

# Rolf Apweiler

## List of Publications by Citations

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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 | 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      |
| 181 | UniProt: the Universal Protein knowledgebase. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D115-9   | 20.1 | 2195      |
| 180 | InterProScan--an integration platform for the signature-recognition methods in InterPro. <i>Bioinformatics</i> , <b>2001</b> , 17, 847-8   | 7.2  | 2126      |
| 179 | ProteomeXchange provides globally coordinated proteomics data submission and dissemination. <i>Nature Biotechnology</i> , <b>2014</b> , 32, 223-6  | 44.5 | 2053      |
| 178 | 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      |
| 177 | Pindel: a pattern growth approach to detect break points of large deletions and medium sized insertions from paired-end short reads. <i>Bioinformatics</i> , <b>2009</b> , 25, 2865-71   | 7.2  | 1423      |
| 176 | InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D211-5   | 20.1 | 1379      |
| 175 | Comparative genomics of the eukaryotes. <i>Science</i> , <b>2000</b> , 287, 2204-15  | 33.3 | 1364      |
| 174 | The Universal Protein Resource (UniProt). <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D154-9   | 20.1 | 1231      |
| 173 | InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D306-12   | 20.1 | 844       |
| 172 | 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       |
| 171 | Evaluation of methods for the prediction of membrane spanning regions. <i>Bioinformatics</i> , <b>2001</b> , 17, 646-53  | 7.2  | 811       |
| 170 | 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> , <b>2005</b> , 5, 3226-45 | 4.8  | 672       |
| 169 | IntAct: an open source molecular interaction database. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D452-5  | 20.1 | 670       |
| 168 | The International Protein Index: an integrated database for proteomics experiments. <i>Proteomics</i> , <b>2004</b> , 4, 1985-8  | 4.8  | 650       |
| 167 | The Gene Ontology Annotation (GOA) Database: sharing knowledge in Uniprot with Gene Ontology. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D262-6   | 20.1 | 643       |
| 166 | A common open representation of mass spectrometry data and its application to proteomics research. <i>Nature Biotechnology</i> , <b>2004</b> , 22, 1459-66   | 44.5 | 632       |

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|-----|---|------|-----|
| 165 | The minimum information about a proteomics experiment (MIAPE). <i>Nature Biotechnology</i> , <b>2007</b> , 25, 887-935  | 44.5 | 583 |
| 164 | The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 315-8   | 20.1 | 556 |
| 163 | QuickGO: a web-based tool for Gene Ontology searching. <i>Bioinformatics</i> , <b>2009</b> , 25, 3045-6   | 7.2  | 529 |
| 162 | The HUPO PSI3 molecular interaction format--a community standard for the representation of protein interaction data. <i>Nature Biotechnology</i> , <b>2004</b> , 22, 177-83 | 44.5 | 504 |
| 161 | PRIDE: the proteomics identifications database. <i>Proteomics</i> , <b>2005</b> , 5, 3537-45  | 4.8  | 454 |
| 160 | The GOA database in 2009--an integrated Gene Ontology Annotation resource. <i>Nucleic Acids Research</i> , <b>2009</b> , 37, D396-403                                       | 20.1 | 447 |
| 159 | InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D201-5   | 20.1 | 426 |
| 158 | Promoting coherent minimum reporting guidelines for biological and biomedical investigations: the MIBBI project. <i>Nature Biotechnology</i> , <b>2008</b> , 26, 889-96     | 44.5 | 417 |
| 157 | New developments in the InterPro database. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D224-8   | 20.1 | 397 |
| 156 | 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 |
| 155 | The UniProt-GO Annotation database in 2011. <i>Nucleic Acids Research</i> , <b>2012</b> , 40, D565-70   | 20.1 | 265 |
| 154 | The Rice Annotation Project Database (RAP-DB): 2008 update. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, D1028-33  | 20.1 | 262 |
| 153 | Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , <b>2004</b> , 2, e162  | 9.7  | 255 |
| 152 | InterPro and InterProScan: tools for protein sequence classification and comparison. <i>Methods in Molecular Biology</i> , <b>2007</b> , 396, 59-70                         | 1.4  | 253 |
| 151 | The Gene Ontology Annotation (GOA) project: implementation of GO in SWISS-PROT, TrEMBL, and InterPro. <i>Genome Research</i> , <b>2003</b> , 13, 662-72                     | 9.7  | 251 |
| 150 | Recommendations for biomarker identification and qualification in clinical proteomics. <i>Science Translational Medicine</i> , <b>2010</b> , 2, 46ps42                      | 17.5 | 237 |
| 149 | Clinical proteomics: A need to define the field and to begin to set adequate standards. <i>Proteomics - Clinical Applications</i> , <b>2007</b> , 1, 148-56                 | 3.1  | 237 |
| 148 | The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , <b>2007</b> , 25, 894-8                            | 44.5 | 229 |

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| 147 | PRIDE: a public repository of protein and peptide identifications for the proteomics community. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D659-63                           | 20.1 | 222 |
| 146 | High-quality protein knowledge resource: SWISS-PROT and TrEMBL. <i>Briefings in Bioinformatics</i> , <b>2002</b> , 3, 275-84  | 13.4 | 206 |
| 145 | Broadening the horizon--level 2.5 of the HUPO-PSI format for molecular interactions. <i>BMC Biology</i> , <b>2007</b> , 5, 44   | 7.3  | 204 |
| 144 | Curated genome annotation of <i>Oryza sativa ssp. japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , <b>2007</b> , 17, 175-83 | 9.7  | 200 |
| 143 | Finding one's way in proteomics: a protein species nomenclature. <i>Chemistry Central Journal</i> , <b>2009</b> , 3, 11   |      | 199 |
| 142 | The EMBL Nucleotide Sequence Database. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D29-33   | 20.1 | 199 |
| 141 | Prepublication data sharing. <i>Nature</i> , <b>2009</b> , 461, 168-70  | 50.4 | 197 |
| 140 | The speciation of the proteome. <i>Chemistry Central Journal</i> , <b>2008</b> , 2, 16  |      | 183 |
| 139 | Protein sequence databases. <i>Current Opinion in Chemical Biology</i> , <b>2004</b> , 8, 76-80   | 9.7  | 173 |
| 138 | Increase of functional diversity by alternative splicing. <i>Trends in Genetics</i> , <b>2003</b> , 19, 124-8   | 8.5  | 171 |
| 137 | The proteomics standards initiative. <i>Proteomics</i> , <b>2003</b> , 3, 1374-6  | 4.8  | 159 |
| 136 | Systematic comparison of the human saliva and plasma proteomes. <i>Proteomics - Clinical Applications</i> , <b>2009</b> , 3, 116-134  | 3.1  | 142 |
| 135 | The Ontology Lookup Service, a lightweight cross-platform tool for controlled vocabulary queries. <i>BMC Bioinformatics</i> , <b>2006</b> , 7, 97                                   | 3.6  | 142 |
| 134 | UniProt archive. <i>Bioinformatics</i> , <b>2004</b> , 20, 3236-7   | 7.2  | 137 |
| 133 | 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 |
| 132 | IntEnz, the integrated relational enzyme database. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D434-7   | 20.1 | 134 |
| 131 | The EMBL Nucleotide Sequence Database. <i>Nucleic Acids Research</i> , <b>2004</b> , 32, D27-30   | 20.1 | 123 |
| 130 | Integr8 and Genome Reviews: integrated views of complete genomes and proteomes. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, D297-302  | 20.1 | 116 |

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|-----|---|------|-----|
| 129 | EMBL Nucleotide Sequence Database in 2006. <i>Nucleic Acids Research</i> , <b>2007</b> , 35, D16-20   | 20.1 | 114 |
| 128 | An evaluation of GO annotation retrieval for BioCreAtIvE and GOA. <i>BMC Bioinformatics</i> , <b>2005</b> , 6 Suppl 1, S17  | 3.6  | 106 |
| 127 | The Protein Identifier Cross-Referencing (PICR) service: reconciling protein identifiers across multiple source databases. <i>BMC Bioinformatics</i> , <b>2007</b> , 8, 401                   | 3.6  | 102 |
| 126 | Approaching clinical proteomics: current state and future fields of application in fluid proteomics. <i>Clinical Chemistry and Laboratory Medicine</i> , <b>2009</b> , 47, 724-44             | 5.9  | 94  |
| 125 | The EBI SRS server--recent developments. <i>Bioinformatics</i> , <b>2002</b> , 18, 368-73   | 7.2  | 93  |
| 124 | The European Bioinformatics Institute in 2016: Data growth and integration. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D20-6   | 20.1 | 91  |
| 123 | Common interchange standards for proteomics data: Public availability of tools and schema. <i>Proteomics</i> , <b>2004</b> , 4, 490-1   | 4.8  | 88  |
| 122 | Systematic characterization of the murine mitochondrial proteome using functionally validated cardiac mitochondria. <i>Proteomics</i> , <b>2008</b> , 8, 1564-75                              | 4.8  | 84  |
| 121 | The Functional Genomics Experiment model (FuGE): an extensible framework for standards in functional genomics. <i>Nature Biotechnology</i> , <b>2007</b> , 25, 1127-33                        | 44.5 | 81  |
| 120 | ASTD: The Alternative Splicing and Transcript Diversity database. <i>Genomics</i> , <b>2009</b> , 93, 213-20  | 4.3  | 80  |
| 119 | Phosphoproteome analysis reveals regulatory sites in major pathways of cardiac mitochondria. <i>Molecular and Cellular Proteomics</i> , <b>2011</b> , 10, M110.000117                         | 7.6  | 79  |
| 118 | EMBL Nucleotide Sequence Database: developments in 2005. <i>Nucleic Acids Research</i> , <b>2006</b> , 34, D10-5  | 20.1 | 76  |
| 117 | The EBI SRS server-new features. <i>Bioinformatics</i> , <b>2002</b> , 18, 1149-50  | 7.2  | 76  |
| 116 | The human proteomics initiative (HPI). <i>Trends in Biotechnology</i> , <b>2001</b> , 19, 178-81  | 15.1 | 74  |
| 115 | On the importance of comprehensible classification models for protein function prediction. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2010</b> , 7, 172-82 | 3    | 63  |
| 114 | LipidHome: a database of theoretical lipids optimized for high throughput mass spectrometry lipidomics. <i>PLoS ONE</i> , <b>2013</b> , 8, e61951   | 3.7  | 59  |
| 113 | Recommendations from the 2008 International Summit on Proteomics Data Release and Sharing Policy: the Amsterdam principles. <i>Journal of Proteome Research</i> , <b>2009</b> , 8, 3689-92    | 5.6  | 58  |
| 112 | The Ontology Lookup Service: more data and better tools for controlled vocabulary queries. <i>Nucleic Acids Research</i> , <b>2008</b> , 36, W372-6   | 20.1 | 58  |

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| 111 | The InterPro database and tools for protein domain analysis. <i>Current Protocols in Bioinformatics</i> , <b>2008</b> , Chapter 2, Unit 2.7  | 24.2 | 57 |
| 110 | The work of the Human Proteome Organisation® Proteomics Standards Initiative (HUPO PSI). <i>OMICS A Journal of Integrative Biology</i> , <b>2006</b> , 10, 145-51  | 3.8  | 57 |
| 109 | The Proteome Analysis database: a tool for the in silico analysis of whole proteomes. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 414-7  | 20.1 | 55 |
| 108 | The European Bioinformatics Institute® data resources 2014. <i>Nucleic Acids Research</i> , <b>2014</b> , 42, D18-25   | 20.1 | 54 |
| 107 | Altered proteome biology of cardiac mitochondria under stress conditions. <i>Journal of Proteome Research</i> , <b>2008</b> , 7, 2204-14   | 5.6  | 51 |
| 106 | Automated reprocessing pipeline for searching heterogeneous mass spectrometric data of the HUPO Brain Proteome Project pilot phase. <i>Proteomics</i> , <b>2006</b> , 6, 5015-29   | 4.8  | 50 |
| 105 | Characterization, design, and function of the mitochondrial proteome: from organs to organisms. <i>Journal of Proteome Research</i> , <b>2014</b> , 13, 433-46   | 5.6  | 49 |
| 104 | Applications of InterPro in protein annotation and genome analysis. <i>Briefings in Bioinformatics</i> , <b>2002</b> , 3, 285-95   | 13.4 | 48 |
| 103 | In silico characterization of proteins: UniProt, InterPro and Integr8. <i>Molecular Biotechnology</i> , <b>2008</b> , 38, 165-77   | 3    | 47 |
| 102 | HUPO Brain Proteome Project: summary of the pilot phase and introduction of a comprehensive data reprocessing strategy. <i>Proteomics</i> , <b>2006</b> , 6, 4890-8  | 4.8  | 45 |
| 101 | VARSP LIC: alternatively-spliced protein sequences derived from SWISS-PROT and TrEMBL. <i>Bioinformatics</i> , <b>2000</b> , 16, 1048-9  | 7.2  | 44 |
| 100 | Identifying ELIXIR Core Data Resources. <i>F1000Research</i> , <b>2016</b> , 5,  | 3.6  | 44 |
| 99  | Missing in action: enzyme functional annotations in biological databases. <i>Nature Chemical Biology</i> , <b>2009</b> , 5, 521-5  | 11.7 | 43 |
| 98  | Integration of cardiac proteome biology and medicine by a specialized knowledgebase. <i>Circulation Research</i> , <b>2013</b> , 113, 1043-53  | 15.7 | 42 |
| 97  | 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> , <b>2009</b> , 75, 816-32 | 4.6  | 41 |
| 96  | GOAnnotator: linking protein GO annotations to evidence text. <i>Journal of Biomedical Discovery and Collaboration</i> , <b>2006</b> , 1, 19   |      | 41 |
| 95  | The predictive power of the CluSTr database. <i>Bioinformatics</i> , <b>2005</b> , 21, 3604-9  | 7.2  | 40 |
| 94  | 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> , <b>2008</b> , 36, D5-12                        | 20.1 | 39 |

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| 93 | Cellular resolution models for even skipped regulation in the entire Drosophila embryo. <i>ELife</i> , <b>2013</b> , 2, e00522   | 8.9  | 39 |
| 92 | The European Bioinformatics Institute's data resources. <i>Nucleic Acids Research</i> , <b>2003</b> , 31, 43-50  | 20.1 | 38 |
| 91 | Plant protein annotation in the UniProt Knowledgebase. <i>Plant Physiology</i> , <b>2005</b> , 138, 59-66  | 6.6  | 38 |
| 90 | Clustering and analysis of protein families. <i>Current Opinion in Structural Biology</i> , <b>2001</b> , 11, 334-9  | 8.1  | 38 |
| 89 | Whither systems medicine?. <i>Experimental and Molecular Medicine</i> , <b>2018</b> , 50, e453   | 12.8 | 37 |
| 88 | The European Bioinformatics Institute in 2017: data coordination and integration. <i>Nucleic Acids Research</i> , <b>2018</b> , 46, D21-D29  | 20.1 | 36 |
| 87 | Analyzing large-scale proteomics projects with latent semantic indexing. <i>Journal of Proteome Research</i> , <b>2008</b> , 7, 182-91   | 5.6  | 36 |
| 86 | QuickGO: a user tutorial for the web-based Gene Ontology browser. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2009</b> , 2009, bap010                                     | 5    | 33 |
| 85 | UniProtJAPI: a remote API for accessing UniProt data. <i>Bioinformatics</i> , <b>2008</b> , 24, 1321-2   | 7.2  | 32 |
| 84 | Comparative proteomics profiling reveals role of smooth muscle progenitors in extracellular matrix production. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , <b>2010</b> , 30, 1325-32 | 9.4  | 31 |
| 83 | The Gene Ontology Annotation (GOA) Project--Application of GO in SWISS-PROT, TrEMBL and InterPro. <i>Comparative and Functional Genomics</i> , <b>2003</b> , 4, 71-4                                 |      | 31 |
| 82 | Linking publication, gene and protein data. <i>Nature Cell Biology</i> , <b>2006</b> , 8, 1183-9   | 23.4 | 28 |
| 81 | Annotating the human proteome: beyond establishing a parts list. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , <b>2007</b> , 1774, 175-91   | 4    | 26 |
| 80 | The power of cooperative investigation: summary and comparison of the HUPO Brain Proteome Project pilot study results. <i>Proteomics</i> , <b>2006</b> , 6, 4997-5014                                | 4.8  | 26 |
| 79 | A posteriori quality control for the curation and reuse of public proteomics data. <i>Proteomics</i> , <b>2011</b> , 11, 2182-94   | 4.8  | 25 |
| 78 | Genome Reviews: standardizing content and representation of information about complete genomes. <i>OMICS A Journal of Integrative Biology</i> , <b>2006</b> , 10, 114-8                              | 3.8  | 25 |
| 77 | A comparison of the HUPO Brain Proteome Project pilot with other proteomics studies. <i>Proteomics</i> , <b>2006</b> , 6, 5076-86  | 4.8  | 25 |
| 76 | Current status of proteomic standards development. <i>Expert Review of Proteomics</i> , <b>2004</b> , 1, 179-83  | 4.2  | 25 |

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| 75 | Consequences of the discontinuation of the International Protein Index (IPI) database and its substitution by the UniProtKB "complete proteome" sets. <i>Proteomics</i> , <b>2011</b> , 11, 4434-8  | 4.8  | 24 |
| 74 | Advances in the development of common interchange standards for proteomic data. <i>Proteomics</i> , <b>2004</b> , 4, 2363-5   | 4.8  | 24 |
| 73 | Functional annotation of proteins identified in human brain during the HUPO Brain Proteome Project pilot study. <i>Proteomics</i> , <b>2006</b> , 6, 5059-75  | 4.8  | 23 |
| 72 | The impact of focused Gene Ontology curation of specific mammalian systems. <i>PLoS ONE</i> , <b>2011</b> , 6, e27541   | 3.7  | 22 |
| 71 | The Gene Ontology [Providing a Functional Role in Proteomic Studies. <i>Proteomics</i> , <b>2008</b> , 8, n/a-n/a   | 4.8  | 22 |
| 70 | Evidence standards in experimental and inferential INSDC Third Party Annotation data. <i>OMICS A Journal of Integrative Biology</i> , <b>2006</b> , 10, 105-13                                      | 3.8  | 22 |
| 69 | The HUPO Proteomics Standards Initiative Meeting: Towards Common Standards for Exchanging Proteomics Data. <i>Comparative and Functional Genomics</i> , <b>2003</b> , 4, 16-9                       |      | 22 |
| 68 | Dasty and UniProt DAS: a perfect pair for protein feature visualization. <i>Bioinformatics</i> , <b>2005</b> , 21, 3198-9   | 7.2  | 22 |
| 67 | Annotating the human proteome. <i>Molecular and Cellular Proteomics</i> , <b>2005</b> , 4, 435-40   | 7.6  | 22 |
| 66 | MINT and IntAct contribute to the Second BioCreative challenge: serving the text-mining community with high quality molecular interaction data. <i>Genome Biology</i> , <b>2008</b> , 9 Suppl 2, S5 | 18.3 | 21 |
| 65 | Towards data management of the HUPO Human Brain Proteome Project pilot phase. <i>Proteomics</i> , <b>2004</b> , 4, 2361-2   | 4.8  | 21 |
| 64 | The European Bioinformatics Institute in 2018: tools, infrastructure and training. <i>Nucleic Acids Research</i> , <b>2019</b> , 47, D15-D22  | 20.1 | 21 |
| 63 | The Integr8 project--a resource for genomic and proteomic data. <i>In Silico Biology</i> , <b>2005</b> , 5, 179-85  | 2    | 21 |
| 62 | UniSave: the UniProtKB sequence/annotation version database. <i>Bioinformatics</i> , <b>2006</b> , 22, 1284-5   | 7.2  | 20 |
| 61 | Analysis of the experimental detection of central nervous system-related genes in human brain and cerebrospinal fluid datasets. <i>Proteomics</i> , <b>2008</b> , 8, 1138-48                        | 4.8  | 18 |
| 60 | The importance of uniformity in reporting protein-function data. <i>Trends in Biochemical Sciences</i> , <b>2005</b> , 30, 11-2   | 10.3 | 18 |
| 59 | The role SWISS-PROT and TrEMBL play in the genome research environment. <i>Journal of Biotechnology</i> , <b>2000</b> , 78, 221-34  | 3.7  | 18 |
| 58 | The European Bioinformatics Institute in 2020: building a global infrastructure of interconnected data resources for the life sciences. <i>Nucleic Acids Research</i> , <b>2020</b> , 48, D17-D23   | 20.1 | 18 |



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| 57 | A large-scale protein-function database. <i>Nature Chemical Biology</i> , <b>2010</b> , 6, 785   | 11.7 | 17 |
| 56 | The COVID-19 Data Portal: accelerating SARS-CoV-2 and COVID-19 research through rapid open access data sharing. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, W619-W623  | 20.1 | 17 |
| 55 | Use of Gene Ontology Annotation to understand the peroxisome proteome in humans. <i>Database: the Journal of Biological Databases and Curation</i> , <b>2013</b> , 2013, bas062  | 5    | 16 |
| 54 | Representing kidney development using the gene ontology. <i>PLoS ONE</i> , <b>2014</b> , 9, e99864   | 3.7  | 15 |
| 53 | Bioinformatics database infrastructure for biotechnology research. <i>Journal of Biotechnology</i> , <b>2006</b> , 124, 629-39   | 3.7  | 15 |
| 52 | Tools and resources for identifying protein families, domains and motifs. <i>Genome Biology</i> , <b>2002</b> , 3, REVIEWS20015  | 10.5 | 15 |
| 51 | A guide to UniProt for protein scientists. <i>Methods in Molecular Biology</i> , <b>2011</b> , 694, 25-35  | 1.4  | 14 |
| 50 | Getting a grip on proteomics data - Proteomics Data Collection (ProDaC). <i>Proteomics</i> , <b>2009</b> , 9, 3928-33  | 4.8  | 14 |
| 49 | Progress in Establishing Common Standards for Exchanging Proteomics Data: The Second Meeting of the HUPO Proteomics Standards Initiative. <i>Comparative and Functional Genomics</i> , <b>2003</b> , 4, 203-6                        |      | 14 |
| 48 | 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> , <b>2005</b> , 186-96 | 1.3  | 14 |
| 47 | The Renal Gene Ontology Annotation Initiative. <i>Organogenesis</i> , <b>2010</b> , 6, 71-5  | 1.7  | 13 |
| 46 | Gaining knowledge from previously unexplained spectra-application of the PTM-Explorer software to detect PTM in HUPO BPP MS/MS data. <i>Proteomics</i> , <b>2006</b> , 6, 5048-58  | 4.8  | 13 |
| 45 | Human Proteome Organization Proteomics Standards Initiative. <i>Molecular and Cellular Proteomics</i> , <b>2007</b> , 6, 1666-1667   | 7.6  | 13 |
| 44 | The EMBL Nucleotide Sequence and Genome Reviews Databases. <i>Methods in Molecular Biology</i> , <b>2007</b> , 406, 1-21   | 1.4  | 12 |
| 43 | Cardiovascular GO annotation initiative year 1 report: why cardiovascular GO?. <i>Proteomics</i> , <b>2008</b> , 8, 1950-38  | 4.3  | 12 |
| 42 | 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> , <b>2006</b> , 6, 4439-43   | 4.8  | 12 |
| 41 | The European Bioinformatics Institute: empowering cooperation in response to a global health crisis. <i>Nucleic Acids Research</i> , <b>2021</b> , 49, D29-D37   | 20.1 | 12 |
| 40 | Protein sequence databases. <i>Advances in Protein Chemistry</i> , <b>2000</b> , 54, 31-71   |      | 11 |

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