

# Amos Bairoch

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/8534428/amos-bairoch-publications-by-citations.pdf>

**Version:** 2024-04-24

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Protein Identification and Analysis Tools on the ExPASy Server <b>2005</b> , 571-607		3376
191	ExPASy: The proteomics server for in-depth protein knowledge and analysis. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3784-8	20.1	2989
190	The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 365-70	20.1	2375
189	UniProt: the Universal Protein knowledgebase. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D115-9	20.1	2195
188	The SWISS-PROT protein sequence database and its supplement TrEMBL in 2000. <i>Nucleic Acids Research</i> , <b>2000</b> , 28, 45-8	20.1	1933
187	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D211-5	20.1	1379
186	The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D154-9	20.1	1231
185	Protein identification and analysis tools in the ExPASy server. <i>Methods in Molecular Biology</i> , <b>1999</b> , 112, 531-52	1.4	1209
184	Updating the sequence-based classification of glycosyl hydrolases. <i>Biochemical Journal</i> , <b>1996</b> , 316 (Pt 2), 695-6	3.8	1175
183	ScanProsite: detection of PROSITE signature matches and ProRule-associated functional and structural residues in proteins. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, W362-5	20.1	1055
182	The Universal Protein Resource (UniProt) in 2010. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D142-8	20.1	1035
181	The PROSITE database, its status in 1999. <i>Nucleic Acids Research</i> , <b>1999</b> , 27, 215-9	20.1	1001
180	The UDP glycosyltransferase gene superfamily: recommended nomenclature update based on evolutionary divergence. <i>Pharmacogenetics and Genomics</i> , <b>1997</b> , 7, 255-69		927
179	The Universal Protein Resource (UniProt): an expanding universe of protein information. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D187-91	20.1	839
178	The PROSITE database, its status in 2002. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, 235-8	20.1	787
177	The InterPro database, an integrated documentation resource for protein families, domains and functional sites. <i>Nucleic Acids Research</i> , <b>2001</b> , 29, 37-40	20.1	743
176	The PROSITE database, its status in 1997. <i>Nucleic Acids Research</i> , <b>1997</b> , 25, 217-21	20.1	742

175	The ENZYME database in 2000. <i>Nucleic Acids Research</i> , <b>2000</b> , 28, 304-5	20.1	707
174	PROSITE: a documented database using patterns and profiles as motif descriptors. <i>Briefings in Bioinformatics</i> , <b>2002</b> , 3, 265-74	13.4	676
173	IntAct: an open source molecular interaction database. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D452-5	20.1	670
172	Molecular basis of symbiosis between Rhizobium and legumes. <i>Nature</i> , <b>1997</b> , 387, 394-401	50.4	661
171	The PROSITE database. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D227-30	20.1	649
170	PROSITE, a protein domain database for functional characterization and annotation. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D161-6	20.1	600
169	Ongoing and future developments at the Universal Protein Resource. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D214-9	20.1	592
168	A large-scale evaluation of computational protein function prediction. <i>Nature Methods</i> , <b>2013</b> , 10, 221-7	21.6	587
167	PROSITE: a dictionary of sites and patterns in proteins. <i>Nucleic Acids Research</i> , <b>1991</b> , 19 Suppl, 2241-5	20.1	571
166	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 315-8	20.1	556
165	A new generation of information retrieval tools for biologists: the example of the ExPASy WWW server. <i>Trends in Biochemical Sciences</i> , <b>1994</b> , 19, 258-60	10.3	511
164	The Universal Protein Resource (UniProt) 2009. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D169-74	20.1	509
163	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D201-5	20.1	426
162	The SWISS-PROT protein sequence data bank and its supplement TrEMBL in 1999. <i>Nucleic Acids Research</i> , <b>1999</b> , 27, 49-54	20.1	424
161	UniProtKB/Swiss-Prot. <i>Methods in Molecular Biology</i> , <b>2007</b> , 406, 89-112	1.4	405
160	New developments in the InterPro database. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D224-8	20.1	397
159	Mass spectrometry in high-throughput proteomics: ready for the big time. <i>Nature Methods</i> , <b>2010</b> , 7, 681-5	21.6	390
158	The 20 years of PROSITE. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D245-9	20.1	375

157	A unique signature identifies a family of zinc-dependent metallopeptidases. <i>FEBS Letters</i> , <b>1989</b> , 242, 211-4	3.8	375
156	The SWISS-PROT protein sequence data bank. <i>Nucleic Acids Research</i> , <b>1991</b> , 19 Suppl, 2247-9	20.1	370
155	The Gene Ontology in 2010: extensions and refinements. <i>Nucleic Acids Research</i> , <b>2010</b> , 38, D331-5	20.1	367
154	Infrastructure for the life sciences: design and implementation of the UniProt website. <i>BMC Bioinformatics</i> , <b>2009</b> , 10, 136	3.6	366
153	The SWISS-PROT protein sequence data bank and its supplement TrEMBL. <i>Nucleic Acids Research</i> , <b>1997</b> , 25, 31-6	20.1	325
152	The PROSITE dictionary of sites and patterns in proteins, its current status. <i>Nucleic Acids Research</i> , <b>1993</b> , 21, 3097-103	20.1	316
151	GPCRDB: an information system for G protein-coupled receptors. <i>Nucleic Acids Research</i> , <b>1998</b> , 26, 275-9	20.1	311
150	Recent improvements to the PROSITE database. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D134-7	20.1	299
149	Detailed peptide characterization using PEPTIDEMASS--a World-Wide-Web-accessible tool. <i>Electrophoresis</i> , <b>1997</b> , 18, 403-8	3.6	294
148	The SWISS-PROT protein sequence data bank and its new supplement TREMBL. <i>Nucleic Acids Research</i> , <b>1996</b> , 24, 21-5	20.1	290
147	Swiss-Prot: juggling between evolution and stability. <i>Briefings in Bioinformatics</i> , <b>2004</b> , 5, 39-55	13.4	287
146	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> , <b>1992</b> , 267, 22190-7	5.4	284
145	ScanProsite: a reference implementation of a PROSITE scanning tool. <i>Applied Bioinformatics</i> , <b>2002</b> , 1, 107-8		275
144	High-throughput mass spectrometric discovery of protein post-translational modifications. <i>Journal of Molecular Biology</i> , <b>1999</b> , 289, 645-57	6.5	266
143	CTdatabase: a knowledge-base of high-throughput and curated data on cancer-testis antigens. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D816-9	20.1	257
142	The human proteome project: current state and future direction. <i>Molecular and Cellular Proteomics</i> , <b>2011</b> , 10, M111.009993	7.6	249
141	The Chromosome-Centric Human Proteome Project for cataloging proteins encoded in the genome. <i>Nature Biotechnology</i> , <b>2012</b> , 30, 221-3	44.5	244
140	The Sulfinator: predicting tyrosine sulfation sites in protein sequences. <i>Bioinformatics</i> , <b>2002</b> , 18, 769-70	7.2	225

139	Inside SWISS-2DPAGE database. <i>Electrophoresis</i> , <b>1995</b> , 16, 1131-51	3.6	222
138	ViralZone: a knowledge resource to understand virus diversity. <i>Nucleic Acids Research</i> , <b>2011</b> , 39, D576-82	20.1	216
137	The Cellosaurus, a Cell-Line Knowledge Resource. <i>Journal of Biomolecular Techniques</i> , <b>2018</b> , 29, 25-38	1.1	212
136	The PROSITE database, its status in 1995. <i>Nucleic Acids Research</i> , <b>1996</b> , 24, 189-96	20.1	211
135	The SWISS-PROT protein sequence data bank. <i>Nucleic Acids Research</i> , <b>1992</b> , 20 Suppl, 2019-22	20.1	208
134	High-quality protein knowledge resource: SWISS-PROT and TrEMBL. <i>Briefings in Bioinformatics</i> , <b>2002</b> , 3, 275-84	13.4	206
133	Complementation of the DNA repair defect in xeroderma pigmentosum group G cells by a human cDNA related to yeast RAD2. <i>Nature</i> , <b>1993</b> , 363, 182-5	50.4	197
132	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> , <b>1991</b> , 173, 5385-95	3.5	192
131	The SWISS-PROT protein sequence data bank and its supplement TrEMBL in 1998. <i>Nucleic Acids Research</i> , <b>1998</b> , 26, 38-42	20.1	180
130	Two-dimensional gel electrophoresis for proteome projects: the effects of protein hydrophobicity and copy number. <i>Electrophoresis</i> , <b>1998</b> , 19, 1501-5	3.6	176
129	Protein sequence databases. <i>Current Opinion in Chemical Biology</i> , <b>2004</b> , 8, 76-80	9.7	173
128	The ENZYME data bank. <i>Nucleic Acids Research</i> , <b>1994</b> , 22, 3626-3627	20.1	168
127	neXtProt: a knowledge platform for human proteins. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D76-83	20.1	142
126	The SWISS-PROT protein sequence data bank, recent developments. <i>Nucleic Acids Research</i> , <b>1993</b> , 21, 3093-6	20.1	142
125	InterPro: an integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , <b>2002</b> , 3, 225-35	13.4	137
124	A superfamily of metalloenzymes unifies phosphopentomutase and cofactor-independent phosphoglycerate mutase with alkaline phosphatases and sulfatases. <i>Protein Science</i> , <b>1998</b> , 7, 1829-35	6.3	134
123	IntEnz, the integrated relational enzyme database. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D434-7	20.1	134
122	Federated two-dimensional electrophoresis database: a simple means of publishing two-dimensional electrophoresis data. <i>Electrophoresis</i> , <b>1996</b> , 17, 540-6	3.6	133

121	Human liver protein map: a reference database established by microsequencing and gel comparison. <i>Electrophoresis</i> , <b>1992</b> , 13, 992-1001	3.6	127
120	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> , <b>1991</b> , 173, 7540-8	3.5	125
119	Plasma and red blood cell protein maps: update 1993. <i>Electrophoresis</i> , <b>1993</b> , 14, 1223-31	3.6	124
118	The neXtProt knowledgebase on human proteins: 2017 update. <i>Nucleic Acids Research</i> , <b>2017</b> , 45, D177-D182	18.2	123
117	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> , <b>1998</b> , 8, 348-53	9.7	122
116	Standard guidelines for the chromosome-centric human proteome project. <i>Journal of Proteome Research</i> , <b>2012</b> , 11, 2005-13	5.6	121
115	A molecular scanner to automate proteomic research and to display proteome images. <i>Analytical Chemistry</i> , <b>1999</b> , 71, 4981-8	7.8	118
114	SWISS-2DPAGE: a database of two-dimensional gel electrophoresis images. <i>Electrophoresis</i> , <b>1993</b> , 14, 1232-8	3.6	118
113	HAMAP: a database of completely sequenced microbial proteome sets and manually curated microbial protein families in UniProtKB/Swiss-Prot. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D471-8	20.1	117
112	Improving protein identification from peptide mass fingerprinting through a parameterized multi-level scoring algorithm and an optimized peak detection. <i>Electrophoresis</i> , <b>1999</b> , 20, 3535-50	3.6	117
111	The Swiss-Prot variant page and the ModSNP database: a resource for sequence and structure information on human protein variants. <i>Human Mutation</i> , <b>2004</b> , 23, 464-70	4.7	116
110	Metrics for the Human Proteome Project 2013-2014 and strategies for finding missing proteins. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 15-20	5.6	113
109	Automated annotation of microbial proteomes in SWISS-PROT. <i>Computational Biology and Chemistry</i> , <b>2003</b> , 27, 49-58	3.6	112
108	neXtProt: organizing protein knowledge in the context of human proteome projects. <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 293-8	5.6	110
107	Calling on a million minds for community annotation in WikiProteins. <i>Genome Biology</i> , <b>2008</b> , 9, R89	18.3	101
106	Industrial-scale proteomics: from liters of plasma to chemically synthesized proteins. <i>Proteomics</i> , <b>2004</b> , 4, 2125-50	4.8	97
105	FindPept, a tool to identify unmatched masses in peptide mass fingerprinting protein identification. <i>Proteomics</i> , <b>2002</b> , 2, 1435-44	4.8	89
104	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> , <b>1987</b> , 210, 241-7		89

103	Protein identification with N and C-terminal sequence tags in proteome projects. <i>Journal of Molecular Biology</i> , <b>1998</b> , 278, 599-608	6.5	88
102	Annotating single amino acid polymorphisms in the UniProt/Swiss-Prot knowledgebase. <i>Human Mutation</i> , <b>2008</b> , 29, 361-6	4.7	87
101	Annotation of post-translational modifications in the Swiss-Prot knowledge base. <i>Proteomics</i> , <b>2004</b> , 4, 1537-50	4.8	87
100	Go hunting in sequence databases but watch out for the traps. <i>Trends in Genetics</i> , <b>1996</b> , 12, 425-7	8.5	87
99	98 Escherichia coli SWISS-2DPAGE database update. <i>Electrophoresis</i> , <b>1998</b> , 19, 1960-71	3.6	81
98	Protein variety and functional diversity: Swiss-Prot annotation in its biological context. <i>Comptes Rendus - Biologies</i> , <b>2005</b> , 328, 882-99	1.4	80
97	Tox-Prot, the toxin protein annotation program of the Swiss-Prot protein knowledgebase. <i>Toxicon</i> , <b>2005</b> , 45, 293-301	2.8	79
96	The neXtProt knowledgebase on human proteins: current status. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D764-70.1	7.1	76
95	UniPathway: a resource for the exploration and annotation of metabolic pathways. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D761-9	20.1	76
94	The human proteomics initiative (HPI). <i>Trends in Biotechnology</i> , <b>2001</b> , 19, 178-81	15.1	74
93	Two-dimensional gel electrophoresis of Escherichia coli homogenates: the Escherichia coli SWISS-2DPAGE database. <i>Electrophoresis</i> , <b>1996</b> , 17, 547-55	3.6	73
92	Human liver protein map: update 1993. <i>Electrophoresis</i> , <b>1993</b> , 14, 1216-22	3.6	73
91	The 1999 SWISS-2DPAGE database update. <i>Nucleic Acids Research</i> , <b>2000</b> , 28, 286-8	20.1	70
90	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. <i>FEBS Journal</i> , <b>1992</b> , 204, 113-20		70
89	The neXtProt knowledgebase in 2020: data, tools and usability improvements. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D328-D334	20.1	67
88	The UniProtKB/Swiss-Prot knowledgebase and its Plant Proteome Annotation Program. <i>Journal of Proteomics</i> , <b>2009</b> , 72, 567-73	3.9	63
87	The ENZYME data bank. <i>Nucleic Acids Research</i> , <b>1993</b> , 21, 3155-6	20.1	60
86	Protein annotation: detective work for function prediction. <i>Trends in Genetics</i> , <b>1998</b> , 14, 248-50	8.5	59

85	A high-stringency blueprint of the human proteome. <i>Nature Communications</i> , <b>2020</b> , 11, 5301	17.4	59
84	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> , <b>1999</b> , 105, 399-409	6.3	58
83	The xylS gene positive regulator of TOL plasmid pWWO: identification, sequence analysis and overproduction leading to constitutive expression of meta cleavage operon. <i>Molecular Genetics and Genomics</i> , <b>1987</b> , 207, 349-54		58
82	The SWISS-PROT protein sequence database: its relevance to human molecular medical research. <i>Journal of Molecular Medicine</i> , <b>1997</b> , 75, 312-6	5.5	57
81	Low molecular weight proteins: a challenge for post-genomic research. <i>Electrophoresis</i> , <b>1998</b> , 19, 536-44	3.6	56
80	The Swiss-Prot protein knowledgebase and ExPASy: providing the plant community with high quality proteomic data and tools. <i>Plant Physiology and Biochemistry</i> , <b>2004</b> , 42, 1013-21	5.4	54
79	ProRule: a new database containing functional and structural information on PROSITE profiles. <i>Bioinformatics</i> , <b>2005</b> , 21, 4060-6	7.2	54
78	Multiple parameter cross-species protein identification using Multident--a world-wide web accessible tool. <i>Electrophoresis</i> , <b>1998</b> , 19, 3199-206	3.6	51
77	EF-hand motifs in inositol phospholipid-specific phospholipase C. <i>FEBS Letters</i> , <b>1990</b> , 269, 454-6	3.8	50
76	Standards for Reporting Enzyme Data: The STRENDA Consortium: What it aims to do and why it should be helpful. <i>Perspectives in Science</i> , <b>2014</b> , 1, 131-137	0.8	47
75	Human aldehyde dehydrogenase genes: alternatively spliced transcriptional variants and their suggested nomenclature. <i>Pharmacogenetics and Genomics</i> , <b>2009</b> , 19, 893-902	1.9	46
74	Annotation of glycoproteins in the SWISS-PROT database. <i>Proteomics</i> , <b>2001</b> , 1, 262-8	4.8	45
73	C11orf83, a mitochondrial cardiolipin-binding protein involved in bc1 complex assembly and supercomplex stabilization. <i>Molecular and Cellular Biology</i> , <b>2015</b> , 35, 1139-56	4.8	44
72	N-terminome analysis of the human mitochondrial proteome. <i>Proteomics</i> , <b>2015</b> , 15, 2519-24	4.8	43
71	Biocuration: Distilling data into knowledge. <i>PLoS Biology</i> , <b>2018</b> , 16, e2002846	9.7	42
70	The ENZYME data bank in 1995. <i>Nucleic Acids Research</i> , <b>1996</b> , 24, 221-2	20.1	42
69	The SIB Swiss Institute of Bioinformatics Resources: focus on curated databases. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D27-37	20.1	41
68	A Standard Nomenclature for Referencing and Authentication of Pluripotent Stem Cells. <i>Stem Cell Reports</i> , <b>2018</b> , 10, 1-6	8	39



67	Plant protein annotation in the UniProt Knowledgebase. <i>Plant Physiology</i> , <b>2005</b> , 138, 59-66	6.6	38
66	Sequence patterns in protein kinases. <i>Nature</i> , <b>1988</b> , 331, 22	50.4	37
65	The yeast SWISS-2DPAGE database. <i>Electrophoresis</i> , <b>1996</b> , 17, 556-65	3.6	36
64	Proto-vav and gene expression. <i>Nature</i> , <b>1992</b> , 358, 113	50.4	34
63	A chromosome-centric human proteome project (C-HPP) to characterize the sets of proteins encoded in chromosome 17. <i>Journal of Proteome Research</i> , <b>2013</b> , 12, 45-57	5.6	31
62	NEWT, a new taxonomy portal. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 3822-3	20.1	31
61	The ENZYME data bank in 1999. <i>Nucleic Acids Research</i> , <b>1999</b> , 27, 310-1	20.1	30
60	OpenFluDB, a database for human and animal influenza virus. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2010</b> , 2010, baq004	5	29
59	The human proteome project: Current state and future direction. <i>Molecular and Cellular Proteomics</i> , <b>2011</b> ,	7.6	28
58	A possible mechanism for metal-ion induced DNA-protein dissociation in a family of prokaryotic transcriptional regulators. <i>Nucleic Acids Research</i> , <b>1993</b> , 21, 2515	20.1	26
57	Proposals for the naming of chloroplast genes. III. Nomenclature for open reading frames encoded in chloroplast genomes. <i>Plant Molecular Biology Reporter</i> , <b>1994</b> , 12, S29-S30	1.7	26
56	Integrating two-dimensional gel databases using the Melanie II software. <i>Trends in Biochemical Sciences</i> , <b>1996</b> , 21, 496-7	10.3	25
55	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> , <b>1993</b> , 144, 341-7	4	23
54	Sequence similarities in calcium-binding proteins. <i>Nature</i> , <b>1988</b> , 331, 491	50.4	21
53	CLASTR: The Cellosaurus STR similarity search tool - A precious help for cell line authentication. <i>International Journal of Cancer</i> , <b>2020</b> , 146, 1299-1306	7.5	21
52	DERA is the human deoxyribose phosphate aldolase and is involved in stress response. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , <b>2014</b> , 1843, 2913-25	4.9	19
51	Current status of the SWISS-2DPAGE database. <i>Nucleic Acids Research</i> , <b>1998</b> , 26, 332-3	20.1	19
50	Functional identification of APIP as human mttnB, a key enzyme in the methionine salvage pathway. <i>PLoS ONE</i> , <b>2012</b> , 7, e52877	3.7	19

49	Animal Toxins: How is Complexity Represented in Databases?. <i>Toxins</i> , <b>2010</b> , 2, 262-282	4.9	18
48	A comprehensive web resource on RNA helicases from the baker's yeast <i>Saccharomyces cerevisiae</i> . <i>Yeast</i> , <b>2000</b> , 16, 507-9	3.4	18
47	The SWISS-2DPAGE database of two-dimensional polyacrylamide gel electrophoresis, its status in 1995. <i>Nucleic Acids Research</i> , <b>1996</b> , 24, 180-1	20.1	18
46	A large-scale protein-function database. <i>Nature Chemical Biology</i> , <b>2010</b> , 6, 785	11.7	17
45	Exploring the Uncharacterized Human Proteome Using neXtProt. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 4211-4226	5.6	17
44	The SWISS-2DPAGE database: what has changed during the last year. <i>Nucleic Acids Research</i> , <b>1999</b> , 27, 289-91	20.1	16
43	A novel zinc-binding motif found in two ubiquitous deaminase families. <i>Protein Science</i> , <b>1994</b> , 3, 853-6	6.3	15
42	The ABCD database: a repository for chemically defined antibodies. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D261-D264	20.1	15
41	C2orf62 and TTC17 are involved in actin organization and ciliogenesis in zebrafish and human. <i>PLoS ONE</i> , <b>2014</b> , 9, e86476	3.7	13
40	Deep Question Answering for protein annotation. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2015</b> , 2015,	5	12
39	Fifteen years SIB Swiss Institute of Bioinformatics: life science databases, tools and support. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, W436-41	20.1	12
38	Missing Protein Landscape of Human Chromosomes 2 and 14: Progress and Current Status. <i>Journal of Proteome Research</i> , <b>2016</b> , 15, 3971-3978	5.6	12
37	Querying neXtProt nanopublications and their value for insights on sequence variants and tissue expression. <i>Web Semantics</i> , <b>2014</b> , 29, 3-11	2.9	11
36	Incidences of problematic cell lines are lower in papers that use RRIDs to identify cell lines. <i>ELife</i> , <b>2019</b> , 8,	8.9	11
35	Annotation of functional impact of voltage-gated sodium channel mutations. <i>Human Mutation</i> , <b>2017</b> , 38, 485-493	4.7	10
34	Converting neXtProt into Linked Data and nanopublications. <i>Semantic Web</i> , <b>2015</b> , 6, 147-153	2.4	10
33	Quality control in databanks for molecular biology. <i>BioEssays</i> , <b>2000</b> , 22, 1024-34	4.1	10
32	Large-Scale Reanalysis of Publicly Available HeLa Cell Proteomics Data in the Context of the Human Proteome Project. <i>Journal of Proteome Research</i> , <b>2018</b> , 17, 4160-4170	5.6	10

31	Collaborative annotation of genes and proteins between UniProtKB/Swiss-Prot and dictyBase. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2009</b> , 2009, bap016	5	9
30	The Feature-Viewer: a visualization tool for positional annotations on a sequence. <i>Bioinformatics</i> , <b>2020</b> , 36, 3244-3245	7.2	8
29	Sequences and topology: Predicting evolution. <i>Current Opinion in Structural Biology</i> , <b>1997</b> , 7, 367-8	8.1	8
28	A new bioinformatics tool to help assess the significance of BRCA1 variants. <i>Human Genomics</i> , <b>2018</b> , 12, 36	6.8	7
27	Triage by ranking to support the curation of protein interactions. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2017</b> , 2017,	5	7
26	ICEPO: the ion channel electrophysiology ontology. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2016</b> , 2016,	5	7
25	Cell Lines as Biological Models: Practical Steps for More Reliable Research. <i>Chemical Research in Toxicology</i> , <b>2019</b> , 32, 1733-1736	4	6
24	Constructing a 2-D database for the World Wide Web. <i>Methods in Molecular Biology</i> , <b>1999</b> , 112, 411-6	1.4	6
23	Animal Toxins: How is Complexity Represented in Databases?. <i>Toxins</i> , <b>2010</b> , 2, 262-82	4.9	6
22	Proteome Databases. <i>Principles and Practice</i> , <b>1997</b> , 93-148		6
21	Internet Resources for Protein Identification and Characterization 277-299		6
20	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> , <b>2015</b> , 2015, bav063	5	5
19	The future of annotation/biocuration. <i>Nature Precedings</i> , <b>2009</b> ,		5
18	2-D databases on the World Wide Web. <i>Methods in Molecular Biology</i> , <b>1999</b> , 112, 383-91	1.4	5
17	LISTA, LISTA-HOP and LISTA-HON: a comprehensive compilation of protein encoding sequences and its associated homology databases from the yeast <i>Saccharomyces</i> . <i>Nucleic Acids Research</i> , <b>1996</b> , 24, 50-2	20.1	4
16	LISTA, LISTA-HOP and LISTA-HON: a comprehensive compilation of protein encoding sequences and its associated homology databases from the yeast <i>Saccharomyces</i> . <i>Nucleic Acids Research</i> , <b>1994</b> , 22, 3459-61	20.1	4
15	SEQANALREF: a sequence analysis bibliographic reference databank. <i>Bioinformatics</i> , <b>1991</b> , 7, 268	7.2	4
14	Amino acid sequence determination by gas chromatography-mass spectrometry of permethylated peptides. <i>Journal of Chromatography A</i> , <b>1983</b> , 268, 197-206	4.5	4

13	Bioinformatics for Human Proteomics: Current State and Future Status. <i>Nature Precedings</i> , <b>2010</b> ,		2
12	Querying NeXtProt Nanopublications and Their Value for Insights on Sequence Variants and Tissue Expression. <i>SSRN Electronic Journal</i> ,	1	2
11	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> , <b>2021</b> , 2021,	5	2
10	Review of the selected proceedings of the Fifth International Workshop on Data Integration in the Life Sciences 2008. <i>BMC Bioinformatics</i> , <b>2008</b> , 9 Suppl 8, S1	3.6	1
9	Proteome Analysis. <i>Methods and Principles in Medicinal Chemistry</i> , <b>2001</b> , 69-118	0.4	1
8	UniProtKB/Swiss-Prot: New and Future Developments. <i>Lecture Notes in Computer Science</i> , <b>2008</b> , 204-206.	0.9	1
7	A Preliminary Study on the Prediction of Human Protein Functions. <i>Lecture Notes in Computer Science</i> , <b>2011</b> , 334-343	0.9	1
6	UniProtKB/Swiss-Prot Manual and Automated Annotation of Complete Proteomes: The Dictyostelium discoideum Case Study <b>2009</b> , 149-168		
5	Protein Variations: Resources and Tools <b>2004</b> , 389-422		
4	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> , <b>1996</b> , 44-51	0.9	
3	Evidence for the existence of a mutated enkephalin sequence in preproenkephalin. <i>FEBS Letters</i> , <b>1982</b> , 145, 121-2	3.8	
2	Protein Sequence Variants: Resources and Tools 389		
1	The Impact of 3D Structures on a Protein Knowledgebase: From Proteins to Systems <b>2008</b> , 51-77		