

Heinz Himmelbauer

List of Publications by Year in descending order

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122
papers

15,058
citations

87843

38
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19169

118
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125
all docs

125
docs citations

125
times ranked

24283
citing authors

#	ARTICLE	IF	CITATIONS
1	Prediction of <i>NLR</i> resistance genes based on full-length sequence homology. <i>Plant Journal</i> , 2022, 110, 1592-1602.	2.8	13
2	Genomic distances reveal relationships of wild and cultivated beets. <i>Nature Communications</i> , 2022, 13, 2021.	5.8	17
3	Adaptive Evolution in Producing Microtiter Cultivations Generates Genetically Stable <i>Escherichia coli</i> Production Hosts for Continuous Bioprocessing. <i>Biotechnology Journal</i> , 2021, 16, e2000376.	1.8	2
4	Subgenome evolution in allotetraploid plants. <i>Plant Journal</i> , 2021, 106, 672-688.	2.8	23
5	Assembly and characterization of the genome of chard (<i>Beta vulgaris</i> ssp. <i>vulgaris</i> var. <i>cicla</i>). <i>Journal of Biotechnology</i> , 2021, 333, 67-76.	1.9	7
6	Quinoa genome assembly employing genomic variation for guided scaffolding. <i>Theoretical and Applied Genetics</i> , 2021, 134, 3577-3594.	1.8	4
7	Parental origin of the allotetraploid tobacco <i>Nicotiana benthamiana</i> . <i>Plant Journal</i> , 2020, 102, 541-554.	2.8	31
8	Container-aided integrative QTL and RNA-seq analysis of Collaborative Cross mice supports distinct sex-oriented molecular modes of response in obesity. <i>BMC Genomics</i> , 2020, 21, 761.	1.2	7
9	Benchmarking of long-read correction methods. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa037.	1.5	75
10	Comparative genome characterization of the periodontal pathogen <i>Tannerella forsythia</i> . <i>BMC Genomics</i> , 2020, 21, 150.	1.2	9
11	The genome of <i>Ectocarpus subulatus</i> – A highly stress-tolerant brown alga. <i>Marine Genomics</i> , 2020, 52, 100740.	0.4	26
12	Genome and transcriptome characterization of the glycoengineered <i>Nicotiana benthamiana</i> line XT/FT. <i>BMC Genomics</i> , 2019, 20, 594.	1.2	20
13	Genomes of the wild beets <i>Beta patula</i> and <i>Beta vulgaris</i> ssp. <i>maritima</i> . <i>Plant Journal</i> , 2019, 99, 1242-1253.	2.8	28
14	Genetic and Epigenetic Variation across Genes Involved in Energy Metabolism and Mitochondria of Chinese Hamster Ovary Cell Lines. <i>Biotechnology Journal</i> , 2019, 14, e1800681.	1.8	13
15	Comparative transcriptome analysis of a <i>Trichoplusia ni</i> cell line reveals distinct host responses to intracellular and secreted protein products expressed by recombinant baculoviruses. <i>Journal of Biotechnology</i> , 2018, 270, 61-69.	1.9	23
16	nextPARS: parallel probing of RNA structures in Illumina. <i>Rna</i> , 2018, 24, 609-619.	1.6	23
17	A General Protein O-Glycosylation Gene Cluster Encodes the Species-Specific Glycan of the Oral Pathogen <i>Tannerella forsythia</i> : O-Glycan Biosynthesis and Immunological Implications. <i>Frontiers in Microbiology</i> , 2018, 9, 2008.	1.5	23
18	Haplotype selection as an adaptive mechanism in the protozoan pathogen <i>Leishmania donovani</i> . <i>Nature Ecology and Evolution</i> , 2017, 1, 1961-1969.	3.4	95

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19	Dissecting the Effect of Genetic Variation on the Hepatic Expression of Drug Disposition Genes across the Collaborative Cross Mouse Strains. <i>Frontiers in Genetics</i> , 2016, 7, 172.	1.1	12
20	Genome and transcriptome analysis of the Mesoamerican common bean and the role of gene duplications in establishing tissue and temporal specialization of genes. <i>Genome Biology</i> , 2016, 17, 32.	3.8	166
21	Diversification, evolution and methylation of short interspersed nuclear element families in sugar beet and related Amaranthaceae species. <i>Plant Journal</i> , 2016, 85, 229-244.	2.8	29
22	Oligoadenylation of 3' decay intermediates promotes cytoplasmic mRNA degradation in <i>Drosophila</i> cells. <i>Rna</i> , 2016, 22, 428-442.	1.6	12
23	The 474-Kilobase-Pair Complete Genome Sequence of CeV-01B, a Virus Infecting <i>Haptolina</i> (<i>Tj ETQq1 1 0.784314 rgBT /Overlock 0.8 17</i>)	0.8	17
24	Exploiting single-molecule transcript sequencing for eukaryotic gene prediction. <i>Genome Biology</i> , 2015, 16, 184.	3.8	148
25	Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13970-13975.	3.3	192
26	Genomic analysis of the blood attributed to Louis XVI (1754-1793), king of France. <i>Scientific Reports</i> , 2015, 4, 4666.	1.6	16
27	Identification of ALK Gene Alterations in Urothelial Carcinoma. <i>PLoS ONE</i> , 2014, 9, e103325.	1.1	9
28	Differential Expression Patterns of Non-Symbiotic Hemoglobins in Sugar Beet (<i>Beta vulgaris</i> ssp.) <i>Tj ETQq0 0 0 rgBT /Overlock 1.5 21 Tf 50 3</i>	1.5	21
29	Cytosine Methylation of an Ancient Satellite Family in the Wild Beet <i>Beta procumbens</i> . <i>Cytogenetic and Genome Research</i> , 2014, 143, 157-167.	0.6	11
30	Formation of hepatic DNA adducts by methyleugenol in mouse models: drastic decrease by <i>Sult1a1</i> knockout and strong increase by transgenic human <i>SULT1A1/2</i> . <i>Carcinogenesis</i> , 2014, 35, 935-941.	1.3	50
31	The CHH motif in sugar beet satellite DNA: a modulator for cytosine methylation. <i>Plant Journal</i> , 2014, 78, 937-950.	2.8	17
32	Determination of Sulfotransferase Forms Involved in the Metabolic Activation of the Genotoxicant 1-Hydroxymethylpyrene Using Bacterially Expressed Enzymes and Genetically Modified Mouse Models. <i>Chemical Research in Toxicology</i> , 2014, 27, 1060-1069.	1.7	34
33	Profiling of extensively diversified plant LINEs reveals distinct plant-specific subclades. <i>Plant Journal</i> , 2014, 79, 385-397.	2.8	35
34	The genome of the recently domesticated crop plant sugar beet (<i>Beta vulgaris</i>). <i>Nature</i> , 2014, 505, 546-549.	18.7	569
35	Klf4 and Klf5 differentially inhibit mesoderm and endoderm differentiation in embryonic stem cells. <i>Nature Communications</i> , 2014, 5, 3719.	5.8	94
36	Reliable In Silico Identification of Sequence Polymorphisms and Their Application for Extending the Genetic Map of Sugar Beet (<i>Beta vulgaris</i>). <i>PLoS ONE</i> , 2014, 9, e110113.	1.1	18

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37	Highly diverse chromoviruses of <i>Beta vulgaris</i> are classified by chromodomains and chromosomal integration. <i>Mobile DNA</i> , 2013, 4, 8.	1.3	36
38	Microarray and deep sequencing cross-platform analysis of the mirNome and isomiR variation in response to epidermal growth factor. <i>BMC Genomics</i> , 2013, 14, 371.	1.2	33
39	Comparative transcriptomics of early dipteran development. <i>BMC Genomics</i> , 2013, 14, 123.	1.2	41
40	Architecture and evolution of a minute plant genome. <i>Nature</i> , 2013, 498, 94-98.	13.7	293
41	Conventional Knockout of <i>Tbc1d1</i> in Mice Impairs Insulin- and AICAR-Stimulated Glucose Uptake in Skeletal Muscle. <i>Endocrinology</i> , 2013, 154, 3502-3514.	1.4	61
42	Evolutionary reshuffling in the Errantivirus lineage Elbe within the <i>Beta vulgaris</i> genome. <i>Plant Journal</i> , 2012, 72, 636-651.	2.8	26
43	Maturation of mammalian H/ACA box snoRNAs: PAPD5-dependent adenylation and PARN-dependent trimming. <i>Rna</i> , 2012, 18, 958-972.	1.6	133
44	Identification of a mutation in the extracellular domain of the Epidermal Growth Factor Receptor conferring cetuximab resistance in colorectal cancer. <i>Nature Medicine</i> , 2012, 18, 221-223.	15.2	434
45	Induction and Selection of Sox17-Expressing Endoderm Cells Generated from Murine Embryonic Stem Cells. <i>Cells Tissues Organs</i> , 2012, 195, 507-523.	1.3	10
46	Exome sequencing identifies recurrent mutations of the splicing factor SF3B1 gene in chronic lymphocytic leukemia. <i>Nature Genetics</i> , 2012, 44, 47-52.	9.4	893
47	The Role of a Pseudo-Response Regulator Gene in Life Cycle Adaptation and Domestication of Beet. <i>Current Biology</i> , 2012, 22, 1095-1101.	1.8	135
48	Palaeohexaploid ancestry for Caryophyllales inferred from extensive gene-based physical and genetic mapping of the sugar beet genome (<i>Beta vulgaris</i>). <i>Plant Journal</i> , 2012, 70, 528-540.	2.8	58
49	Survey of sugar beet (<i>Beta vulgaris</i> L.) hAT transposons and MITE-like hATpin derivatives. <i>Plant Molecular Biology</i> , 2012, 78, 393-405.	2.0	16
50	Identification of mediator complex 26 (<i>Crsp7</i>) gametologs on platypus X1 and Y5 sex chromosomes: a candidate testis-determining gene in monotremes?. <i>Chromosome Research</i> , 2012, 20, 127-138.	1.0	8
51	Whole-genome sequencing identifies recurrent mutations in chronic lymphocytic leukaemia. <i>Nature</i> , 2011, 475, 101-105.	13.7	1,364
52	p53 Gene Repair with Zinc Finger Nucleases Optimised by Yeast 1-Hybrid and Validated by Solexa Sequencing. <i>PLoS ONE</i> , 2011, 6, e20913.	1.1	34
53	Partial short-read sequencing of a highly inbred Iberian pig and genomics inference thereof. <i>Heredity</i> , 2011, 107, 256-264.	1.2	16
54	Epigenetic profiling of heterochromatic satellite DNA. <i>Chromosoma</i> , 2011, 120, 409-422.	1.0	31

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55	Evaluation of genomic high-throughput sequencing data generated on Illumina HiSeq and Genome Analyzer systems. <i>Genome Biology</i> , 2011, 12, R112.	13.9	513
56	Multiple platform assessment of the EGF dependent transcriptome by microarray and deep tag sequencing analysis. <i>BMC Genomics</i> , 2011, 12, 326.	1.2	19
57	Expression analysis of proline rich 15 (<i>Prr15</i>) in mouse and human gastrointestinal tumors. <i>Molecular Carcinogenesis</i> , 2011, 50, 8-15.	1.3	13
58	Role of Medium- and Short-Chain L-3-Hydroxyacyl-CoA Dehydrogenase in the Regulation of Body Weight and Thermogenesis. <i>Endocrinology</i> , 2011, 152, 4641-4651.	1.4	33
59	Altered tissue distribution of 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine-DNA adducts in mice transgenic for human sulfotransferases 1A1 and 1A2. <i>Carcinogenesis</i> , 2011, 32, 1734-1740.	1.3	29
60	High-throughput identification of genetic markers using representational oligonucleotide microarray analysis. <i>Theoretical and Applied Genetics</i> , 2010, 121, 549-565.	1.8	6
61	Global transcriptomic analysis of murine embryonic stem cell-derived brachyury ⁺ (T) cells. <i>Genes To Cells</i> , 2010, 15, 209-228.	0.5	5
62	International network of cancer genome projects. <i>Nature</i> , 2010, 464, 993-998.	13.7	2,114
63	Strand-specific deep sequencing of the transcriptome. <i>Genome Research</i> , 2010, 20, 989-999.	2.4	76
64	<i>ojoplano</i> -mediated basal constriction is essential for optic cup morphogenesis. <i>Development (Cambridge)</i> , 2009, 136, 2165-2175.	1.2	84
65	Cloning of mouse <i>ojoplano</i> , a reticular cytoplasmic protein expressed during embryonic development. <i>Gene Expression Patterns</i> , 2009, 9, 562-567.	0.3	6
66	Higher-order genome organization in platypus and chicken sperm and repositioning of sex chromosomes during mammalian evolution. <i>Chromosoma</i> , 2009, 118, 53-69.	1.0	22
67	Haplotype divergence in <i>Beta vulgaris</i> and microsynteny with sequenced plant genomes. <i>Plant Journal</i> , 2009, 57, 14-26.	2.8	19
68	The FunGenES Database: A Genomics Resource for Mouse Embryonic Stem Cell Differentiation. <i>PLoS ONE</i> , 2009, 4, e6804.	1.1	54
69	A mouse translocation associated with <i>Caspr5-2</i> disruption and perinatal lethality. <i>Mammalian Genome</i> , 2008, 19, 675-686.	1.0	8
70	Construction and characterization of a sugar beet (<i>Beta vulgaris</i>) fosmid library. <i>Genome</i> , 2008, 51, 948-951.	0.9	25
71	Characterizing the mouse ES cell transcriptome with Illumina sequencing. <i>Genomics</i> , 2008, 92, 187-194.	1.3	79
72	Pronounced Alterations of Cellular Metabolism and Structure Due to Hyper- or Hypo-Osmosis. <i>Journal of Proteome Research</i> , 2008, 7, 3968-3983.	1.8	17

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73	Substantial biases in ultra-short read data sets from high-throughput DNA sequencing. <i>Nucleic Acids Research</i> , 2008, 36, e105.	6.5	914
74	Neuronal functions, feeding behavior, and energy balance in <i>Slc2a3</i> ^{+/-} mice. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2008, 295, E1084-E1094.	1.8	30
75	WDR55 Is a Nucleolar Modulator of Ribosomal RNA Synthesis, Cell Cycle Progression, and Teleost Organ Development. <i>PLoS Genetics</i> , 2008, 4, e1000171.	1.5	23
76	SHARCGS, a fast and highly accurate short-read assembly algorithm for de novo genomic sequencing. <i>Genome Research</i> , 2007, 17, 1697-1706.	2.4	230
77	The DNA sequence of medaka chromosome LG22. <i>Genomics</i> , 2007, 89, 124-133.	1.3	14
78	Disruption and pseudoautosomal localization of the major histocompatibility complex in monotremes. <i>Genome Biology</i> , 2007, 8, R175.	13.9	55
79	Proteomic Shifts in Embryonic Stem Cells with Gene Dose Modifications Suggest the Presence of Balancer Proteins in Protein Regulatory Networks. <i>PLoS ONE</i> , 2007, 2, e1218.	1.1	24
80	Comparative genomics of medaka and fugu. <i>Comparative Biochemistry and Physiology Part D: Genomics and Proteomics</i> , 2006, 1, 6-12.	0.4	7
81	Mobilization and evolutionary history of miniature inverted-repeat transposable elements (MITEs) in <i>Beta vulgaris</i> L.. <i>Chromosome Research</i> , 2006, 14, 831-844.	1.0	31
82	New members of the neurexin superfamily: multiple rodent homologues of the human CASPR5 gene. <i>Mammalian Genome</i> , 2006, 17, 723-731.	1.0	29
83	Positional cloning of the Hybrid sterility 1 gene: fine genetic mapping and evaluation of two candidate genes. <i>Biological Journal of the Linnean Society</i> , 2005, 84, 637-641.	0.7	19
84	Comparison of PCR-based mutation detection methods and application for identification of mouse <i>Sult1a1</i> mutant embryonic stem cell clones using pooled templates. <i>Human Mutation</i> , 2005, 25, 483-490.	1.1	11
85	A proteomic method for the analysis of changes in protein concentrations in response to systemic perturbations using metabolic incorporation of stable isotopes and mass spectrometry. <i>Proteomics</i> , 2005, 5, 3563-3570.	1.3	33
86	MEPD: a resource for medaka gene expression patterns. <i>Bioinformatics</i> , 2005, 21, 3195-3197.	1.8	24
87	Mouse splice mutant generation from ENU-treated ES cells: A gene-driven approach. <i>Genomics</i> , 2005, 85, 557-562.	1.3	8
88	Integrated and Sequence-Ordered BAC- and YAC-Based Physical Maps for the Rat Genome. <i>Genome Research</i> , 2004, 14, 766-779.	2.4	44
89	The Genomic Sequence and Comparative Analysis of the Rat Major Histocompatibility Complex. <i>Genome Research</i> , 2004, 14, 631-639.	2.4	108
90	The Collaborative Cross, a community resource for the genetic analysis of complex traits. <i>Nature Genetics</i> , 2004, 36, 1133-1137.	9.4	1,034

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91	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	13.7	1,943
92	An endoribonuclease-prepared siRNA screen in human cells identifies genes essential for cell division. <i>Nature</i> , 2004, 432, 1036-1040.	13.7	369
93	Divergent genetic and epigenetic post-zygotic isolation mechanisms in <i>Mus</i> and <i>Peromyscus</i> . <i>Journal of Evolutionary Biology</i> , 2004, 17, 453-460.	0.8	29
94	A first generation physical map of the medaka genome in BACs essential for positional cloning and clone-by-clone based genomic sequencing. <i>Mechanisms of Development</i> , 2004, 121, 903-913.	1.7	32
95	Current Status of Medaka Genetics and Genomics. <i>Methods in Cell Biology</i> , 2004, 77, 173-199.	0.5	8
96	Characterization of trimethylpsoralen as a mutagen for mouse embryonic stem cells. <i>Mutation Research - Fundamental and Molecular Mechanisms of Mutagenesis</i> , 2003, 525, 67-76.	0.4	9
97	The nature and identification of quantitative trait loci: a community's view. <i>Nature Reviews Genetics</i> , 2003, 4, 911-916.	7.7	390
98	Physical mapping of the major histocompatibility complex class II and class III regions of the rat. <i>Immunogenetics</i> , 2002, 54, 268-275.	1.2	15
99	Genetic analysis of the mouse brain proteome. <i>Nature Genetics</i> , 2002, 30, 385-393.	9.4	293
100	Advanced Integrated Mouse YAC Map Including BAC Framework. <i>Genome Research</i> , 2001, 11, 2142-2150.	2.4	7
101	UniGene cDNA array-based monitoring of transcriptome changes during mouse placental development. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 13126-13131.	3.3	46
102	Molecular cloning and characterization of murine ICOS and identification of B7h as ICOS ligand. <i>European Journal of Immunology</i> , 2000, 30, 1040-1047.	1.6	162
103	cDNA subtraction cloning reveals novel genes whose temporal and spatial expression indicates association with trophoblast invasion. <i>Developmental Biology</i> , 2000, 222, 158-169.	0.9	46
104	The Mouse <i>Psma1</i> Gene Coding for the $\hat{\pm}$ -Type C2 Proteasome Subunit: Structural and Functional Analysis, Mapping, and Colocalization with <i>Pde3b</i> on Mouse Chromosome 7. <i>Genomics</i> , 2000, 66, 313-323.	1.3	6
105	High-Throughput Scanning of the Rat Genome Using Interspersed Repetitive Sequence-PCR Markers. <i>Genomics</i> , 2000, 69, 287-294.	1.3	16
106	Expression of the von Hippel-Lindau-binding protein-1 (<i>Vbp1</i>) in fetal and adult mouse tissues. <i>Human Molecular Genetics</i> , 1999, 8, 229-236.	1.4	9
107	Panel of Microsatellite Markers for Whole-Genome Scans and Radiation Hybrid Mapping and a Mouse Family Tree. <i>Genome Research</i> , 1999, 9, 878-887.	2.4	30
108	Technology development at the interface of proteome research and genomics: Mapping nonpolymorphic proteins on the physical map of mouse chromosomes. <i>Electrophoresis</i> , 1999, 20, 1027-1032.	1.3	8

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109	Identification and characterization of C90, a novel mouse RNA that lacks an extensive open reading frame. <i>Gene</i> , 1999, 232, 35-42.	1.0	18
110	Comparative Mapping of Mouse and Rat Chromosomes by Fluorescence in Situ Hybridization. <i>Genomics</i> , 1999, 55, 306-313.	1.3	46
111	Refined radiation hybrid map of mouse Chromosome 17. <i>Mammalian Genome</i> , 1998, 9, 807-811.	1.0	6
112	IRS-PCR-based genetic mapping of the huntingtin interacting protein gene (HIP1) on mouse Chromosome 5. <i>Mammalian Genome</i> , 1998, 9, 26-31.	1.0	15
113	Complex probes for high-throughput parallel genetic mapping of genomic mouse BAC clones. <i>Mammalian Genome</i> , 1998, 9, 611-616.	1.0	4
114	Characterization of the Mouse Src Homology 3 Domain Gene Sh3d2con Chr 7 Demonstrates Coexpression with Huntingtin in the Brain and Identifies the Processed Pseudogene Sh3d2c-ps1 on Chr 2. <i>Genomics</i> , 1998, 54, 505-510.	1.3	11
115	Localization of the Human HIP1 Gene Close to the Elastin (ELN) Locus on 7q11.23. <i>Genomics</i> , 1997, 46, 313-315.	1.3	12
116	High-resolution genetic analysis of a deletion on mouse Chromosome 17 extending over the Fused, tufted, and homeobox Nkx2-5 loci. <i>Mammalian Genome</i> , 1994, 5, 814-816.	1.0	13
117	Mouse chromosome 17. <i>Mammalian Genome</i> , 1993, 4, S230-S252.	1.0	18
118	High-Resolution Comparative Mapping of Mouse Chromosome 17. <i>Genomics</i> , 1993, 17, 110-120.	1.3	28
119	Construction of a map of chromosome 16 by using radiation hybrids. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1992, 89, 104-108.	3.3	30
120	The gene for autosomal dominant polycystic kidney disease lies in a 750-kb CpG-rich region. <i>Genomics</i> , 1992, 13, 144-151.	1.3	80
121	Human-mouse homologies in the region of the polycystic kidney disease gene (PKD1). <i>Genomics</i> , 1992, 13, 35-38.	1.3	25
122	Fine genetic localization of the gene for autosomal dominant polycystic kidney disease (PKD1) with respect to physically mapped markers. <i>Genomics</i> , 1992, 13, 152-158.	1.3	37