> , 2009, 10, 136.	2.6	405
66	The UniProtKB/Swiss-Prot knowledgebase and its Plant Proteome Annotation Program. <i>Journal of Proteomics</i> , 2009, 72, 567-573.	2.4	80
67	Human aldehyde dehydrogenase genes: alternatively spliced transcriptional variants and their suggested nomenclature. <i>Pharmacogenetics and Genomics</i> , 2009, 19, 893-902.	1.5	55
68	UniProtKB/Swiss-Prot Manual and Automated Annotation of Complete Proteomes: The <i>Dictyostelium discoideum</i> Case Study. , 2009, , 149-168.		0
69	Annotating single amino acid polymorphisms in the UniProt/Swiss-Prot knowledgebase. <i>Human Mutation</i> , 2008, 29, 361-366.	2.5	105
70	Review of the selected proceedings of the Fifth International Workshop on Data Integration in the Life Sciences 2008. <i>BMC Bioinformatics</i> , 2008, 9, S1.	2.6	1
71	Calling on a million minds for community annotation in WikiProteins. <i>Genome Biology</i> , 2008, 9, R89.	9.6	117
72	UniProtKB/Swiss-Prot: New and Future Developments. <i>Lecture Notes in Computer Science</i> , 2008, , 204-206.	1.3	1

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73	The Impact of 3D Structures on a Protein Knowledgebase: From Proteins to Systems. , 2008, , 51-77.		0
74	New developments in the InterPro database. Nucleic Acids Research, 2007, 35, D224-D228.	14.5	444
75	The 20 years of PROSITE. Nucleic Acids Research, 2007, 36, D245-D249.	14.5	441
76	UniProtKB/Swiss-Prot. , 2007, 406, 89-112.		569
77	Data Integration in Proteomics. , 2007, , 145-168.		2
78	ScanProsite: detection of PROSITE signature matches and ProRule-associated functional and structural residues in proteins. Nucleic Acids Research, 2006, 34, W362-W365.	14.5	1,428
79	The PROSITE database. Nucleic Acids Research, 2006, 34, D227-D230.	14.5	800
80	The Universal Protein Resource (UniProt): an expanding universe of protein information. Nucleic Acids Research, 2006, 34, D187-D191.	14.5	961
81	Functionally and structurally relevant residues in PROSITE motif descriptors. , 2005, , .		0
82	Plant Protein Annotation in the UniProt Knowledgebase. Plant Physiology, 2005, 138, 59-66.	4.8	42
83	ProRule: a new database containing functional and structural information on PROSITE profiles. Bioinformatics, 2005, 21, 4060-4066.	4.1	73
84	Protein variety and functional diversity: Swiss-Prot annotation in its biological context. Comptes Rendus - Biologies, 2005, 328, 882-899.	0.2	107
85	Tox-Prot, the toxin protein annotation program of the Swiss-Prot protein knowledgebase. Toxicon, 2005, 45, 293-301.	1.6	97
86	Protein Identification and Analysis Tools on the ExPASy Server. , 2005, , 571-607.		4,810
87	Title Page / Table of Contents / Editorial. Complexus, 2004, 2, 56-60.	0.6	0
88	Protein Variations: Resources and Tools. , 2004, , 389-422.		0
89	IntEnz, the integrated relational enzyme database. Nucleic Acids Research, 2004, 32, 434D-437.	14.5	160
90	InterPro, progress and status in 2005. Nucleic Acids Research, 2004, 33, D201-D205.	14.5	478

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91	Swiss-Prot: Juggling between evolution and stability. Briefings in Bioinformatics, 2004, 5, 39-55.	6.5	338
92	IntAct: an open source molecular interaction database. Nucleic Acids Research, 2004, 32, 452D-455.	14.5	864
93	The Universal Protein Resource (UniProt). Nucleic Acids Research, 2004, 33, D154-D159.	14.5	1,681
94	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.	5.8	69
95	Industrial-scale proteomics: From liters of plasma to chemically synthesized proteins. Proteomics, 2004, 4, 2125-2150.	2.2	103
96	Annotation of post-translational modifications in the Swiss-Prot knowledge base. Proteomics, 2004, 4, 1537-1550.	2.2	99
97	Post-translational modifications: A challenge for proteomics and bioinformatics. Proteomics, 2004, 4, 1525-1526.	2.2	12
98	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.	2.5	127
99	Protein sequence databases. Current Opinion in Chemical Biology, 2004, 8, 76-80.	6.1	201
100	UniProt: the Universal Protein knowledgebase. Nucleic Acids Research, 2004, 32, 115D-119.	14.5	2,994
101	Recent improvements to the PROSITE database. Nucleic Acids Research, 2004, 32, 134D-137.	14.5	350
102	Automated annotation of microbial proteomes in SWISS-PROT. Computational Biology and Chemistry, 2003, 27, 49-58.	2.3	125
103	ExPASy: the proteomics server for in-depth protein knowledge and analysis. Nucleic Acids Research, 2003, 31, 3784-3788.	14.5	4,128
104	NEWT, a new taxonomy portal. Nucleic Acids Research, 2003, 31, 3822-3823.	14.5	36
105	The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. Nucleic Acids Research, 2003, 31, 365-370.	14.5	3,096
106	The InterPro Database, 2003 brings increased coverage and new features. Nucleic Acids Research, 2003, 31, 315-318.	14.5	640
107	PROSITE: A documented database using patterns and profiles as motif descriptors. Briefings in Bioinformatics, 2002, 3, 265-274.	6.5	802
108	The PROSITE database, its status in 2002. Nucleic Acids Research, 2002, 30, 235-238.	14.5	908

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109	InterPro: An integrated documentation resource for protein families, domains and functional sites. Briefings in Bioinformatics, 2002, 3, 225-235.	6.5	155
110	High-quality protein knowledge resource: SWISS-PROT and TrEMBL. Briefings in Bioinformatics, 2002, 3, 275-284.	6.5	273
111	The Sulfinator: predicting tyrosine sulfation sites in protein sequences. Bioinformatics, 2002, 18, 769-770.	4.1	263
112	Editorial: Proteomics 10/2002. Proteomics, 2002, 2, 1363-1364.	2.2	0
113	FindPept, a tool to identify unmatched masses in peptide mass fingerprinting protein identification. Proteomics, 2002, 2, 1435-1444.	2.2	100
114	ScanProsite: a reference implementation of a PROSITE scanning tool. Applied Bioinformatics, 2002, 1, 107-8.	1.6	289
115	The InterPro database, an integrated documentation resource for protein families, domains and functional sites. Nucleic Acids Research, 2001, 29, 37-40.	14.5	928
116	Annotation of glycoproteins in the SWISS-PROT database. Proteomics, 2001, 1, 262-268.	2.2	47
117	The human proteomics initiative (HPI). Trends in Biotechnology, 2001, 19, 178-181.	9.3	87
118	A comprehensive web resource on RNA helicases from the baker's yeast <i>Saccharomyces cerevisiae</i> . Yeast, 2000, 16, 507-509.	1.7	19
119	Quality control in databanks for molecular biology. BioEssays, 2000, 22, 1024-1034.	2.5	16
120	The ENZYME database in 2000. Nucleic Acids Research, 2000, 28, 304-305.	14.5	919
121	The 1999 SWISS-2DPAGE database update. Nucleic Acids Research, 2000, 28, 286-288.	14.5	100
122	The SWISS-PROT protein sequence database and its supplement TrEMBL in 2000. Nucleic Acids Research, 2000, 28, 45-48.	14.5	2,603
123	Constructing a 2-D Database for the World Wide Web. , 1999, 112, 411-416.		6
124	Protein Identification and Analysis Tools in the ExPASy Server. , 1999, 112, 531-552.		1,932
125	D Databases on the World Wide Web. , 1999, 112, 383-392.		7
126	The SWISS-PROT protein sequence data bank and its supplement TrEMBL in 1999. Nucleic Acids Research, 1999, 27, 49-54.	14.5	1,592



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127	The SWISS-2DPAGE database: what has changed during the last year. Nucleic Acids Research, 1999, 27, 289-291.	14.5	18
128	The PROSITE database, its status in 1999. Nucleic Acids Research, 1999, 27, 215-219.	14.5	1,089
129	The ENZYME data bank in 1999. Nucleic Acids Research, 1999, 27, 310-311.	14.5	39
130	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.	3.8	69
131	Improving protein identification from peptide mass fingerprinting through a parameterized multi-level scoring algorithm and an optimized peak detection. Electrophoresis, 1999, 20, 3535-3550.	2.4	140
132	A Molecular Scanner To Automate Proteomic Research and To Display Proteome Images. Analytical Chemistry, 1999, 71, 4981-4988.	6.5	127
133	High-throughput mass spectrometric discovery of protein post-translational modifications. Journal of Molecular Biology, 1999, 289, 645-657.	4.2	296
134	Improving protein identification from peptide mass fingerprinting through a parameterized multi-level scoring algorithm and an optimized peak detection. Electrophoresis, 1999, 20, 3535-3550.	2.4	2
135	Protein annotation: detective work for function prediction. Trends in Genetics, 1998, 14, 248-250.	6.7	66
136	Low molecular weight proteins: A challenge for post-genomic research. Electrophoresis, 1998, 19, 536-544.	2.4	58
137	Two-dimensional gel electrophoresis for proteome projects: The effects of protein hydrophobicity and copy number. Electrophoresis, 1998, 19, 1501-1505.	2.4	196
138	'98Escherichia coli SWISS-2DPAGE database update. Electrophoresis, 1998, 19, 1960-1971.	2.4	90
139	Multiple parameter cross-species protein identification using MultIdent - a world-wide web accessible tool. Electrophoresis, 1998, 19, 3199-3206.	2.4	60
140	A superfamily of metalloenzymes unifies phosphopentomutase and cofactor-independent phosphoglycerate mutase with alkaline phosphatases and sulfatases. Protein Science, 1998, 7, 1829-1835.	7.6	148
141	Protein identification with N and C-terminal sequence tags in proteome projects. Journal of Molecular Biology, 1998, 278, 599-608.	4.2	95
142	Current status of the SWISS-2DPAGE database. Nucleic Acids Research, 1998, 26, 332-333.	14.5	23
143	The SWISS-PROT protein sequence data bank and its supplement TrEMBL in 1998. Nucleic Acids Research, 1998, 26, 38-42.	14.5	193
144	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.	5.5	138

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145	GPCRDB: an information system for G protein-coupled receptors. Nucleic Acids Research, 1998, 26, 275-279.	14.5	326
146	The PROSITE database, its status in 1997. Nucleic Acids Research, 1997, 25, 217-221.	14.5	963
147	The SWISS-PROT protein sequence data bank and its supplement TrEMBL. Nucleic Acids Research, 1997, 25, 31-36.	14.5	451
148	The UDP glycosyltransferase gene superfamily: recommended nomenclature update based on evolutionary divergence. Pharmacogenetics and Genomics, 1997, 7, 255-269.	5.7	1,055
149	Sequences and topology predicting evolution. Current Opinion in Structural Biology, 1997, 7, 367-368.	5.7	8
150	Molecular basis of symbiosis between Rhizobium and legumes. Nature, 1997, 387, 394-401.	27.8	753
151	Detailed peptide characterization using PEPTIDEMASS - a World-Wide-Web-accessible tool. Electrophoresis, 1997, 18, 403-408.	2.4	334
152	Proteome Databases. Principles and Practice, 1997, , 93-148.	0.3	11
153	The SWISS-PROT protein sequence database: its relevance to human molecular medical research. Journal of Molecular Medicine, 1997, 75, 312-6.	3.9	63
154	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.	1.3	0
155	Go hunting in sequence databases but watch out for the traps. Trends in Genetics, 1996, 12, 425-427.	6.7	94
156	Integrating two-dimensional gel databases using the melanie II software. Trends in Biochemical Sciences, 1996, 21, 496-497.	7.5	31
157	Federated two-dimensional electrophoresis database: A simple means of publishing two-dimensional electrophoresis data. Electrophoresis, 1996, 17, 540-546.	2.4	149
158	Two-dimensional gel electrophoresis of Escherichia coli homogenates: The Escherichia coli SWISS-2DPAGE database. Electrophoresis, 1996, 17, 547-555.	2.4	80
159	The yeast SWISS-2DPAGE database. Electrophoresis, 1996, 17, 556-565.	2.4	40
160	The SWISS-PROT protein sequence data bank and its new supplement TREMBL. Nucleic Acids Research, 1996, 24, 21-25.	14.5	389
161	The SWISS-2DPAGE database of two-dimensional polyacrylamide gel electrophoresis, its status in 1995. Nucleic Acids Research, 1996, 24, 180-181.	14.5	21
162	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.	14.5	6

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163	The PROSITE database, its status in 1995. Nucleic Acids Research, 1996, 24, 189-196.	14.5	259
164	The ENZYME data bank in 1995. Nucleic Acids Research, 1996, 24, 221-222.	14.5	49
165	Updating the sequence-based classification of glycosyl hydrolases. Biochemical Journal, 1996, 316, 695-696.	3.7	1,293
166	Inside SWISS-2DPAGE database. Electrophoresis, 1995, 16, 1131-1151.	2.4	241
167	LISTA, LISTA-HOP and LISTA-HON: a comprehensive compilation of protein encoding sequences and its associated homology databases from the yeast <i>Saccharomyces</i> . Nucleic Acids Research, 1994, 22, 3459-3461.	14.5	6
168	A novel zinc-binding motif found in two ubiquitous deaminase families. Protein Science, 1994, 3, 853-856.	7.6	15
169	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.	1.8	28
170	A new generation of information retrieval tools for biologists: the example of the ExPASy WWW server. Trends in Biochemical Sciences, 1994, 19, 258-260.	7.5	552
171	The ENZYME data bank. Nucleic Acids Research, 1994, 22, 3626-3627.	14.5	192
172	Human liver protein map: Update 1993. Electrophoresis, 1993, 14, 1216-1218.	2.4	77
173	Plasma and red blood cell protein maps: Update 1993. Electrophoresis, 1993, 14, 1223-1226.	2.4	129
174	SWISS-2DPAGE: A database of two-dimensional gel electrophoresis images. Electrophoresis, 1993, 14, 1232-1238.	2.4	126
175	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.	27.8	215
176	A diverse transketolase family that includes the RecP protein of <i>Streptococcus pneumoniae</i> , a protein implicated in genetic recombination. Research in Microbiology, 1993, 144, 341-347.	2.1	26
177	The ENZYME data bank. Nucleic Acids Research, 1993, 21, 3155-3156.	14.5	66
178	A possible mechanism for metal-ion induced DNA-protein dissociation in a family of prokaryotic transcriptional regulators. Nucleic Acids Research, 1993, 21, 2515-2515.	14.5	29
179	The SWISS-PROT protein sequence data bank, recent developments. Nucleic Acids Research, 1993, 21, 3093-3096.	14.5	158
180	The PROSITE dictionary of sites and patterns in proteins, its current status. Nucleic Acids Research, 1993, 21, 3097-3103.	14.5	362

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181	The SWISS-PROT protein sequence data bank. Nucleic Acids Research, 1992, 20, 2019-2022.	14.5	366
182	Proto-vav and gene expression. Nature, 1992, 358, 113-113.	27.8	36
183	Cis-diol dehydrogenases encoded by the TOL pWWO 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
184	Human liver protein map: A reference database established by microsequencing and gel comparison. Electrophoresis, 1992, 13, 992-1001.	2.4	132
185	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.	3.4	313
186	SEQANALREF: a sequence analysis bibliographic reference databank. Bioinformatics, 1991, 7, 268-268.	4.1	6
187	Potential DNA slippage structures acquired during evolutionary divergence of Acinetobacter calcoaceticus chromosomal benABC and Pseudomonas putida TOL pWWO plasmid xylXYZ, genes encoding benzoate dioxygenases. Journal of Bacteriology, 1991, 173, 7540-7548.	2.2	145
188	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.	2.2	244
189	The SWISS-PROT protein sequence data bank. Nucleic Acids Research, 1991, 19, 2247-2249.	14.5	409
190	Prosite: a dictionary of sites and patterns in proteins. Nucleic Acids Research, 1991, 19, 2241-2245.	14.5	618
191	EF-hand motifs in inositol phospholipid-specific phospholipase C. FEBS Letters, 1990, 269, 454-456.	2.8	50
192	A unique signature identifies a family of zinc-dependent metallopeptidases. FEBS Letters, 1989, 242, 211-214.	2.8	435
193	Sequence patterns in protein kinases. Nature, 1988, 331, 22-22.	27.8	43
194	Sequence similarities in calcium-binding proteins. Nature, 1988, 331, 491-491.	27.8	21
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