

Rolf Apweiler

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.

182
papers

35,326
citations

67
h-index

187
g-index

210
ext. papers

39,921
ext. citations

11.1
avg. IF

6.69
L-index

| # | Paper | IF | Citations |
|-----|---|------|-----------|
| 182 | Data Mining, Quality and Management in the Life Sciences.. <i>Methods in Molecular Biology</i> , 2022 , 2449, 3-25 | 1.4 | |
| 181 | The European Bioinformatics Institute (EMBL-EBI) in 2021. <i>Nucleic Acids Research</i> , 2021 , | 20.1 | 2 |
| 180 | The European Bioinformatics Institute: empowering cooperation in response to a global health crisis. <i>Nucleic Acids Research</i> , 2021 , 49, D29-D37 | 20.1 | 12 |
| 179 | Data Sharing Under the General Data Protection Regulation: Time to Harmonize Law and Research Ethics?. <i>Hypertension</i> , 2021 , 77, 1029-1035 | 8.5 | 10 |
| 178 | The COVID-19 Data Portal: accelerating SARS-CoV-2 and COVID-19 research through rapid open access data sharing. <i>Nucleic Acids Research</i> , 2021 , 49, W619-W623 | 20.1 | 17 |
| 177 | The European Bioinformatics Institute in 2020: building a global infrastructure of interconnected data resources for the life sciences. <i>Nucleic Acids Research</i> , 2020 , 48, D17-D23 | 20.1 | 18 |
| 176 | Biomolecular Data Resources: Bioinformatics Infrastructure for Biomedical Data Science. <i>Annual Review of Biomedical Data Science</i> , 2019 , 2, 199-222 | 5.6 | 6 |
| 175 | The European Bioinformatics Institute in 2018: tools, infrastructure and training. <i>Nucleic Acids Research</i> , 2019 , 47, D15-D22 | 20.1 | 21 |
| 174 | Whither systems medicine?. <i>Experimental and Molecular Medicine</i> , 2018 , 50, e453 | 12.8 | 37 |
| 173 | The European Bioinformatics Institute in 2017: data coordination and integration. <i>Nucleic Acids Research</i> , 2018 , 46, D21-D29 | 20.1 | 36 |
| 172 | The European Bioinformatics Institute in 2016: Data growth and integration. <i>Nucleic Acids Research</i> , 2016 , 44, D20-6 | 20.1 | 91 |
| 171 | Identifying ELIXIR Core Data Resources. <i>F1000Research</i> , 2016 , 5, | 3.6 | 44 |
| 170 | ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , 2014 , 32, 223-6 | 44.5 | 2053 |
| 169 | Characterization, design, and function of the mitochondrial proteome: from organs to organisms. <i>Journal of Proteome Research</i> , 2014 , 13, 433-46 | 5.6 | 49 |
| 168 | The European Bioinformatics Institute's data resources 2014. <i>Nucleic Acids Research</i> , 2014 , 42, D18-25 | 20.1 | 54 |
| 167 | Representing kidney development using the gene ontology. <i>PLoS ONE</i> , 2014 , 9, e99864 | 3.7 | 15 |
| 166 | Use of Gene Ontology Annotation to understand the peroxisome proteome in humans. <i>Database: the Journal of Biological Databases and Curation</i> , 2013 , 2013, bas062 | 5 | 16 |

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| 165 | Integration of cardiac proteome biology and medicine by a specialized knowledgebase. <i>Circulation Research</i> , 2013 , 113, 1043-53 | 15.7 | 42 |
| 164 | LipidHome: a database of theoretical lipids optimized for high throughput mass spectrometry lipidomics. <i>PLoS ONE</i> , 2013 , 8, e61951 | 3.7 | 59 |
| 163 | Cellular resolution models for even skipped regulation in the entire <i>Drosophila</i> embryo. <i>ELife</i> , 2013 , 2, e00522 | 8.9 | 39 |
| 162 | The HUPO initiative on Model Organism Proteomes, iMOP. <i>Proteomics</i> , 2012 , 12, 340-5 | 4.8 | 8 |
| 161 | The UniProt-GO Annotation database in 2011. <i>Nucleic Acids Research</i> , 2012 , 40, D565-70 | 20.1 | 265 |
| 160 | InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012 , 40, D306-12 | 20.1 | 844 |
| 159 | A guide to UniProt for protein scientists. <i>Methods in Molecular Biology</i> , 2011 , 694, 25-35 | 1.4 | 14 |
| 158 | The impact of focused Gene Ontology curation of specific mammalian systems. <i>PLoS ONE</i> , 2011 , 6, e27547 | 3.7 | 22 |
| 157 | A posteriori quality control for the curation and reuse of public proteomics data. <i>Proteomics</i> , 2011 , 11, 2182-94 | 4.8 | 25 |
| 156 | Consequences of the discontinuation of the International Protein Index (IPI) database and its substitution by the UniProtKB "complete proteome" sets. <i>Proteomics</i> , 2011 , 11, 4434-8 | 4.8 | 24 |
| 155 | Phosphoproteome analysis reveals regulatory sites in major pathways of cardiac mitochondria. <i>Molecular and Cellular Proteomics</i> , 2011 , 10, M110.000117 | 7.6 | 79 |
| 154 | "4D Biology for health and disease" workshop report. <i>New Biotechnology</i> , 2011 , 28, 291-3 | 6.4 | 2 |
| 153 | A large-scale protein-function database. <i>Nature Chemical Biology</i> , 2010 , 6, 785 | 11.7 | 17 |
| 152 | Comparative proteomics profiling reveals role of smooth muscle progenitors in extracellular matrix production. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2010 , 30, 1325-32 | 9.4 | 31 |
| 151 | Practical Applications of the Gene Ontology Resource 2010 , 319-339 | | |
| 150 | The Renal Gene Ontology Annotation Initiative. <i>Organogenesis</i> , 2010 , 6, 71-5 | 1.7 | 13 |
| 149 | Design, Implementation and Updating of Knowledge Bases 2010 , 87-105 | | |
| 148 | Recommendations for biomarker identification and qualification in clinical proteomics. <i>Science Translational Medicine</i> , 2010 , 2, 46ps42 | 17.5 | 237 |

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| 147 | On the importance of comprehensible classification models for protein function prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2010 , 7, 172-82 | 3 | 63 |
| 146 | Mining Unique- Substrings from Genomes. <i>Journal of Proteomics and Bioinformatics</i> , 2010 , 3, 099-103 | 2.1 | 2 |
| 145 | Approaching clinical proteomics: current state and future fields of application in fluid proteomics. <i>Clinical Chemistry and Laboratory Medicine</i> , 2009 , 47, 724-44 | 5.9 | 94 |
| 144 | QuickGO: a user tutorial for the web-based Gene Ontology browser. <i>Database: the Journal of Biological Databases and Curation</i> , 2009 , 2009, bap010 | 5 | 33 |
| 143 | The GOA database in 2009--an integrated Gene Ontology Annotation resource. <i>Nucleic Acids Research</i> , 2009 , 37, D396-403 | 20.1 | 447 |
| 142 | QuickGO: a web-based tool for Gene Ontology searching. <i>Bioinformatics</i> , 2009 , 25, 3045-6 | 7.2 | 529 |
| 141 | Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. <i>Bioinformatics</i> , 2009 , 25, 2865-71 | 7.2 | 1423 |
| 140 | InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009 , 37, D211-5 | 20.1 | 1379 |
| 139 | Approaching clinical proteomics: current state and future fields of application in cellular proteomics. <i>Cytometry Part A: the Journal of the International Society for Analytical Cytology</i> , 2009 , 75, 816-32 | 4.6 | 41 |
| 138 | Proteomics data collection--4th ProDaC workshop 15 August 2008, Amsterdam, The Netherlands. <i>Proteomics</i> , 2009 , 9, 218-22 | 4.8 | 1 |
| 137 | Getting a grip on proteomics data - Proteomics Data Collection (ProDaC). <i>Proteomics</i> , 2009 , 9, 3928-33 | 4.8 | 14 |
| 136 | Systematic comparison of the human saliva and plasma proteomes. <i>Proteomics - Clinical Applications</i> , 2009 , 3, 116-134 | 3.1 | 142 |
| 135 | Finding one's way in proteomics: a protein species nomenclature. <i>Chemistry Central Journal</i> , 2009 , 3, 11 | | 199 |
| 134 | Prepublication data sharing. <i>Nature</i> , 2009 , 461, 168-70 | 50.4 | 197 |
| 133 | Missing in action: enzyme functional annotations in biological databases. <i>Nature Chemical Biology</i> , 2009 , 5, 521-5 | 11.7 | 43 |
| 132 | Know your limits: assumptions, constraints and interpretation in systems biology. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2009 , 1794, 1280-7 | 4 | 5 |
| 131 | ASTD: The Alternative Splicing and Transcript Diversity database. <i>Genomics</i> , 2009 , 93, 213-20 | 4.3 | 80 |
| 130 | Recommendations from the 2008 International Summit on Proteomics Data Release and Sharing Policy: the Amsterdam principles. <i>Journal of Proteome Research</i> , 2009 , 8, 3689-92 | 5.6 | 58 |

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| 129 | Algorithms and databases. <i>Methods in Molecular Biology</i> , 2009 , 564, 245-59 | 1.4 | 3 |
| 128 | Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , 2008 , 26, 889-96 | 44.5 | 417 |
| 127 | MINT and IntAct contribute to the Second BioCreative challenge: serving the text-mining community with high quality molecular interaction data. <i>Genome Biology</i> , 2008 , 9 Suppl 2, S5 | 18.3 | 21 |
| 126 | Analyzing large-scale proteomics projects with latent semantic indexing. <i>Journal of Proteome Research</i> , 2008 , 7, 182-91 | 5.6 | 36 |
| 125 | The InterPro database and tools for protein domain analysis. <i>Current Protocols in Bioinformatics</i> , 2008 , Chapter 2, Unit 2.7 | 24.2 | 57 |
| 124 | Altered proteome biology of cardiac mitochondria under stress conditions. <i>Journal of Proteome Research</i> , 2008 , 7, 2204-14 | 5.6 | 51 |
| 123 | The Ontology Lookup Service: more data and better tools for controlled vocabulary queries. <i>Nucleic Acids Research</i> , 2008 , 36, W372-6 | 20.1 | 58 |
| 122 | UniProtJAPI: a remote API for accessing UniProt data. <i>Bioinformatics</i> , 2008 , 24, 1321-2 | 7.2 | 32 |
| 121 | Building a biological space based on protein sequence similarities and biological ontologies. <i>Combinatorial Chemistry and High Throughput Screening</i> , 2008 , 11, 653-60 | 1.3 | 1 |
| 120 | In silico characterization of proteins: UniProt, InterPro and Integr8. <i>Molecular Biotechnology</i> , 2008 , 38, 165-77 | 3 | 47 |
| 119 | The speciation of the proteome. <i>Chemistry Central Journal</i> , 2008 , 2, 16 | | 183 |
| 118 | Analysis of the experimental detection of central nervous system-related genes in human brain and cerebrospinal fluid datasets. <i>Proteomics</i> , 2008 , 8, 1138-48 | 4.8 | 18 |
| 117 | Systematic characterization of the murine mitochondrial proteome using functionally validated cardiac mitochondria. <i>Proteomics</i> , 2008 , 8, 1564-75 | 4.8 | 84 |
| 116 | The Gene Ontology [Providing a Functional Role in Proteomic Studies. <i>Proteomics</i> , 2008 , 8, n/a-n/a | 4.8 | 22 |
| 115 | Cardiovascular GO annotation initiative year 1 report: why cardiovascular GO?. <i>Proteomics</i> , 2008 , 8, 1950-38 | 4.8 | 12 |
| 114 | The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , 2008 , 36, D1028-33 | 20.1 | 262 |
| 113 | Priorities for nucleotide trace, sequence and annotation data capture at the Ensembl Trace Archive and the EMBL Nucleotide Sequence Database. <i>Nucleic Acids Research</i> , 2008 , 36, D5-12 | 20.1 | 39 |
| 112 | Annotating the Human Proteome 2008 , 211-235 | | |

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| 111 | InterPro and InterProScan: tools for protein sequence classification and comparison. <i>Methods in Molecular Biology</i> , 2007 , 396, 59-70 | 1.4 | 253 |
| 110 | Annotating the human proteome: beyond establishing a parts list. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2007 , 1774, 175-91 | 4 | 26 |
| 109 | Broadening the horizon--level 2.5 of the HUPO-PSI format for molecular interactions. <i>BMC Biology</i> , 2007 , 5, 44 | 7.3 | 204 |
| 108 | Clinical proteomics: A need to define the field and to begin to set adequate standards. <i>Proteomics - Clinical Applications</i> , 2007 , 1, 148-56 | 3.1 | 237 |
| 107 | The minimum information required for reporting a molecular interaction experiment (MIMIX). <i>Nature Biotechnology</i> , 2007 , 25, 894-8 | 44.5 | 229 |
| 106 | The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , 2007 , 25, 887-91 | 44.5 | 583 |
| 105 | The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics. <i>Nature Biotechnology</i> , 2007 , 25, 1127-33 | 44.5 | 81 |
| 104 | The EMBL Nucleotide Sequence and Genome Reviews Databases. <i>Methods in Molecular Biology</i> , 2007 , 406, 1-21 | 1.4 | 12 |
| 103 | Proteomic data exchange and storage: the need for common standards and public repositories. <i>Methods in Molecular Biology</i> , 2007 , 367, 261-70 | 1.4 | 9 |
| 102 | New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007 , 35, D224-8 | 20.1 | 397 |
| 101 | EMBL Nucleotide Sequence Database in 2006. <i>Nucleic Acids Research</i> , 2007 , 35, D16-20 | 20.1 | 114 |
| 100 | Curated genome annotation of <i>Oryza sativa</i> ssp. <i>japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007 , 17, 175-83 | 9.7 | 200 |
| 99 | The Protein Identifier Cross-Referencing (PICR) service: reconciling protein identifiers across multiple source databases. <i>BMC Bioinformatics</i> , 2007 , 8, 401 | 3.6 | 102 |
| 98 | Human Proteome Organization Proteomics Standards Initiative. <i>Molecular and Cellular Proteomics</i> , 2007 , 6, 1666-1667 | 7.6 | 13 |
| 97 | The Ontology Lookup Service, a lightweight cross-platform tool for controlled vocabulary queries. <i>BMC Bioinformatics</i> , 2006 , 7, 97 | 3.6 | 142 |
| 96 | UniSave: the UniProtKB sequence/annotation version database. <i>Bioinformatics</i> , 2006 , 22, 1284-5 | 7.2 | 20 |
| 95 | EMBL Nucleotide Sequence Database: developments in 2005. <i>Nucleic Acids Research</i> , 2006 , 34, D10-5 | 20.1 | 76 |
| 94 | PRIDE: a public repository of protein and peptide identifications for the proteomics community. <i>Nucleic Acids Research</i> , 2006 , 34, D659-63 | 20.1 | 222 |

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| 93 | The Universal Protein Resource (UniProt): an expanding universe of protein information. <i>Nucleic Acids Research</i> , 2006 , 34, D187-91 | 20.1 | 839 |
| 92 | GOAnnotator: linking protein GO annotations to evidence text. <i>Journal of Biomedical Discovery and Collaboration</i> , 2006 , 1, 19 | | 41 |
| 91 | The work of the Human Proteome Organisation & Proteomics Standards Initiative (HUPO PSI). <i>OMICS A Journal of Integrative Biology</i> , 2006 , 10, 145-51 | 3.8 | 57 |
| 90 | Genome Reviews: standardizing content and representation of information about complete genomes. <i>OMICS A Journal of Integrative Biology</i> , 2006 , 10, 114-8 | 3.8 | 25 |
| 89 | Evidence standards in experimental and inferential INSDC Third Party Annotation data. <i>OMICS A Journal of Integrative Biology</i> , 2006 , 10, 105-13 | 3.8 | 22 |
| 88 | Bioinformatics database infrastructure for biotechnology research. <i>Journal of Biotechnology</i> , 2006 , 124, 629-39 | 3.7 | 15 |
| 87 | Proteomic Data Standardization, Deposition and Exchange. <i>Methods and Principles in Medicinal Chemistry</i> , 2006 , 19-30 | 0.4 | |
| 86 | Gaining knowledge from previously unexplained spectra-application of the PTM-Explorer software to detect PTM in HUPO BPP MS/MS data. <i>Proteomics</i> , 2006 , 6, 5048-58 | 4.8 | 13 |
| 85 | Functional annotation of proteins identified in human brain during the HUPO Brain Proteome Project pilot study. <i>Proteomics</i> , 2006 , 6, 5059-75 | 4.8 | 23 |
| 84 | A comparison of the HUPO Brain Proteome Project pilot with other proteomics studies. <i>Proteomics</i> , 2006 , 6, 5076-86 | 4.8 | 25 |
| 83 | Automated reprocessing pipeline for searching heterogeneous mass spectrometric data of the HUPO Brain Proteome Project pilot phase. <i>Proteomics</i> , 2006 , 6, 5015-29 | 4.8 | 50 |
| 82 | HUPO Brain Proteome Project: summary of the pilot phase and introduction of a comprehensive data reprocessing strategy. <i>Proteomics</i> , 2006 , 6, 4890-8 | 4.8 | 45 |
| 81 | The power of cooperative investigation: summary and comparison of the HUPO Brain Proteome Project pilot study results. <i>Proteomics</i> , 2006 , 6, 4997-5014 | 4.8 | 26 |
| 80 | Proteomics and Beyond: a report on the 3rd Annual Spring Workshop of the HUPO-PSI 21-23 April 2006, San Francisco, CA, USA. <i>Proteomics</i> , 2006 , 6, 4439-43 | 4.8 | 12 |
| 79 | Linking publication, gene and protein data. <i>Nature Cell Biology</i> , 2006 , 8, 1183-9 | 23.4 | 28 |
| 78 | Protein Sequence Databases 2005 , 609-618 | | |
| 77 | Integr8 and Genome Reviews: integrated views of complete genomes and proteomes. <i>Nucleic Acids Research</i> , 2005 , 33, D297-302 | 20.1 | 116 |
| 76 | The EMBL Nucleotide Sequence Database. <i>Nucleic Acids Research</i> , 2005 , 33, D29-33 | 20.1 | 199 |

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| 75 | InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2005 , 33, D201-5 | 20.1 | 426 |
| 74 | The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , 2005 , 33, D154-9 | 20.1 | 1231 |
| 73 | Biological Databases: Infrastructure, Content and Integration 2005 , 11-28 | | 3 |
| 72 | In Silico Characterization of Proteins InterPro and Proteome Analysis 2005 , 619-627 | | |
| 71 | The importance of uniformity in reporting protein-function data. <i>Trends in Biochemical Sciences</i> , 2005 , 30, 11-2 | 10.3 | 18 |
| 70 | An evaluation of GO annotation retrieval for BioCreAtIvE and GOA. <i>BMC Bioinformatics</i> , 2005 , 6 Suppl 1, S17 | 3.6 | 106 |
| 69 | PRIDE: the proteomics identifications database. <i>Proteomics</i> , 2005 , 5, 3537-45 | 4.8 | 454 |
| 68 | Overview of the HUPO Plasma Proteome Project: results from the pilot phase with 35 collaborating laboratories and multiple analytical groups, generating a core dataset of 3020 proteins and a publicly-available database. <i>Proteomics</i> , 2005 , 5, 3226-45 | 4.8 | 672 |
| 67 | Databases and Resources for in silico Proteome Analysis. <i>Methods of Biochemical Analysis</i> , 2005 , 395-414 | | 1 |
| 66 | The predictive power of the CluSTr database. <i>Bioinformatics</i> , 2005 , 21, 3604-9 | 7.2 | 40 |
| 65 | Plant protein annotation in the UniProt Knowledgebase. <i>Plant Physiology</i> , 2005 , 138, 59-66 | 6.6 | 38 |
| 64 | Dasty and UniProt DAS: a perfect pair for protein feature visualization. <i>Bioinformatics</i> , 2005 , 21, 3198-9 | 7.2 | 22 |
| 63 | Annotating the human proteome. <i>Molecular and Cellular Proteomics</i> , 2005 , 4, 435-40 | 7.6 | 22 |
| 62 | Do you do text?. <i>Bioinformatics</i> , 2005 , 21, 4199-200 | 7.2 | 5 |
| 61 | The use of common ontologies and controlled vocabularies to enable data exchange and deposition for complex proteomic experiments. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2005 , 186-96 | 1.3 | 14 |
| 60 | The Integr8 project--a resource for genomic and proteomic data. <i>In Silico Biology</i> , 2005 , 5, 179-85 | 2 | 21 |
| 59 | The EMBL Nucleotide Sequence Database. <i>Nucleic Acids Research</i> , 2004 , 32, D27-30 | 20.1 | 123 |
| 58 | UniProt archive. <i>Bioinformatics</i> , 2004 , 20, 3236-7 | 7.2 | 137 |

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| 57 | The Gene Ontology Annotation (GOA) Database: sharing knowledge in Uniprot with Gene Ontology. <i>Nucleic Acids Research</i> , 2004 , 32, D262-6 | 20.1 | 643 |
| 56 | IntEnz, the integrated relational enzyme database. <i>Nucleic Acids Research</i> , 2004 , 32, D434-7 | 20.1 | 134 |
| 55 | IntAct: an open source molecular interaction database. <i>Nucleic Acids Research</i> , 2004 , 32, D452-5 | 20.1 | 670 |
| 54 | Current status of proteomic standards development. <i>Expert Review of Proteomics</i> , 2004 , 1, 179-83 | 4.2 | 25 |
| 53 | Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , 2004 , 2, e162 | 9.7 | 255 |
| 52 | A common open representation of mass spectrometry data and its application to proteomics research. <i>Nature Biotechnology</i> , 2004 , 22, 1459-66 | 44.5 | 632 |
| 51 | The HUPO PSI ³ molecular interaction format--a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , 2004 , 22, 177-83 | 44.5 | 504 |
| 50 | Common interchange standards for proteomics data: Public availability of tools and schema. <i>Proteomics</i> , 2004 , 4, 490-1 | 4.8 | 88 |
| 49 | The International Protein Index: an integrated database for proteomics experiments. <i>Proteomics</i> , 2004 , 4, 1985-8 | 4.8 | 650 |
| 48 | Towards data management of the HUPO Human Brain Proteome Project pilot phase. <i>Proteomics</i> , 2004 , 4, 2361-2 | 4.8 | 21 |
| 47 | Advances in the development of common interchange standards for proteomic data. <i>Proteomics</i> , 2004 , 4, 2363-5 | 4.8 | 24 |
| 46 | Protein sequence databases. <i>Current Opinion in Chemical Biology</i> , 2004 , 8, 76-80 | 9.7 | 173 |
| 45 | UniProt: the Universal Protein knowledgebase. <i>Nucleic Acids Research</i> , 2004 , 32, D115-9 | 20.1 | 2195 |
| 44 | Proteomics and data standardisation. <i>Drug Discovery Today Biosilico</i> , 2004 , 2, 91-93 | | 2 |
| 43 | InterPro and Proteome Analysis In silico Analysis of Proteins and Proteomes. <i>Principles and Practice</i> , 2004 , 307-318 | | |
| 42 | Protein Sequence Database Methods 2004 , 13-17 | | |
| 41 | Managing core resources for genomics and proteomics. <i>Pharmacogenomics</i> , 2003 , 4, 343-50 | 2.6 | 4 |
| 40 | The InterPro Database and Tools for Protein Domain Analysis. <i>Current Protocols in Bioinformatics</i> , 2003 , 2, 2.7.1 | 24.2 | 2 |

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| 39 | Bioinformatics Resources for In Silico Proteome Analysis. <i>Journal of Biomedicine and Biotechnology</i> , 2003 , 2003, 231-236 | | 6 |
| 38 | Increase of functional diversity by alternative splicing. <i>Trends in Genetics</i> , 2003 , 19, 124-8 | 8.5 | 171 |
| 37 | The HUPO Proteomics Standards Initiative Meeting: Towards Common Standards for Exchanging Proteomics Data. <i>Comparative and Functional Genomics</i> , 2003 , 4, 16-9 | | 22 |
| 36 | The Gene Ontology Annotation (GOA) Project--Application of GO in SWISS-PROT, TrEMBL and InterPro. <i>Comparative and Functional Genomics</i> , 2003 , 4, 71-4 | | 31 |
| 35 | Progress in Establishing Common Standards for Exchanging Proteomics Data: The Second Meeting of the HUPO Proteomics Standards Initiative. <i>Comparative and Functional Genomics</i> , 2003 , 4, 203-6 | | 14 |
| 34 | The proteomics standards initiative. <i>Proteomics</i> , 2003 , 3, 1374-6 | 4.8 | 159 |
| 33 | The Gene Ontology Annotation (GOA) project: implementation of GO in SWISS-PROT, TrEMBL, and InterPro. <i>Genome Research</i> , 2003 , 13, 662-72 | 9.7 | 251 |
| 32 | The SWISS-PROT protein knowledgebase and its supplement TrEMBL in 2003. <i>Nucleic Acids Research</i> , 2003 , 31, 365-70 | 20.1 | 2375 |
| 31 | The Proteome Analysis database: a tool for the in silico analysis of whole proteomes. <i>Nucleic Acids Research</i> , 2003 , 31, 414-7 | 20.1 | 55 |
| 30 | The European Bioinformatics Institute's data resources. <i>Nucleic Acids Research</i> , 2003 , 31, 43-50 | 20.1 | 38 |
| 29 | The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003 , 31, 315-8 | 20.1 | 556 |
| 28 | TEMBLOR - Perspectives of EBI Database Services. <i>Comparative and Functional Genomics</i> , 2002 , 3, 47-50 | | 3 |
| 27 | InterPro: an integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002 , 3, 225-35 | 13.4 | 137 |
| 26 | The EBI SRS server--recent developments. <i>Bioinformatics</i> , 2002 , 18, 368-73 | 7.2 | 93 |
| 25 | Applications of InterPro in protein annotation and genome analysis. <i>Briefings in Bioinformatics</i> , 2002 , 3, 285-95 | 13.4 | 48 |
| 24 | Focus on InterPro. <i>Briefings in Bioinformatics</i> , 2002 , 3, 221-223 | 13.4 | 1 |
| 23 | High-quality protein knowledge resource: SWISS-PROT and TrEMBL. <i>Briefings in Bioinformatics</i> , 2002 , 3, 275-84 | 13.4 | 206 |
| 22 | The EBI SRS server-new features. <i>Bioinformatics</i> , 2002 , 18, 1149-50 | 7.2 | 76 |

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|----|--|------|------|
| 21 | Tools and resources for identifying protein families, domains and motifs. <i>Genome Biology</i> , 2002 , 3, REVIEW | 18.5 | 2015 |
| 20 | Organisation and standardisation of information in SWISS-PROT and TrEMBL. <i>Data Science Journal</i> , 2002 , 1, 13-18 | 2 | 2 |
| 19 | Application of InterPro for the functional classification of the proteins of fish origin in SWISS-PROT and TrEMBL. <i>Journal of Biosciences</i> , 2001 , 26, 277-84 | 2.3 | 4 |
| 18 | Consistent integration of non-reliable heterogeneous information resources applied to the annotation of transmembrane proteins. <i>Computers & Chemistry</i> , 2001 , 26, 41-9 | | 10 |
| 17 | The human proteomics initiative (HPI). <i>Trends in Biotechnology</i> , 2001 , 19, 178-81 | 15.1 | 74 |
| 16 | Clustering and analysis of protein families. <i>Current Opinion in Structural Biology</i> , 2001 , 11, 334-9 | 8.1 | 38 |
| 15 | Evaluation of methods for the prediction of membrane spanning regions. <i>Bioinformatics</i> , 2001 , 17, 646-53 | 3.2 | 811 |
| 14 | InterProScan--an integration platform for the signature-recognition methods in InterPro. <i>Bioinformatics</i> , 2001 , 17, 847-8 | 7.2 | 2126 |
| 13 | Using the Molecular Biology Data 2001 , 281-300 | | 0 |
| 12 | Mus musculus in the SWISS-PROT database: its relevance to developmental research. <i>Genesis</i> , 2000 , 26, 1-4 | 1.9 | |
| 11 | Comparative genomics of the eukaryotes. <i>Science</i> , 2000 , 287, 2204-15 | 33.3 | 1364 |
| 10 | Protein sequence databases. <i>Advances in Protein Chemistry</i> , 2000 , 54, 31-71 | | 11 |
| 9 | VARSPPLIC: alternatively-spliced protein sequences derived from SWISS-PROT and TrEMBL. <i>Bioinformatics</i> , 2000 , 16, 1048-9 | 7.2 | 44 |
| 8 | The SWISS-PROT protein sequence database and its supplement TrEMBL in 2000. <i>Nucleic Acids Research</i> , 2000 , 28, 45-8 | 20.1 | 1933 |
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