

Amos Bairoch

List of Publications by Year in Descending Order

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

192
papers

48,523
citations

89
h-index

207
g-index

207
ext. papers

54,632
ext. citations

11.4
avg, IF

7.59
L-index

#	Paper	IF	Citations
192	Functionathon: a manual data mining workflow to generate functional hypotheses for uncharacterized human proteins and its application by undergraduate students. <i>Database: the Journal of Biological Databases and Curation</i> , 2021 , 2021,	5	2
191	The Feature-Viewer: a visualization tool for positional annotations on a sequence. <i>Bioinformatics</i> , 2020 , 36, 3244-3245	7.2	8
190	The neXtProt knowledgebase in 2020: data, tools and usability improvements. <i>Nucleic Acids Research</i> , 2020 , 48, D328-D334	20.1	67
189	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , 2020 , 11, 5301	17.4	59
188	The ABCD database: a repository for chemically defined antibodies. <i>Nucleic Acids Research</i> , 2020 , 48, D261-D264	20.1	15
187	CLASTR: The Cellosaurus STR similarity search tool - A precious help for cell line authentication. <i>International Journal of Cancer</i> , 2020 , 146, 1299-1306	7.5	21
186	Cell Lines as Biological Models: Practical Steps for More Reliable Research. <i>Chemical Research in Toxicology</i> , 2019 , 32, 1733-1736	4	6
185	Incidences of problematic cell lines are lower in papers that use RRIDs to identify cell lines. <i>ELife</i> , 2019 , 8,	8.9	11
184	A Standard Nomenclature for Referencing and Authentication of Pluripotent Stem Cells. <i>Stem Cell Reports</i> , 2018 , 10, 1-6	8	39
183	A new bioinformatics tool to help assess the significance of BRCA1 variants. <i>Human Genomics</i> , 2018 , 12, 36	6.8	7
182	Biocuration: Distilling data into knowledge. <i>PLoS Biology</i> , 2018 , 16, e2002846	9.7	42
181	The Cellosaurus, a Cell-Line Knowledge Resource. <i>Journal of Biomolecular Techniques</i> , 2018 , 29, 25-38	1.1	212
180	Exploring the Uncharacterized Human Proteome Using neXtProt. <i>Journal of Proteome Research</i> , 2018 , 17, 4211-4226	5.6	17
179	Large-Scale Reanalysis of Publicly Available HeLa Cell Proteomics Data in the Context of the Human Proteome Project. <i>Journal of Proteome Research</i> , 2018 , 17, 4160-4170	5.6	10
178	Annotation of functional impact of voltage-gated sodium channel mutations. <i>Human Mutation</i> , 2017 , 38, 485-493	4.7	10
177	The neXtProt knowledgebase on human proteins: 2017 update. <i>Nucleic Acids Research</i> , 2017 , 45, D177-D182	21.2	123
176	Triage by ranking to support the curation of protein interactions. <i>Database: the Journal of Biological Databases and Curation</i> , 2017 , 2017,	5	7

175	The SIB Swiss Institute of Bioinformatics Resources: focus on curated databases. <i>Nucleic Acids Research</i> , 2016 , 44, D27-37	20.1	41
174	ICEPO: the ion channel electrophysiology ontology. <i>Database: the Journal of Biological Databases and Curation</i> , 2016 , 2016,	5	7
173	Missing Protein Landscape of Human Chromosomes 2 and 14: Progress and Current Status. <i>Journal of Proteome Research</i> , 2016 , 15, 3971-3978	5.6	12
172	C11orf83, a mitochondrial cardiolipin-binding protein involved in bc1 complex assembly and supercomplex stabilization. <i>Molecular and Cellular Biology</i> , 2015 , 35, 1139-56	4.8	44
171	Converting neXtProt into Linked Data and nanopublications. <i>Semantic Web</i> , 2015 , 6, 147-153	2.4	10
170	Creating a specialist protein resource network: a meeting report for the protein bioinformatics and community resources retreat. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015, bav063	5	5
169	N-terminome analysis of the human mitochondrial proteome. <i>Proteomics</i> , 2015 , 15, 2519-24	4.8	43
168	Deep Question Answering for protein annotation. <i>Database: the Journal of Biological Databases and Curation</i> , 2015 , 2015,	5	12
167	The neXtProt knowledgebase on human proteins: current status. <i>Nucleic Acids Research</i> , 2015 , 43, D764-70.1	20.1	76
166	Metrics for the Human Proteome Project 2013-2014 and strategies for finding missing proteins. <i>Journal of Proteome Research</i> , 2014 , 13, 15-20	5.6	113
165	Querying neXtProt nanopublications and their value for insights on sequence variants and tissue expression. <i>Web Semantics</i> , 2014 , 29, 3-11	2.9	11
164	DERA is the human deoxyribose phosphate aldolase and is involved in stress response. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014 , 1843, 2913-25	4.9	19
163	Standards for Reporting Enzyme Data: The STRENDA Consortium: What it aims to do and why it should be helpful. <i>Perspectives in Science</i> , 2014 , 1, 131-137	0.8	47
162	C2orf62 and TTC17 are involved in actin organization and ciliogenesis in zebrafish and human. <i>PLoS ONE</i> , 2014 , 9, e86476	3.7	13
161	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. <i>Nucleic Acids Research</i> , 2014 , 42, W436-41	20.1	12
160	A chromosome-centric human proteome project (C-HPP) to characterize the sets of proteins encoded in chromosome 17. <i>Journal of Proteome Research</i> , 2013 , 12, 45-57	5.6	31
159	neXtProt: organizing protein knowledge in the context of human proteome projects. <i>Journal of Proteome Research</i> , 2013 , 12, 293-8	5.6	110
158	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , 2013 , 10, 221-7	21.6	587

157	Standard guidelines for the chromosome-centric human proteome project. <i>Journal of Proteome Research</i> , 2012 , 11, 2005-13	5.6	121
156	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. <i>Nature Biotechnology</i> , 2012 , 30, 221-3	44.5	244
155	UniPathway: a resource for the exploration and annotation of metabolic pathways. <i>Nucleic Acids Research</i> , 2012 , 40, D761-9	20.1	76
154	neXtProt: a knowledge platform for human proteins. <i>Nucleic Acids Research</i> , 2012 , 40, D76-83	20.1	142
153	Functional identification of APIP as human mtnB, a key enzyme in the methionine salvage pathway. <i>PLoS ONE</i> , 2012 , 7, e52877	3.7	19
152	The human proteome project: current state and future direction. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M111.009993	7.6	249
151	ViralZone: a knowledge resource to understand virus diversity. <i>Nucleic Acids Research</i> , 2011 , 39, D576-82	20.1	216
150	Ongoing and future developments at the Universal Protein Resource. <i>Nucleic Acids Research</i> , 2011 , 39, D214-9	20.1	592
149	The human proteome project: Current state and future direction. <i>Molecular and Cellular Proteomics</i> , 2011 ,	7.6	28
148	A Preliminary Study on the Prediction of Human Protein Functions. <i>Lecture Notes in Computer Science</i> , 2011 , 334-343	0.9	1
147	A large-scale protein-function database. <i>Nature Chemical Biology</i> , 2010 , 6, 785	11.7	17
146	Mass spectrometry in high-throughput proteomics: ready for the big time. <i>Nature Methods</i> , 2010 , 7, 681-5	11.6	390
145	Bioinformatics for Human Proteomics: Current State and Future Status. <i>Nature Precedings</i> , 2010 ,		2
144	Animal Toxins: How is Complexity Represented in Databases?. <i>Toxins</i> , 2010 , 2, 262-282	4.9	18
143	PROSITE, a protein domain database for functional characterization and annotation. <i>Nucleic Acids Research</i> , 2010 , 38, D161-6	20.1	600
142	The Gene Ontology in 2010: extensions and refinements. <i>Nucleic Acids Research</i> , 2010 , 38, D331-5	20.1	367
141	OpenFluDB, a database for human and animal influenza virus. <i>Database: the Journal of Biological Databases and Curation</i> , 2010 , 2010, baq004	5	29
140	The Universal Protein Resource (UniProt) in 2010. <i>Nucleic Acids Research</i> , 2010 , 38, D142-8	20.1	1035

139	Animal Toxins: How is Complexity Represented in Databases?. <i>Toxins</i> , 2010 , 2, 262-82	4.9	6
138	CTdatabase: a knowledge-base of high-throughput and curated data on cancer-testis antigens. <i>Nucleic Acids Research</i> , 2009 , 37, D816-9	20.1	257
137	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, D471-8	20.1	117
136	The Universal Protein Resource (UniProt) 2009. <i>Nucleic Acids Research</i> , 2009 , 37, D169-74	20.1	509
135	The future of annotation/biocuration. <i>Nature Precedings</i> , 2009 ,		5
134	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009 , 37, D211-5	20.1	1379
133	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	5	9
132	Infrastructure for the life sciences: design and implementation of the UniProt website. <i>BMC Bioinformatics</i> , 2009 , 10, 136	3.6	366
131	The UniProtKB/Swiss-Prot knowledgebase and its Plant Proteome Annotation Program. <i>Journal of Proteomics</i> , 2009 , 72, 567-73	3.9	63
130	Human aldehyde dehydrogenase genes: alternatively spliced transcriptional variants and their suggested nomenclature. <i>Pharmacogenetics and Genomics</i> , 2009 , 19, 893-902	1.9	46
129	UniProtKB/Swiss-Prot Manual and Automated Annotation of Complete Proteomes: The Dictyostelium discoideum Case Study 2009 , 149-168		
128	Review of the selected proceedings of the Fifth International Workshop on Data Integration in the Life Sciences 2008. <i>BMC Bioinformatics</i> , 2008 , 9 Suppl 8, S1	3.6	1
127	Calling on a million minds for community annotation in WikiProteins. <i>Genome Biology</i> , 2008 , 9, R89	18.3	101
126	Annotating single amino acid polymorphisms in the UniProt/Swiss-Prot knowledgebase. <i>Human Mutation</i> , 2008 , 29, 361-6	4.7	87
125	The 20 years of PROSITE. <i>Nucleic Acids Research</i> , 2008 , 36, D245-9	20.1	375
124	The Impact of 3D Structures on a Protein Knowledgebase: From Proteins to Systems 2008 , 51-77		
123	UniProtKB/Swiss-Prot: New and Future Developments. <i>Lecture Notes in Computer Science</i> , 2008 , 204-206	0.9	1
122	UniProtKB/Swiss-Prot. <i>Methods in Molecular Biology</i> , 2007 , 406, 89-112	1.4	405

121	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007 , 35, D224-8	20.1	397
120	The Universal Protein Resource (UniProt): an expanding universe of protein information. <i>Nucleic Acids Research</i> , 2006 , 34, D187-91	20.1	839
119	ScanProsite: detection of PROSITE signature matches and ProRule-associated functional and structural residues in proteins. <i>Nucleic Acids Research</i> , 2006 , 34, W362-5	20.1	1055
118	The PROSITE database. <i>Nucleic Acids Research</i> , 2006 , 34, D227-30	20.1	649
117	Protein variety and functional diversity: Swiss-Prot annotation in its biological context. <i>Comptes Rendus - Biologies</i> , 2005 , 328, 882-99	1.4	80
116	Tox-Prot, the toxin protein annotation program of the Swiss-Prot protein knowledgebase. <i>Toxicon</i> , 2005 , 45, 293-301	2.8	79
115	Protein Identification and Analysis Tools on the ExPASy Server 2005 , 571-607		3376
114	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2005 , 33, D201-5	20.1	426
113	The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2005 , 33, D154-9	20.1	1231
112	Plant protein annotation in the UniProt Knowledgebase. <i>Plant Physiology</i> , 2005 , 138, 59-66	6.6	38
111	ProRule: a new database containing functional and structural information on PROSITE profiles. <i>Bioinformatics</i> , 2005 , 21, 4060-6	7.2	54
110	Protein Variations: Resources and Tools 2004 , 389-422		
109	IntEnz, the integrated relational enzyme database. <i>Nucleic Acids Research</i> , 2004 , 32, D434-7	20.1	134
108	Swiss-Prot: juggling between evolution and stability. <i>Briefings in Bioinformatics</i> , 2004 , 5, 39-55	13.4	287
107	IntAct: an open source molecular interaction database. <i>Nucleic Acids Research</i> , 2004 , 32, D452-5	20.1	670
106	The Swiss-Prot protein knowledgebase and ExPASy: providing the plant community with high quality proteomic data and tools. <i>Plant Physiology and Biochemistry</i> , 2004 , 42, 1013-21	5.4	54
105	Industrial-scale proteomics: from liters of plasma to chemically synthesized proteins. <i>Proteomics</i> , 2004 , 4, 2125-50	4.8	97
104	Annotation of post-translational modifications in the Swiss-Prot knowledge base. <i>Proteomics</i> , 2004 , 4, 1537-50	4.8	87

103	The Swiss-Prot variant page and the ModSNP database: a resource for sequence and structure information on human protein variants. <i>Human Mutation</i> , 2004 , 23, 464-70	4.7	116
102	Protein sequence databases. <i>Current Opinion in Chemical Biology</i> , 2004 , 8, 76-80	9.7	173
101	UniProt: the Universal Protein knowledgebase. <i>Nucleic Acids Research</i> , 2004 , 32, D115-9	20.1	2195
100	Recent improvements to the PROSITE database. <i>Nucleic Acids Research</i> , 2004 , 32, D134-7	20.1	299
99	Automated annotation of microbial proteomes in SWISS-PROT. <i>Computational Biology and Chemistry</i> , 2003 , 27, 49-58	3.6	112
98	ExPASy: The proteomics server for in-depth protein knowledge and analysis. <i>Nucleic Acids Research</i> , 2003 , 31, 3784-8	20.1	2989
97	NEWT, a new taxonomy portal. <i>Nucleic Acids Research</i> , 2003 , 31, 3822-3	20.1	31
96	The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. <i>Nucleic Acids Research</i> , 2003 , 31, 365-70	20.1	2375
95	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003 , 31, 315-8	20.1	556
94	FindPept, a tool to identify unmatched masses in peptide mass fingerprinting protein identification. <i>Proteomics</i> , 2002 , 2, 1435-44	4.8	89
93	PROSITE: a documented database using patterns and profiles as motif descriptors. <i>Briefings in Bioinformatics</i> , 2002 , 3, 265-74	13.4	676
92	The PROSITE database, its status in 2002. <i>Nucleic Acids Research</i> , 2002 , 30, 235-8	20.1	787
91	InterPro: an integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002 , 3, 225-35	13.4	137
90	High-quality protein knowledge resource: SWISS-PROT and TrEMBL. <i>Briefings in Bioinformatics</i> , 2002 , 3, 275-84	13.4	206
89	The Sulfinator: predicting tyrosine sulfation sites in protein sequences. <i>Bioinformatics</i> , 2002 , 18, 769-70	7.2	225
88	ScanProsite: a reference implementation of a PROSITE scanning tool. <i>Applied Bioinformatics</i> , 2002 , 1, 107-8		275
87	Proteome Analysis. <i>Methods and Principles in Medicinal Chemistry</i> , 2001 , 69-118	0.4	1
86	Annotation of glycoproteins in the SWISS-PROT database. <i>Proteomics</i> , 2001 , 1, 262-8	4.8	45

85	The human proteomics initiative (HPI). <i>Trends in Biotechnology</i> , 2001 , 19, 178-81	15.1	74
84	The InterPro database, an integrated documentation resource for protein families, domains and functional sites. <i>Nucleic Acids Research</i> , 2001 , 29, 37-40	20.1	743
83	A comprehensive web resource on RNA helicases from the baker's yeast <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , 2000 , 16, 507-9	3.4	18
82	Quality control in databanks for molecular biology. <i>BioEssays</i> , 2000 , 22, 1024-34	4.1	10
81	The ENZYME database in 2000. <i>Nucleic Acids Research</i> , 2000 , 28, 304-5	20.1	707
80	The 1999 SWISS-2DPAGE database update. <i>Nucleic Acids Research</i> , 2000 , 28, 286-8	20.1	70
79	The SWISS-PROT protein sequence database and its supplement TrEMBL in 2000. <i>Nucleic Acids Research</i> , 2000 , 28, 45-8	20.1	1933
78	Constructing a 2-D database for the World Wide Web. <i>Methods in Molecular Biology</i> , 1999 , 112, 411-6	1.4	6
77	Protein identification and analysis tools in the ExPASy server. <i>Methods in Molecular Biology</i> , 1999 , 112, 531-52	1.4	1209
76	2-D databases on the World Wide Web. <i>Methods in Molecular Biology</i> , 1999 , 112, 383-91	1.4	5
75	The SWISS-PROT protein sequence data bank and its supplement TrEMBL in 1999. <i>Nucleic Acids Research</i> , 1999 , 27, 49-54	20.1	424
74	The SWISS-2DPAGE database: what has changed during the last year. <i>Nucleic Acids Research</i> , 1999 , 27, 289-91	20.1	16
73	The PROSITE database, its status in 1999. <i>Nucleic Acids Research</i> , 1999 , 27, 215-9	20.1	1001
72	The ENZYME data bank in 1999. <i>Nucleic Acids Research</i> , 1999 , 27, 310-1	20.1	30
71	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. <i>Human Genetics</i> , 1999 , 105, 399-409	6.3	58
70	Improving protein identification from peptide mass fingerprinting through a parameterized multi-level scoring algorithm and an optimized peak detection. <i>Electrophoresis</i> , 1999 , 20, 3535-50	3.6	117
69	A molecular scanner to automate proteomic research and to display proteome images. <i>Analytical Chemistry</i> , 1999 , 71, 4981-8	7.8	118
68	High-throughput mass spectrometric discovery of protein post-translational modifications. <i>Journal of Molecular Biology</i> , 1999 , 289, 645-57	6.5	266

67	Protein annotation: detective work for function prediction. <i>Trends in Genetics</i> , 1998 , 14, 248-50	8.5	59
66	Low molecular weight proteins: a challenge for post-genomic research. <i>Electrophoresis</i> , 1998 , 19, 536-44	3.6	56
65	Two-dimensional gel electrophoresis for proteome projects: the effects of protein hydrophobicity and copy number. <i>Electrophoresis</i> , 1998 , 19, 1501-5	3.6	176
64	Ø8 Escherichia coli SWISS-2DPAGE database update. <i>Electrophoresis</i> , 1998 , 19, 1960-71	3.6	81
63	Multiple parameter cross-species protein identification using Multident--a world-wide web accessible tool. <i>Electrophoresis</i> , 1998 , 19, 3199-206	3.6	51
62	A superfamily of metalloenzymes unifies phosphopentomutase and cofactor-independent phosphoglycerate mutase with alkaline phosphatases and sulfatases. <i>Protein Science</i> , 1998 , 7, 1829-35	6.3	134
61	Protein identification with N and C-terminal sequence tags in proteome projects. <i>Journal of Molecular Biology</i> , 1998 , 278, 599-608	6.5	88
60	Current status of the SWISS-2DPAGE database. <i>Nucleic Acids Research</i> , 1998 , 26, 332-3	20.1	19
59	The SWISS-PROT protein sequence data bank and its supplement TrEMBL in 1998. <i>Nucleic Acids Research</i> , 1998 , 26, 38-42	20.1	180
58	New insulin-like proteins with atypical disulfide bond pattern characterized in <i>Caenorhabditis elegans</i> by comparative sequence analysis and homology modeling. <i>Genome Research</i> , 1998 , 8, 348-53	9.7	122
57	GPCRDB: an information system for G protein-coupled receptors. <i>Nucleic Acids Research</i> , 1998 , 26, 275-9	20.1	311
56	The PROSITE database, its status in 1997. <i>Nucleic Acids Research</i> , 1997 , 25, 217-21	20.1	742
55	The SWISS-PROT protein sequence data bank and its supplement TrEMBL. <i>Nucleic Acids Research</i> , 1997 , 25, 31-6	20.1	325
54	The UDP glycosyltransferase gene superfamily: recommended nomenclature update based on evolutionary divergence. <i>Pharmacogenetics and Genomics</i> , 1997 , 7, 255-69		927
53	Sequences and topology: Predicting evolution. <i>Current Opinion in Structural Biology</i> , 1997 , 7, 367-8	8.1	8
52	Molecular basis of symbiosis between <i>Rhizobium</i> and legumes. <i>Nature</i> , 1997 , 387, 394-401	50.4	661
51	Detailed peptide characterization using PEPTIDEMASS--a World-Wide-Web-accessible tool. <i>Electrophoresis</i> , 1997 , 18, 403-8	3.6	294
50	Proteome Databases. <i>Principles and Practice</i> , 1997 , 93-148		6

49	The SWISS-PROT protein sequence database: its relevance to human molecular medical research. <i>Journal of Molecular Medicine</i> , 1997 , 75, 312-6	5.5	57
48	Updating the sequence-based classification of glycosyl hydrolases. <i>Biochemical Journal</i> , 1996 , 316 (Pt 2), 695-6	3.8	1175
47	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	0.9	
46	Go hunting in sequence databases but watch out for the traps. <i>Trends in Genetics</i> , 1996 , 12, 425-7	8.5	87
45	Integrating two-dimensional gel databases using the Melanie II software. <i>Trends in Biochemical Sciences</i> , 1996 , 21, 496-7	10.3	25
44	Federated two-dimensional electrophoresis database: a simple means of publishing two-dimensional electrophoresis data. <i>Electrophoresis</i> , 1996 , 17, 540-6	3.6	133
43	Two-dimensional gel electrophoresis of Escherichia coli homogenates: the Escherichia coli SWISS-2DPAGE database. <i>Electrophoresis</i> , 1996 , 17, 547-55	3.6	73
42	The yeast SWISS-2DPAGE database. <i>Electrophoresis</i> , 1996 , 17, 556-65	3.6	36
41	The SWISS-PROT protein sequence data bank and its new supplement TREMBL. <i>Nucleic Acids Research</i> , 1996 , 24, 21-5	20.1	290
40	The SWISS-2DPAGE database of two-dimensional polyacrylamide gel electrophoresis, its status in 1995. <i>Nucleic Acids Research</i> , 1996 , 24, 180-1	20.1	18
39	LISTA, LISTA-HOP and LISTA-HON: a comprehensive compilation of protein encoding sequences and its associated homology databases from the yeast Saccharomyces. <i>Nucleic Acids Research</i> , 1996 , 24, 50-2	20.1	4
38	The PROSITE database, its status in 1995. <i>Nucleic Acids Research</i> , 1996 , 24, 189-96	20.1	211
37	The ENZYME data bank in 1995. <i>Nucleic Acids Research</i> , 1996 , 24, 221-2	20.1	42
36	Inside SWISS-2DPAGE database. <i>Electrophoresis</i> , 1995 , 16, 1131-51	3.6	222
35	LISTA, LISTA-HOP and LISTA-HON: a comprehensive compilation of protein encoding sequences and its associated homology databases from the yeast Saccharomyces. <i>Nucleic Acids Research</i> , 1994 , 22, 3459-61	20.1	4
34	A novel zinc-binding motif found in two ubiquitous deaminase families. <i>Protein Science</i> , 1994 , 3, 853-6	6.3	15
33	Proposals for the naming of chloroplast genes. III. Nomenclature for open reading frames encoded in chloroplast genomes. <i>Plant Molecular Biology Reporter</i> , 1994 , 12, S29-S30	1.7	26
32	A new generation of information retrieval tools for biologists: the example of the EXPASy WWW server. <i>Trends in Biochemical Sciences</i> , 1994 , 19, 258-60	10.3	511

31	The ENZYME data bank. <i>Nucleic Acids Research</i> , 1994 , 22, 3626-3627	20.1	168
30	A diverse transketolase family that includes the RecP protein of <i>Streptococcus pneumoniae</i> , a protein implicated in genetic recombination. <i>Research in Microbiology</i> , 1993 , 144, 341-7	4	23
29	The ENZYME data bank. <i>Nucleic Acids Research</i> , 1993 , 21, 3155-6	20.1	60
28	A possible mechanism for metal-ion induced DNA-protein dissociation in a family of prokaryotic transcriptional regulators. <i>Nucleic Acids Research</i> , 1993 , 21, 2515	20.1	26
27	The SWISS-PROT protein sequence data bank, recent developments. <i>Nucleic Acids Research</i> , 1993 , 21, 3093-6	20.1	142
26	The PROSITE dictionary of sites and patterns in proteins, its current status. <i>Nucleic Acids Research</i> , 1993 , 21, 3097-103	20.1	316
25	Human liver protein map: update 1993. <i>Electrophoresis</i> , 1993 , 14, 1216-22	3.6	73
24	Plasma and red blood cell protein maps: update 1993. <i>Electrophoresis</i> , 1993 , 14, 1223-31	3.6	124
23	SWISS-2DPAGE: a database of two-dimensional gel electrophoresis images. <i>Electrophoresis</i> , 1993 , 14, 1232-8	3.6	118
22	Complementation of the DNA repair defect in xeroderma pigmentosum group G cells by a human cDNA related to yeast RAD2. <i>Nature</i> , 1993 , 363, 182-5	50.4	197
21	The SWISS-PROT protein sequence data bank. <i>Nucleic Acids Research</i> , 1992 , 20 Suppl, 2019-22	20.1	208
20	Proto-vav and gene expression. <i>Nature</i> , 1992 , 358, 113	50.4	34
19	cis-diol dehydrogenases encoded by the TOL pWW0 plasmid xylL gene and the <i>Acinetobacter calcoaceticus</i> chromosomal benD gene are members of the short-chain alcohol dehydrogenase superfamily. <i>FEBS Journal</i> , 1992 , 204, 113-20		70
18	Human liver protein map: a reference database established by microsequencing and gel comparison. <i>Electrophoresis</i> , 1992 , 13, 992-1001	3.6	127
17	Interleukin-1-inducible genes in endothelial cells. Cloning of a new gene related to C-reactive protein and serum amyloid P component. <i>Journal of Biological Chemistry</i> , 1992 , 267, 22190-7	5.4	284
16	The SWISS-PROT protein sequence data bank. <i>Nucleic Acids Research</i> , 1991 , 19 Suppl, 2247-9	20.1	370
15	PROSITE: a dictionary of sites and patterns in proteins. <i>Nucleic Acids Research</i> , 1991 , 19 Suppl, 2241-5	20.1	571
14	SEQANALREF: a sequence analysis bibliographic reference databank. <i>Bioinformatics</i> , 1991 , 7, 268	7.2	4

13	Potential DNA slippage structures acquired during evolutionary divergence of <i>Acinetobacter calcoaceticus</i> chromosomal benABC and <i>Pseudomonas putida</i> TOL pWW0 plasmid xylXYZ, genes encoding benzoate dioxygenases. <i>Journal of Bacteriology</i> , 1991 , 173, 7540-8	3.5	125
12	Nucleotide sequences of the <i>Acinetobacter calcoaceticus</i> benABC genes for benzoate 1,2-dioxygenase reveal evolutionary relationships among multicomponent oxygenases. <i>Journal of Bacteriology</i> , 1991 , 173, 5385-95	3.5	192
11	EF-hand motifs in inositol phospholipid-specific phospholipase C. <i>FEBS Letters</i> , 1990 , 269, 454-6	3.8	50
10	A unique signature identifies a family of zinc-dependent metallopeptidases. <i>FEBS Letters</i> , 1989 , 242, 211-4	3.8	375
9	Sequence patterns in protein kinases. <i>Nature</i> , 1988 , 331, 22	50.4	37
8	Sequence similarities in calcium-binding proteins. <i>Nature</i> , 1988 , 331, 491	50.4	21
7	Evolutionary relationships between catabolic pathways for aromatics: conservation of gene order and nucleotide sequences of catechol oxidation genes of pWW0 and NAH7 plasmids. <i>Molecular Genetics and Genomics</i> , 1987 , 210, 241-7		89
6	The xylS gene positive regulator of TOL plasmid pWW0: identification, sequence analysis and overproduction leading to constitutive expression of meta cleavage operon. <i>Molecular Genetics and Genomics</i> , 1987 , 207, 349-54		58
5	Amino acid sequence determination by gas chromatography-mass spectrometry of permethylated peptides. <i>Journal of Chromatography A</i> , 1983 , 268, 197-206	4.5	4
4	Evidence for the existence of a mutated enkephalin sequence in preproenkephalin. <i>FEBS Letters</i> , 1982 , 145, 121-2	3.8	
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