

Hans-Werner Mewes

List of Publications by Year in descending order

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106
papers

19,046
citations

26630

56
h-index

27406

106
g-index

107
all docs

107
docs citations

107
times ranked

22234
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|---|------|-----------|
| 1 | The genome sequence of the filamentous fungus <i>Neurospora crassa</i> . <i>Nature</i> , 2003, 422, 859-868. | 27.8 | 1,528 |
| 2 | Insights from the genome of the biotrophic fungal plant pathogen <i>Ustilago maydis</i> . <i>Nature</i> , 2006, 444, 97-101. | 27.8 | 1,113 |
| 3 | Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , 2006, 440, 790-794. | 27.8 | 1,075 |
| 4 | The FunCat, a functional annotation scheme for systematic classification of proteins from whole genomes. <i>Nucleic Acids Research</i> , 2004, 32, 5539-5545. | 14.5 | 988 |
| 5 | The complete DNA sequence of yeast chromosome III. <i>Nature</i> , 1992, 357, 38-46. | 27.8 | 924 |
| 6 | Human metabolic individuality in biomedical and pharmaceutical research. <i>Nature</i> , 2011, 477, 54-60. | 27.8 | 916 |
| 7 | Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of <i>Arabidopsis thaliana</i> . <i>Nature</i> , 1998, 391, 485-488. | 27.8 | 844 |
| 8 | The <i>Fusarium graminearum</i> Genome Reveals a Link Between Localized Polymorphism and Pathogen Specialization. <i>Science</i> , 2007, 317, 1400-1402. | 12.6 | 837 |
| 9 | Genetics Meets Metabolomics: A Genome-Wide Association Study of Metabolite Profiles in Human Serum. <i>PLoS Genetics</i> , 2008, 4, e1000282. | 3.5 | 660 |
| 10 | A genome-wide perspective of genetic variation in human metabolism. <i>Nature Genetics</i> , 2010, 42, 137-141. | 21.4 | 618 |
| 11 | Metabolic Footprint of Diabetes: A Multiplatform Metabolomics Study in an Epidemiological Setting. <i>PLoS ONE</i> , 2010, 5, e13953. | 2.5 | 501 |
| 12 | The MIPS mammalian protein-protein interaction database. <i>Bioinformatics</i> , 2005, 21, 832-834. | 4.1 | 500 |
| 13 | Sequence and analysis of chromosome 4 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 1999, 402, 769-777. | 27.8 | 413 |
| 14 | The genome sequence of the thermoacidophilic scavenger <i>Thermoplasma acidophilum</i> . <i>Nature</i> , 2000, 407, 508-513. | 27.8 | 390 |
| 15 | Complete DNA sequence of yeast chromosome XI. <i>Nature</i> , 1994, 369, 371-378. | 27.8 | 382 |
| 16 | Illuminating the Evolutionary History of Chlamydiae. <i>Science</i> , 2004, 304, 728-730. | 12.6 | 373 |
| 17 | Gene selection from microarray data for cancer classification—a machine learning approach. <i>Computational Biology and Chemistry</i> , 2005, 29, 37-46. | 2.3 | 336 |
| 18 | MPact: the MIPS protein interaction resource on yeast. <i>Nucleic Acids Research</i> , 2006, 34, D436-D441. | 14.5 | 305 |

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|----|---|------|-----------|
| 19 | Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162. | 5.6 | 290 |
| 20 | The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007, 25, 894-898. | 17.5 | 274 |
| 21 | Can we estimate the accuracy of ADME-Tox predictions?. <i>Drug Discovery Today</i> , 2006, 11, 700-707. | 6.4 | 242 |
| 22 | Exome sequencing identifies ACAD9 mutations as a cause of complex I deficiency. <i>Nature Genetics</i> , 2010, 42, 1131-1134. | 21.4 | 234 |
| 23 | Sequence-Based Prediction of Type III Secreted Proteins. <i>PLoS Pathogens</i> , 2009, 5, e1000376. | 4.7 | 230 |
| 24 | MIPS: a database for protein sequences, homology data and yeast genome information. <i>Nucleic Acids Research</i> , 1997, 25, 28-30. | 14.5 | 217 |
| 25 | MIPS: a database for genomes and protein sequences. <i>Nucleic Acids Research</i> , 1999, 27, 44-48. | 14.5 | 197 |
| 26 | The Protein Information Resource: an integrated public resource of functional annotation of proteins. <i>Nucleic Acids Research</i> , 2002, 30, 35-37. | 14.5 | 186 |
| 27 | Sequence and analysis of chromosome 5 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 823-826. | 27.8 | 175 |
| 28 | Combining diverse evidence for gene recognition in completely sequenced bacterial genomes. <i>Nucleic Acids Research</i> , 1998, 26, 2941-2947. | 14.5 | 171 |
| 29 | Toward a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs. <i>Genome Research</i> , 2001, 11, 422-435. | 5.5 | 166 |
| 30 | Development of a <i>Fusarium graminearum</i> Affymetrix GeneChip for profiling fungal gene expression in vitro and in planta. <i>Fungal Genetics and Biology</i> , 2006, 43, 316-325. | 2.1 | 164 |
| 31 | Functional modules by relating protein interaction networks and gene expression. <i>Nucleic Acids Research</i> , 2003, 31, 6283-6289. | 14.5 | 162 |
| 32 | MIPS <i>Arabidopsis thaliana</i> Database (MAtdB): an integrated biological knowledge resource based on the first complete plant genome. <i>Nucleic Acids Research</i> , 2002, 30, 91-93. | 14.5 | 159 |
| 33 | Variations of the C2H2 zinc finger motif in the yeast genome and classification of yeast zinc finger proteins. <i>Nucleic Acids Research</i> , 1997, 25, 2464-2469. | 14.5 | 156 |
| 34 | The PIR-International Protein Sequence Database. <i>Nucleic Acids Research</i> , 1999, 27, 39-43. | 14.5 | 149 |
| 35 | Toward a Catalog of Human Genes and Proteins: Sequencing and Analysis of 500 Novel Complete Protein Coding Human cDNAs. <i>Genome Research</i> , 2001, 11, 422-435. | 5.5 | 147 |
| 36 | Functional analysis of 150 deletion mutants in <i>Saccharomyces cerevisiae</i> by a systematic approach. <i>Molecular Genetics and Genomics</i> , 1999, 262, 683-702. | 2.4 | 143 |

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|----|--|------|-----------|
| 37 | A Rapid Vapor-Phase Acid (Hydrochloric Acid and Trifluoroacetic Acid) Hydrolysis of Peptide and Protein. <i>Journal of Biochemistry</i> , 1987, 102, 1593-1597. | 1.7 | 126 |
| 38 | The <i>Fusarium graminearum</i> Genome Reveals More Secondary Metabolite Gene Clusters and Hints of Horizontal Gene Transfer. <i>PLoS ONE</i> , 2014, 9, e110311. | 2.5 | 124 |
| 39 | Bioinformatics Analysis of Targeted Metabolomics—Uncovering Old and New Tales of Diabetic Mice under Medication. <i>Endocrinology</i> , 2008, 149, 3478-3489. | 2.8 | 120 |
| 40 | Molecular evolution of eukaryotic genomes: hemiascomycetous yeast spliceosomal introns. <i>Nucleic Acids Research</i> , 2003, 31, 1121-1135. | 14.5 | 118 |
| 41 | Approaching clinical proteomics: current state and future fields of application in fluid proteomics. <i>Clinical Chemistry and Laboratory Medicine</i> , 2009, 47, 724-44. | 2.3 | 112 |
| 42 | The PEDANT genome database. <i>Nucleic Acids Research</i> , 2003, 31, 207-211. | 14.5 | 110 |
| 43 | The sufficient minimal set of miRNA seed types. <i>Bioinformatics</i> , 2011, 27, 1346-1350. | 4.1 | 110 |
| 44 | PEDANT covers all complete RefSeq genomes. <i>Nucleic Acids Research</i> , 2009, 37, D408-D411. | 14.5 | 97 |
| 45 | PEDANTic genome analysis. <i>Trends in Genetics</i> , 1997, 13, 415-416. | 6.7 | 85 |
| 46 | MIPS: a database for protein sequences and complete genomes. <i>Nucleic Acids Research</i> , 1998, 26, 33-37. | 14.5 | 85 |
| 47 | Functional Characterization of Two Clusters of <i>Brachypodium distachyon</i> UDP-Glycosyltransferases Encoding Putative Deoxynivalenol Detoxification Genes. <i>Molecular Plant-Microbe Interactions</i> , 2013, 26, 781-792. | 2.6 | 85 |
| 48 | MIPS Arabidopsis thaliana Database (MATDB): an integrated biological knowledge resource for plant genomics. <i>Nucleic Acids Research</i> , 2004, 32, 373D-376. | 14.5 | 82 |
| 49 | FGDB: revisiting the genome annotation of the plant pathogen <i>Fusarium graminearum</i> . <i>Nucleic Acids Research</i> , 2011, 39, D637-D639. | 14.5 | 81 |
| 50 | The PIR-International Protein Sequence Database. <i>Nucleic Acids Research</i> , 1998, 26, 27-32. | 14.5 | 79 |
| 51 | FGDB: a comprehensive fungal genome resource on the plant pathogen <i>Fusarium graminearum</i> . <i>Nucleic Acids Research</i> , 2006, 34, D456-D458. | 14.5 | 77 |
| 52 | The PIR-International databases. <i>Nucleic Acids Research</i> , 1993, 21, 3089-3092. | 14.5 | 72 |
| 53 | Protein structural classes in five complete genomes. <i>Nature Structural Biology</i> , 1997, 4, 626-628. | 9.7 | 68 |
| 54 | Sequence and analysis of the Arabidopsis genome. <i>Current Opinion in Plant Biology</i> , 2001, 4, 105-110. | 7.1 | 66 |

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|----|---|------|-----------|
| 55 | PPI spider: A tool for the interpretation of proteomics data in the context of protein-protein interaction networks. <i>Proteomics</i> , 2009, 9, 2740-2749. | 2.2 | 63 |
| 56 | What's in the genome of a filamentous fungus? Analysis of the <i>Neurospora</i> genome sequence. <i>Nucleic Acids Research</i> , 2003, 31, 1944-1954. | 14.5 | 59 |
| 57 | 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, 75A, 816-832. | 1.5 | 52 |
| 58 | Exon discovery by genomic sequence alignment. <i>Bioinformatics</i> , 2002, 18, 777-787. | 4.1 | 51 |
| 59 | The PEDANT genome database in 2005. <i>Nucleic Acids Research</i> , 2004, 33, D308-D310. | 14.5 | 50 |
| 60 | The 2-(dimethylaminostyryl)-1-methylpyridinium cation as indicator of the mitochondrial membrane potential. <i>FEBS Letters</i> , 1981, 131, 7-10. | 2.8 | 46 |
| 61 | Sputnik: a database platform for comparative plant genomics. <i>Nucleic Acids Research</i> , 2003, 31, 128-132. | 14.5 | 44 |
| 62 | Genomic Organization and Molecular Characterization of a Gene Encoding HsPXF, a Human Peroxisomal Farnesylated Protein. <i>Genomics</i> , 1997, 45, 200-210. | 2.9 | 42 |
| 63 | Large Scale Application of Neural Network Based Semantic Role Labeling for Automated Relation Extraction from Biomedical Texts. <i>PLoS ONE</i> , 2009, 4, e6393. | 2.5 | 42 |
| 64 | Conservation of protein-protein interactions - lessons from ascomycota. <i>Trends in Genetics</i> , 2004, 20, 72-76. | 6.7 | 41 |
| 65 | SIMAP - a comprehensive database of pre-calculated protein sequence similarities, domains, annotations and clusters. <i>Nucleic Acids Research</i> , 2010, 38, D223-D226. | 14.5 | 40 |
| 66 | DNA Damage-induced Expression of p53 Suppresses Mitotic Checkpoint Kinase hMps1. <i>Journal of Biological Chemistry</i> , 2006, 281, 8675-8685. | 3.4 | 39 |
| 67 | Uncovering metabolic pathways relevant to phenotypic traits of microbial genomes. <i>Genome Biology</i> , 2009, 10, R28. | 9.6 | 39 |
| 68 | Super paramagnetic clustering of protein sequences. <i>BMC Bioinformatics</i> , 2005, 6, 82. | 2.6 | 37 |
| 69 | How can we deliver the large plant genomes? Strategies and perspectives. <i>Current Opinion in Plant Biology</i> , 2002, 5, 173-177. | 7.1 | 34 |
| 70 | Rare variants in LRRK1 and Parkinson's disease. <i>Neurogenetics</i> , 2014, 15, 49-57. | 1.4 | 33 |
| 71 | TICL - a web tool for network-based interpretation of compound lists inferred by high-throughput metabolomics. <i>FEBS Journal</i> , 2009, 276, 2084-2094. | 4.7 | 30 |
| 72 | Spatiotemporal Expression Control Correlates with Intragenic Scaffold Matrix Attachment Regions (S/MARs) in <i>Arabidopsis thaliana</i> . <i>PLoS Computational Biology</i> , 2006, 2, e21. | 3.2 | 29 |

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|----|--|------|-----------|
| 73 | MITOP: database for mitochondria-related proteins, genes and diseases. <i>Nucleic Acids Research</i> , 1999, 27, 153-155. | 14.5 | 27 |
| 74 | Clearing a path through the jungle: progress in Arabidopsis genomics. <i>BioEssays</i> , 1999, 21, 110-120. | 2.5 | 26 |
| 75 | Large scale analysis of sequences from <i>Neurospora crassa</i> . <i>Journal of Biotechnology</i> , 2002, 94, 3-13. | 3.8 | 25 |
| 76 | PEDANT genome database: 10 years online. <i>Nucleic Acids Research</i> , 2007, 35, D354-D357. | 14.5 | 24 |
| 77 | SIMAP—the database of all-against-all protein sequence similarities and annotations with new interfaces and increased coverage. <i>Nucleic Acids Research</i> , 2014, 42, D279-D284. | 14.5 | 24 |
| 78 | SNAPper: gene order predicts gene function. <i>Bioinformatics</i> , 2002, 18, 1017-1019. | 4.1 | 22 |
| 79 | Stroma-Derived Connective Tissue Growth Factor Maintains Cell Cycle Progression and Repopulation Activity of Hematopoietic Stem Cells In Vitro. <i>Stem Cell Reports</i> , 2015, 5, 702-715. | 4.8 | 21 |
| 80 | Complex Functionality of Gene Groups Identified from High-throughput Data. <i>Journal of Molecular Biology</i> , 2006, 363, 289-296. | 4.2 | 19 |
| 81 | Identification and Characterization of Carboxylesterases from <i>Brachypodium distachyon</i> Deacetylating Trichothecene Mycotoxins. <i>Toxins</i> , 2016, 8, 6. | 3.4 | 17 |
| 82 | Genome-based structural biology. <i>Progress in Biophysics and Molecular Biology</i> , 1999, 72, 1-17. | 2.9 | 16 |
| 83 | Prediction and classification of protein functions. <i>Drug Discovery Today: Technologies</i> , 2006, 3, 145-151. | 4.0 | 16 |
| 84 | Separation of sequences from host-pathogen interface using triplet nucleotide frequencies. <i>Fungal Genetics and Biology</i> , 2007, 44, 231-241. | 2.1 | 16 |
| 85 | A systematic approach to infer biological relevance and biases of gene network structures. <i>Nucleic Acids Research</i> , 2006, 34, e6-e6. | 14.5 | 15 |
| 86 | Structure and organization of the European Yeast Genome Sequencing Network. <i>Journal of Biotechnology</i> , 1995, 41, 131-137. | 3.8 | 13 |
| 87 | Implementing systems medicine within healthcare. <i>Genome Medicine</i> , 2015, 7, 102. | 8.2 | 13 |
| 88 | SmartPhase: Accurate and fast phasing of heterozygous variant pairs for genetic diagnosis of rare diseases. <i>PLoS Computational Biology</i> , 2020, 16, e1007613. | 3.2 | 13 |
| 89 | Beyond the “best” match: machine learning annotation of protein sequences by integration of different sources of information. <i>Bioinformatics</i> , 2008, 24, 621-628. | 4.1 | 12 |
| 90 | Large-scale modeling of condition-specific gene regulatory networks by information integration and inference. <i>Nucleic Acids Research</i> , 2014, 42, e166-e166. | 14.5 | 12 |

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| 91 | PLIPS, an Automatically Collected Database of Protein Lists Reported by Proteomics Studies. <i>Journal of Proteome Research</i> , 2009, 8, 1193-1197. | 3.7 | 10 |
| 92 | Sequence databases: an indispensable source for biotechnological research. <i>Journal of Biotechnology</i> , 1994, 35, 239-256. | 3.8 | 9 |
| 93 | The DICS repository: module-assisted analysis of disease-related gene lists. <i>Bioinformatics</i> , 2009, 25, 830-831. | 4.1 | 9 |
| 94 | Complex phylogenetic profiling reveals fundamental genotype-phenotype associations. <i>Computational Biology and Chemistry</i> , 2008, 32, 412-416. | 2.3 | 8 |
| 95 | An environmental perspective on large-scale genome clustering based on metabolic capabilities. <i>Bioinformatics</i> , 2008, 24, i56-i62. | 4.1 | 7 |
| 96 | A Novel Putative miRNA Target Enhancer Signal. <i>PLoS ONE</i> , 2009, 4, e6473. | 2.5 | 7 |
| 97 | Online genomics facilities in the new millennium. <i>Pharmacogenomics</i> , 2002, 3, 265-271. | 1.3 | 6 |
| 98 | BIOREL: The benchmark resource to estimate the relevance of the gene networks. <i>FEBS Letters</i> , 2006, 580, 844-848. | 2.8 | 5 |
| 99 | Protein sequence databases: database management, data structures and data access. <i>Biochemical Society Transactions</i> , 1989, 17, 843-845. | 3.4 | 3 |
| 100 | Exploiting scale-free information from expression data for cancer classification. <i>Computational Biology and Chemistry</i> , 2005, 29, 288-293. | 2.3 | 3 |
| 101 | PRIME: A graphical interface for integrating genomic/proteomic databases. <i>Proteomics</i> , 2005, 5, 76-80. | 2.2 | 3 |
| 102 | Resources and Tools for Investigating Biomolecular Networks in Mammals. <i>Current Pharmaceutical Design</i> , 2006, 12, 3723-34. | 1.9 | 3 |
| 103 | FunCat functional inference with belief propagation and feature integration. <i>Computational Biology and Chemistry</i> , 2008, 32, 375-377. | 2.3 | 3 |
| 104 | The bioinformatics of the yeast genome—A historical perspective. <i>Yeast</i> , 2019, 36, 161-165. | 1.7 | 3 |
| 105 | 3 The Bioinformatics of the Yeast Genome. <i>Methods in Microbiology</i> , 1998, 26, 33-51. | 0.8 | 2 |
| 106 | Network-based SNP meta-analysis identifies joint and disjoint genetic features across common human diseases. <i>BMC Genomics</i> , 2012, 13, 490. | 2.8 | 1 |