

# 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	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
2	The bioinformatics of the yeast genome—A historical perspective. <i>Yeast</i> , 2019, 36, 161-165.	1.7	3
3	Identification and Characterization of Carboxylesterases from <i>Brachypodium distachyon</i> Deacetylating Trichothecene Mycotoxins. <i>Toxins</i> , 2016, 8, 6.	3.4	17
4	Implementing systems medicine within healthcare. <i>Genome Medicine</i> , 2015, 7, 102.	8.2	13
5	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
6	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
7	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
8	Rare variants in LRRK1 and Parkinson's disease. <i>Neurogenetics</i> , 2014, 15, 49-57.	1.4	33
9	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
10	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
11	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
12	Human metabolic individuality in biomedical and pharmaceutical research. <i>Nature</i> , 2011, 477, 54-60.	27.8	916
13	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
14	The sufficient minimal set of miRNA seed types. <i>Bioinformatics</i> , 2011, 27, 1346-1350.	4.1	110
15	A genome-wide perspective of genetic variation in human metabolism. <i>Nature Genetics</i> , 2010, 42, 137-141.	21.4	618
16	Exome sequencing identifies ACAD9 mutations as a cause of complex I deficiency. <i>Nature Genetics</i> , 2010, 42, 1131-1134.	21.4	234
17	Metabolic Footprint of Diabetes: A Multiplatform Metabolomics Study in an Epidemiological Setting. <i>PLoS ONE</i> , 2010, 5, e13953.	2.5	501
18	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

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19	Large Scale Application of Neural Network Based Semantic Role Labeling for Automated Relation Extraction from Biomedical Texts. PLoS ONE, 2009, 4, e6393.	2.5	42
20	A Novel Putative miRNA Target Enhancer Signal. PLoS ONE, 2009, 4, e6473.	2.5	7
21	Approaching clinical proteomics: current state and future fields of application in fluid proteomics. Clinical Chemistry and Laboratory Medicine, 2009, 47, 724-44.	2.3	112
22	PEDANT covers all complete RefSeq genomes. Nucleic Acids Research, 2009, 37, D408-D411.	14.5	97
23	Sequence-Based Prediction of Type III Secreted Proteins. PLoS Pathogens, 2009, 5, e1000376.	4.7	230
24	The DICS repository: module-assisted analysis of disease-related gene lists. Bioinformatics, 2009, 25, 830-831.	4.1	9
25	Approaching clinical proteomics: Current state and future fields of application in cellular proteomics. Cytometry Part A: the Journal of the International Society for Analytical Cytology, 2009, 75A, 816-832.	1.5	52
26	PPI spider: A tool for the interpretation of proteomics data in the context of proteinâ€“protein interaction networks. Proteomics, 2009, 9, 2740-2749.	2.2	63
27	TICL â€“ a web tool for networkâ€“based interpretation of compound lists inferred by highâ€“throughput metabolomics. FEBS Journal, 2009, 276, 2084-2094.	4.7	30
28	PLIPS, an Automatically Collected Database of Protein Lists Reported by Proteomics Studies. Journal of Proteome Research, 2009, 8, 1193-1197.	3.7	10
29	Uncovering metabolic pathways relevant to phenotypic traits of microbial genomes. Genome Biology, 2009, 10, R28.	9.6	39
30	FunCat functional inference with belief propagation and feature integration. Computational Biology and Chemistry, 2008, 32, 375-377.	2.3	3
31	Complex phylogenetic profiling reveals fundamental genotypeâ€“phenotype associations. Computational Biology and Chemistry, 2008, 32, 412-416.	2.3	8
32	Bioinformatics Analysis of Targeted Metabolomicsâ€“Uncovering Old and New Tales of Diabetic Mice under Medication. Endocrinology, 2008, 149, 3478-3489.	2.8	120
33	An environmental perspective on large-scale genome clustering based on metabolic capabilities. Bioinformatics, 2008, 24, i56-i62.	4.1	7
34	Beyond the â€˜bestâ€™ match: machine learning annotation of protein sequences by integration of different sources of information. Bioinformatics, 2008, 24, 621-628.	4.1	12
35	Genetics Meets Metabolomics: A Genome-Wide Association Study of Metabolite Profiles in Human Serum. PLoS Genetics, 2008, 4, e1000282.	3.5	660
36	PEDANT genome database: 10 years online. Nucleic Acids Research, 2007, 35, D354-D357.	14.5	24

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37	Separation of sequences from host-pathogen interface using triplet nucleotide frequencies. <i>Fungal Genetics and Biology</i> , 2007, 44, 231-241.	2.1	16
38	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
39	The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007, 25, 894-898.	17.5	274
40	Prediction and classification of protein functions. <i>Drug Discovery Today: Technologies</i> , 2006, 3, 145-151.	4.0	16
41	BIOREL: The benchmark resource to estimate the relevance of the gene networks. <i>FEBS Letters</i> , 2006, 580, 844-848.	2.8	5
42	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
43	Complex Functionality of Gene Groups Identified from High-throughput Data. <i>Journal of Molecular Biology</i> , 2006, 363, 289-296.	4.2	19
44	Deciphering the evolution and metabolism of an anammox bacterium from a community genome. <i>Nature</i> , 2006, 440, 790-794.	27.8	1,075
45	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
46	Can we estimate the accuracy of ADME-Tox predictions?. <i>Drug Discovery Today</i> , 2006, 11, 700-707.	6.4	242
47	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
48	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
49	Resources and Tools for Investigating Biomolecular Networks in Mammals. <i>Current Pharmaceutical Design</i> , 2006, 12, 3723-34.	1.9	3
50	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
51	MPact: the MIPS protein interaction resource on yeast. <i>Nucleic Acids Research</i> , 2006, 34, D436-D441.	14.5	305
52	DNA Damage-induced Expression of p53 Suppresses Mitotic Checkpoint Kinase hMps1. <i>Journal of Biological Chemistry</i> , 2006, 281, 8675-8685.	3.4	39
53	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
54	Exploiting scale-free information from expression data for cancer classification. <i>Computational Biology and Chemistry</i> , 2005, 29, 288-293.	2.3	3

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55	Super paramagnetic clustering of protein sequences. <i>BMC Bioinformatics</i> , 2005, 6, 82.	2.6	37
56	PRIME: A graphical interface for integrating genomic/proteomic databases. <i>Proteomics</i> , 2005, 5, 76-80.	2.2	3
57	The MIPS mammalian protein-protein interaction database. <i>Bioinformatics</i> , 2005, 21, 832-834.	4.1	500
58	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
59	The PEDANT genome database in 2005. <i>Nucleic Acids Research</i> , 2004, 33, D308-D310.	14.5	50
60	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
61	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	5.6	290
62	Conservation of protein-protein interactions lessons from ascomycota. <i>Trends in Genetics</i> , 2004, 20, 72-76.	6.7	41
63	Illuminating the Evolutionary History of Chlamydiae. <i>Science</i> , 2004, 304, 728-730.	12.6	373
64	The genome sequence of the filamentous fungus <i>Neurospora crassa</i> . <i>Nature</i> , 2003, 422, 859-868.	27.8	1,528
65	Functional modules by relating protein interaction networks and gene expression. <i>Nucleic Acids Research</i> , 2003, 31, 6283-6289.	14.5	162
66	Sputnik: a database platform for comparative plant genomics. <i>Nucleic Acids Research</i> , 2003, 31, 128-132.	14.5	44
67	The PEDANT genome database. <i>Nucleic Acids Research</i> , 2003, 31, 207-211.	14.5	110
68	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
69	Molecular evolution of eukaryotic genomes: hemiascomycetous yeast spliceosomal introns. <i>Nucleic Acids Research</i> , 2003, 31, 1121-1135.	14.5	118
70	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
71	SNAPper: gene order predicts gene function. <i>Bioinformatics</i> , 2002, 18, 1017-1019.	4.1	22
72	Online genomics facilities in the new millennium. <i>Pharmacogenomics</i> , 2002, 3, 265-271.	1.3	6

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73	Exon discovery by genomic sequence alignment. <i>Bioinformatics</i> , 2002, 18, 777-787.	4.1	51
74	Large scale analysis of sequences from <i>Neurospora crassa</i> . <i>Journal of Biotechnology</i> , 2002, 94, 3-13.	3.8	25
75	MIPS Arabidopsisthaliana 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
76	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
77	Sequence and analysis of the Arabidopsis genome. <i>Current Opinion in Plant Biology</i> , 2001, 4, 105-110.	7.1	66
78	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
79	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
80	The genome sequence of the thermoacidophilic scavenger <i>Thermoplasma acidophilum</i> . <i>Nature</i> , 2000, 407, 508-513.	27.8	390
81	Sequence and analysis of chromosome 5 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 2000, 408, 823-826.	27.8	175
82	The PIR-International Protein Sequence Database. <i>Nucleic Acids Research</i> , 1999, 27, 39-43.	14.5	149
83	MITOP: database for mitochondria-related proteins, genes and diseases. <i>Nucleic Acids Research</i> , 1999, 27, 153-155.	14.5	27
84	MIPS: a database for genomes and protein sequences. <i>Nucleic Acids Research</i> , 1999, 27, 44-48.	14.5	197
85	Sequence and analysis of chromosome 4 of the plant <i>Arabidopsis thaliana</i> . <i>Nature</i> , 1999, 402, 769-777.	27.8	413
86	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
87	Genome-based structural biology. <i>Progress in Biophysics and Molecular Biology</i> , 1999, 72, 1-17.	2.9	16
88	Clearing a path through the jungle: progress in Arabidopsis genomics. <i>BioEssays</i> , 1999, 21, 110-120.	2.5	26
89	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
90	3 The Bioinformatics of the Yeast Genome. <i>Methods in Microbiology</i> , 1998, 26, 33-51.	0.8	2

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91	The PIR-International Protein Sequence Database. <i>Nucleic Acids Research</i> , 1998, 26, 27-32.	14.5	79
92	Combining diverse evidence for gene recognition in completely sequenced bacterial genomes. <i>Nucleic Acids Research</i> , 1998, 26, 2941-2947.	14.5	171
93	MIPS: a database for protein sequences and complete genomes. <i>Nucleic Acids Research</i> , 1998, 26, 33-37.	14.5	85
94	MIPS: a database for protein sequences, homology data and yeast genome information. <i>Nucleic Acids Research</i> , 1997, 25, 28-30.	14.5	217
95	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
96	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
97	Protein structural classes in five complete genomes. <i>Nature Structural Biology</i> , 1997, 4, 626-628.	9.7	68
98	PEDANTic genome analysis. <i>Trends in Genetics</i> , 1997, 13, 415-416.	6.7	85
99	Structure and organization of the European Yeast Genome Sequencing Network. <i>Journal of Biotechnology</i> , 1995, 41, 131-137.	3.8	13
100	Complete DNA sequence of yeast chromosome XI. <i>Nature</i> , 1994, 369, 371-378.	27.8	382
101	Sequence databases: an indispensable source for biotechnological research. <i>Journal of Biotechnology</i> , 1994, 35, 239-256.	3.8	9
102	The PIR-International databases. <i>Nucleic Acids Research</i> , 1993, 21, 3089-3092.	14.5	72
103	The complete DNA sequence of yeast chromosome III. <i>Nature</i> , 1992, 357, 38-46.	27.8	924
104	Protein sequence databases: database management, data structures and data access. <i>Biochemical Society Transactions</i> , 1989, 17, 843-845.	3.4	3
105	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
106	The 2-(dimethylaminostyryl)-1-methylpyridinium cation as indicator of the mitochondrial membrane potential. <i>FEBS Letters</i> , 1981, 131, 7-10.	2.8	46