Morris A Swertz

List of Publications by Year
in descending order

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Version: 2024-02-01

158 papers	33,284 citations	25034 57 h-index	6471 157 g-index
181 all docs	181 docs citations	181 times ranked	58004 citing authors

#	Article	IF	Citations
1	From Inception to ConcePTION: Genesis of a Network to Support Better Monitoring and Communication of Medication Safety During Pregnancy and Breastfeeding. Clinical Pharmacology and Therapeutics, 2022, 111, 321-331.	4.7	30
2	Associations of early-life pet ownership with asthma and allergic sensitization: AÂmeta-analysis of more than 77,000 children from the EU Child Cohort Network. Journal of Allergy and Clinical Immunology, 2022, 150, 82-92.	2.9	21
3	Effect of host genetics on the gut microbiome in 7,738 participants of the Dutch Microbiome Project. Nature Genetics, 2022, 54, 143-151.	21.4	132
4	Genome-wide study of DNA methylation shows alterations in metabolic, inflammatory, and cholesterol pathways in ALS. Science Translational Medicine, 2022, 14, eabj0264.	12.4	38
5	Semantic modelling of common data elements for rare disease registries, and a prototype workflow for their deployment over registry data. Journal of Biomedical Semantics, 2022, 13, 9.	1.6	11
6	LongITools: Dynamic longitudinal exposome trajectories in cardiovascular and metabolic noncommunicable diseases. Environmental Epidemiology, 2022, 6, e184.	3.0	6
7	Road to FAIR genomes: a gap analysis of NGS data generation and sharing in the Netherlands. BMJ Open Science, 2022, 6, e100268.	1.7	2
8	Environmental factors shaping the gut microbiome in a Dutch population. Nature, 2022, 604, 732-739.	27.8	239
9	FAIR Genomes metadata schema promoting Next Generation Sequencing data reuse in Dutch healthcare and research. Scientific Data, 2022, 9, 169.	5.3	8
10	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
11	Lifelines COVID-19 cohort: investigating COVID-19 infection and its health and societal impacts in a Dutch population-based cohort. BMJ Open, 2021, 11, e044474.	1.9	49
12	The EU Child Cohort Networkâ€™s core data: establishing a set of findable, accessible, interoperable and re-usable (FAIR) variables. European Journal of Epidemiology, 2021, 36, 565-580.	5.7	24
13	Strategies in Rapid Genetic Diagnostics of Critically Ill Children: Experiences From a Dutch University Hospital. Frontiers in Pediatrics, 2021, 9, 600556.	1.9	6
14	Feasibility of predicting allele specific expression from DNA sequencing using machine learning. Scientific Reports, 2021, 11, 10606.	3.3	4
15	Solve-RD: systematic pan-European data sharing and collaborative analysis to solve rare diseases. European Journal of Human Genetics, 2021, 29, 1325-1331.	2.8	49
16	FAIRification of data: Great but how?. ISEE Conference Abstracts, 2021, 2021, .	0.0	0
17	Large-scale cis- and trans-eQTL analyses identify thousands of genetic loci and polygenic scores that regulate blood gene expression. Nature Genetics, 2021, 53, 1300-1310.	21.4	590
18	Advancing tools for human early lifecourse exposome research and translation (ATHLETE). Environmental Epidemiology, 2021, 5, e166.	3.0	24

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19	IRF7 and RNH1 are modifying factors of HIV-1 reservoirs: a genome-wide association analysis. BMC Medicine, 2021, 19, 282.	5.5	8
20	The Data Use Ontology to streamline responsible access to human biomedical datasets. Cell Genomics, 2021, 1, 100028.	6.5	31
21	RNA-Sequencing Highlights Inflammation and Impaired Integrity of the Vascular Wall in Brain Arteriovenous Malformations. Stroke, 2020, 51, 268-274.	2.0	22
22	A pipelineâ€friendly software tool for genome diagnostics to prioritize genes by matching patient symptoms to literature. Genetics & Genomics Next, 2020, 1, e10023.	1.5	3
23	The LifeCycle Project-EU Child Cohort Network: a federated analysis infrastructure and harmonized data of more than 250,000 children and parents. European Journal of Epidemiology, 2020, 35, 709-724.	5.7	81
24	Metabolic Age Based on the BBMRI-NL ¹ H-NMR Metabolomics Repository as Biomarker of Age-related Disease. Circulation Genomic and Precision Medicine, 2020, 13, 541-547.	3.6	50
25	CAPICE: a computational method for Consequence-Agnostic Pathogenicity Interpretation of Clinical Exome variations. Genome Medicine, 2020, 12, 75.	8.2	30
26	Gene-educational attainment interactions in a multi-ancestry genome-wide meta-analysis identify novel blood pressure loci. Molecular Psychiatry, 2020, 26, 2111-2125.	7.9	17
27	Refining Attention-Deficit/Hyperactivity Disorder and Autism Spectrum Disorder Genetic Loci by Integrating Summary Data From Genome-wide Association, Gene Expression, and DNA Methylation Studies. Biological Psychiatry, 2020, 88, 470-479.	1.3	14
28	BBMRI-ERICâ€™s contributions to research and knowledge exchange on COVID-19. European Journal of Human Genetics, 2020, 28, 728-731.	2.8	17
29	Deconvolution of bulk blood eQTL effects into immune cell subpopulations. BMC Bioinformatics, 2020, 21, 243.	2.6	38
30	Lack of Association Between Genetic Variants at ACE2 and TMPRSS2 Genes Involved in SARS-CoV-2 Infection and Human Quantitative Phenotypes. Frontiers in Genetics, 2020, 11, 613.	2.3	45
31	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	1.6	5
32	Implementing Individually Tailored Prescription of Physical Activity in Routine Clinical Care: Protocol of the Physicians Implement Exercise = Medicine (PIE=M) Development and Implementation Project. JMIR Research Protocols, 2020, 9, e19397.	1.0	8
33	Dutch genome diagnostic laboratories accelerated and improved variant interpretation and increased accuracy by sharing data. Human Mutation, 2019, 40, 2230-2238.	2.5	32
34	Improving the diagnostic yield of exome- sequencing by predicting geneâ€“phenotype associations using large-scale gene expression analysis. Nature Communications, 2019, 10, 2837.	12.8	107
35	Gene Mosaicism Screening Using Single-Molecule Molecular Inversion Probes in Routine Diagnostics for Systemic Autoinflammatory Diseases. Journal of Molecular Diagnostics, 2019, 21, 943-950.	2.8	5
36	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84

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37	Multi-ancestry sleep-by-SNP interaction analysis in 126,926 individuals reveals lipid loci stratified by sleep duration. Nature Communications, 2019, 10, 5121.	12.8	62
38	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	16.3	69
39	Occupational exposure to gases/fumes and mineral dust affect DNA methylation levels of genes regulating expression. Human Molecular Genetics, 2019, 28, 2477-2485.	2.9	9
40	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. Biological Psychiatry, 2019, 86, 599-607.	1.3	47
41	MOLGENIS research: advanced bioinformatics data software for non-bioinformaticians. Bioinformatics, 2019, 35, 1076-1078.	4.1	58
42	The 1000IBD project: multi-omics data of 1000 inflammatory bowel disease patients; data release 1. BMC Gastroenterology, 2019, 19, 5.	2.0	68
43	The Interaction of Genetic Predisposition and Socioeconomic Position With Type 2 Diabetes Mellitus: Cross-Sectional and Longitudinal Analyses From the Lifelines Cohort and Biobank Study. Psychosomatic Medicine, 2018, 80, 252-262.	2.0	6
44	MYO5B,STX3, andSTXBP2mutations reveal a common disease mechanism that unifies a subset of congenital diarrheal disorders: A mutation update. Human Mutation, 2018, 39, 333-344.	2.5	48
45	New workflow for classification of genetic variantsâ€™ pathogenicity applied to hereditary recurrent fevers by the International Study Group for Systemic Autoinflammatory Diseases (INSAID). Journal of Medical Genetics, 2018, 55, 530-537.	3.2	117
46	Single-cell RNA sequencing identifies celltype-specific cis-eQTLs and co-expression QTLs. Nature Genetics, 2018, 50, 493-497.	21.4	289
47	Runningâ€wheel activity delays mitochondrial respiratory flux decline in aging mouse muscle via a postâ€transcriptional mechanism. Aging Cell, 2018, 17, e12700.	6.7	31
48	NIPTeR: an R package for fast and accurate trisomy prediction in non-invasive prenatal testing. BMC Bioinformatics, 2018, 19, 531.	2.6	7
49	Genetic analysis of over 1 million people identifies 535 new loci associated with blood pressure traits. Nature Genetics, 2018, 50, 1412-1425.	21.4	924
50	Creating Transparent and Reproducible Pipelines: Best Practices for Tools, Data, and Workflow Management Systems. , 2018, , 15-43.		1
51	The phenotypic spectrum of proximal 6q deletions based on a large cohort derived from social media and literature reports. European Journal of Human Genetics, 2018, 26, 1478-1489.	2.8	31
52	GAVIN: Gene-Aware Variant INterpretation for medical sequencing. Genome Biology, 2017, 18, 6.	8.8	55
53	Missing heritability: is the gap closing? An analysis of 32 complex traits in the Lifelines Cohort Study. European Journal of Human Genetics, 2017, 25, 877-885.	2.8	67
54	Genome-wide meta-analysis of 241,258 adults accounting for smoking behaviour identifies novel loci for obesity traits. Nature Communications, 2017, 8, 14977.	12.8	169

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55	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
56	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	21.4	390
57	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	21.4	363
58	Novel Algorithms for Improved Sensitivity in Non-Invasive Prenatal Testing. Scientific Reports, 2017, 7, 1838.	3.3	14
59	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
60	Rapid Targeted Genomics in Critically Ill Newborns. Pediatrics, 2017, 140, .	2.1	99
61	Novel Blood Pressure Locus and Gene Discovery Using Genome-Wide Association Study and Expression Data Sets From Blood and the Kidney. Hypertension, 2017, 70, .	2.7	123
62	BiobankUniverse: automatic matchmaking between datasets for biobank data discovery and integration. Bioinformatics, 2017, 33, 3627-3634.	4.1	3
63	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	6.2	154
64	Impact of common genetic determinants of Hemoglobin A1c on type 2 diabetes risk and diagnosis in ancestrally diverse populations: A transethnic genome-wide meta-analysis. PLoS Medicine, 2017, 14, e1002383.	8.4	341
65	reGenotyper: Detecting mislabeled samples in genetic data. PLoS ONE, 2017, 12, e0171324.	2.5	25
66	Meta-GWAS and Meta-Analysis of Exome Array Studies Do Not Reveal Genetic Determinants of Serum Hepcidin. PLoS ONE, 2016, 11, e0166628.	2.5	2
67	Target and (Astro-)WISE technologies Data federations and its applications. Proceedings of the International Astronomical Union, 2016, 12, 333-340.	0.0	3
68	Inter-individual variability and genetic influences on cytokine responses to bacteria and fungi. Nature Medicine, 2016, 22, 952-960.	30.7	148
69	CoNVaDING: Single Exon Variation Detection in Targeted NGS Data. Human Mutation, 2016, 37, 457-464.	2.5	79
70	Meta-analysis of 49â€…549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant inANGPTL4determining fasting TG levels. Journal of Medical Genetics, 2016, 53, 441-449.	3.2	34
71	BBMRI-ERIC Directory: 515 Biobanks with Over 60 Million Biological Samples. Biopreservation and Biobanking, 2016, 14, 559-562.	1.0	68
72	NIPTRIC: an online tool for clinical interpretation of non-invasive prenatal testing (NIPT) results. Scientific Reports, 2016, 6, 38359.	3.3	10

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73	The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 2016, 3, 160018.	5.3	8,670
74	RNA Sequencing Analysis of Intracranial Aneurysm Walls Reveals Involvement of Lysosomes and Immunoglobulins in Rupture. Stroke, 2016, 47, 1286-1293.	2.0	55
75	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science, 2016, 352, 565-569.	12.6	1,398
76	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
77	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. Genome Biology, 2016, 17, 191.	8.8	120
78	The effect of host genetics on the gut microbiome. Nature Genetics, 2016, 48, 1407-1412.	21.4	672
79	Understanding human immune function using the resources from the Human Functional Genomics Project. Nature Medicine, 2016, 22, 831-833.	30.7	63
80	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
81	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74
82	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99
83	Differential Effects of Environmental and Genetic Factors on T and B Cell Immune Traits. Cell Reports, 2016, 17, 2474-2487.	6.4	154
84	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
85	A Functional Genomics Approach to Understand Variation in Cytokine Production in Humans. Cell, 2016, 167, 1099-1110.e14.	28.9	275
86	Host and Environmental Factors Influencing Individual Human Cytokine Responses. Cell, 2016, 167, 1111-1124.e13.	28.9	364
87	MOLGENIS/connect: a system for semi-automatic integration of heterogeneous phenotype data with applications in biobanks. Bioinformatics, 2016, 32, 2176-2183.	4.1	12
88	Toward Global Biobank Integration by Implementation of the Minimum Information About Biobank Data Sharing (MIABIS 2.0 Core). Biopreservation and Biobanking, 2016, 14, 298-306.	1.0	66
89	Refined mapping of autoimmune disease associated genetic variants with gene expression suggests an important role for non-coding RNAs. Journal of Autoimmunity, 2016, 68, 62-74.	6.5	64
90	Transmission of human mtDNA heteroplasmy in the Genome of the Netherlands families: support for a variable-size bottleneck. Genome Research, 2016, 26, 417-426.	5.5	84

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91	Association analysis of copy numbers of FC-gamma receptor genes for rheumatoid arthritis and other immune-mediated phenotypes. European Journal of Human Genetics, 2016, 24, 263-270.	2.8	25
92	Whole-exome sequencing is a powerful approach for establishing the etiological diagnosis in patients with intellectual disability and microcephaly. BMC Medical Genomics, 2015, 9, 7.	1.5	65
93	Evaluation of CADD Scores in Curated Mismatch Repair Gene Variants Yields a Model for Clinical Validation and Prioritization. Human Mutation, 2015, 36, 712-719.	2.5	39
94	Cafe Variome: General-Purpose Software for Making Genotype-Phenotype Data Discoverable in Restricted or Open Access Contexts. Human Mutation, 2015, 36, 957-964.	2.5	23
95	Cohort profile: LifeLines DEEP, a prospective, general population cohort study in the northern Netherlands: study design and baseline characteristics. BMJ Open, 2015, 5, e006772.	1.9	207
96	Fine mapping the CETP region reveals a common intronic insertion associated to HDL-C. Npj Aging and Mechanisms of Disease, 2015, 1, 15011.	4.5	8
97	SORTA: a system for ontology-based re-coding and technical annotation of biomedical phenotype data. Database: the Journal of Biological Databases and Curation, 2015, 2015, bav089.	3.0	26
98	PyPedia: using the wiki paradigm as crowd sourcing environment for bioinformatics protocols. Source Code for Biology and Medicine, 2015, 10, 14.	1.7	3
99	Calling genotypes from public RNA-sequencing data enables identification of genetic variants that affect gene-expression levels. Genome Medicine, 2015, 7, 30.	8.2	91
100	Lessons Learned from Whole Exome Sequencing in Multiplex Families Affected by a Complex Genetic Disorder, Intracranial Aneurysm. PLoS ONE, 2015, 10, e0121104.	2.5	32
101	The Influence of Age and Sex on Genetic Associations with Adult Body Size and Shape: A Large-Scale Genome-Wide Interaction Study. PLoS Genetics, 2015, 11, e1005378.	3.5	331
102	BiobankConnect: software to rapidly connect data elements for pooled analysis across biobanks using ontological and lexical indexing. Journal of the American Medical Informatics Association: JAMIA, 2015, 22, 65-75.	4.4	24
103	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
104	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
105	The ARVD/C Genetic Variants Database: 2014 Update. Human Mutation, 2015, 36, 403-410.	2.5	77
106	Cohort Profile: LifeLines, a three-generation cohort study and biobank. International Journal of Epidemiology, 2015, 44, 1172-1180.	1.9	578
107	Population-specific genotype imputations using minimac or IMPUTE2. Nature Protocols, 2015, 10, 1285-1296.	12.0	84
108	Improving Phenotypic Prediction by Combining Genetic and Epigenetic Associations. American Journal of Human Genetics, 2015, 97, 75-85.	6.2	116

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109	State-of-the-Art and Future Challenges in the Integration of Biobank Catalogues. Lecture Notes in Computer Science, 2015, , 261-273.	1.3	16
110	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
111	Genome-wide patterns and properties of de novo mutations in humans. Nature Genetics, 2015, 47, 822-826.	21.4	384
112	Molgenis-impute: imputation pipeline in a box. BMC Research Notes, 2015, 8, 359.	1.4	8
113	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
114	Estimation of Genetic Relationships Between Individuals Across Cohorts and Platforms: Application to Childhood Height. Behavior Genetics, 2015, 45, 514-528.	2.1	20
115	The Hybrid Synthetic Microdata Platform: A Method for Statistical Disclosure Control. Biopreservation and Biobanking, 2015, 13, 178-182.	1.0	1
116	Worm variation made accessible. Worm, 2014, 3, e28357.	1.0	11
117	Improved imputation quality of low-frequency and rare variants in European samples using the â€˜Genome of The Netherlandsâ€™. European Journal of Human Genetics, 2014, 22, 1321-1326.	2.8	92
118	Genotype harmonizer: automatic strand alignment and format conversion for genotype data integration. BMC Research Notes, 2014, 7, 901.	1.4	122
119	WormQTLHDâ€”a web database for linking human disease to natural variation data inC. elegans. Nucleic Acids Research, 2014, 42, D794-D801.	14.5	20
120	Fine mapping of the celiac disease-associated LPP locus reveals a potential functional variant. Human Molecular Genetics, 2014, 23, 2481-2489.	2.9	32
121	The prevalence of metabolic syndrome and metabolically healthy obesity in Europe: a collaborative analysis of ten large cohort studies. BMC Endocrine Disorders, 2014, 14, 9.	2.2	440
122	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	2.8	246
123	Defining the role of common variation in the genomic and biological architecture of adult human height. Nature Genetics, 2014, 46, 1173-1186.	21.4	1,818
124	Consensus and conflict cards for metabolic pathway databases. BMC Systems Biology, 2013, 7, 50.	3.0	10
125	Deleterious Alleles in the Human Genome Are on Average Younger Than Neutral Alleles of the Same Frequency. PLoS Genetics, 2013, 9, e1003301.	3.5	63
126	An Overview and Online Registry of Microvillus Inclusion Disease Patients and theirMYO5BMutations. Human Mutation, 2013, 34, 1597-1605.	2.5	62

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127	WormQTLâ€"public archive and analysis web portal for natural variation data in Caenorhabditis spp. Nucleic Acids Research, 2012, 41, D738-D743.	14.5	33
128	Bioinformatics tools and database resources for systems genetics analysis in mice--a short review and an evaluation of future needs. Briefings in Bioinformatics, 2012, 13, 135-142.	6.5	11
129	xQTL workbench: a scalable web environment for multi-level QTL analysis. Bioinformatics, 2012, 28, 1042-1044.	4.1	16
130	Mutations in potassium channel kcnd3 cause spinocerebellar ataxia type 19. Annals of Neurology, 2012, 72, 870-880.	5.3	121
131	VarioML framework for comprehensive variation data representation and exchange. BMC Bioinformatics, 2012, 13, 254.	2.6	17
132	Diagnostic interpretation of array data using public databases and internet sources. Human Mutation, 2012, 33, 930-940.	2.5	87
133	Observ-OM and Observ-TAB: Universal syntax solutions for the integration, search, and exchange of phenotype and genotype information. Human Mutation, 2012, 33, 867-873.	2.5	18
134	Mutation update on the CHD7 gene involved in CHARGE syndrome. Human Mutation, 2012, 33, 1149-1160.	2.5	224
135	PeakML/mzMatch: A File Format, Java Library, R Library, and Tool-Chain for Mass Spectrometry Data Analysis. Analytical Chemistry, 2011, 83, 2786-2793.	6.5	305
136	OntoCAT - an integrated programming toolkit for common ontology application tasks. Nature Precedings, 2011, , .	0.1	0
137	OntoCAT -- simple ontology search and integration in Java, R and REST/JavaScript. BMC Bioinformatics, 2011, 12, 218.	2.6	30
138	The international dystrophic epidermolysis bullosa patient registry: An online database of dystrophic epidermolysis bullosa patients and their COL7A1 mutations. Human Mutation, 2011, 32, 1100-1107.	2.5	74
139	Towards a MOLGENIS Based Computational Framework. , 2011, , .		4
140	<tt>ontoCAT</tt>: an R package for ontology traversal and search. Bioinformatics, 2011, 27, 2468-2470.	4.1	9
141	Modifiers of mutant huntingtin aggregationfunctional conservation of C. elegans-modifiers of polyglutamine aggregation. PLOS Currents, 2011, 3, RRN1255.	1.4	20
142	The MOLGENIS toolkit: rapid prototyping of biosoftware at the push of a button. BMC Bioinformatics, 2010, 11, S12.	2.6	102
143	Towards the integration of mouse databases - definition and implementation of solutions to two use-cases in mouse functional genomics. BMC Research Notes, 2010, 3, 16.	1.4	3
144	Next-Gen Databasing Links Mutations with Prognosis and Clinical Outcome. Human Mutation, 2010, 31, v-v.	2.5	0

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145	Mouse Resource Browser–a database of mouse databases. Database: the Journal of Biological Databases and Curation, 2010, 2010, baq010-baq010.	3.0	3
146	Global Genetic Robustness of the Alternative Splicing Machinery in Caenorhabditis elegans. Genetics, 2010, 186, 405-410.	2.9	55
147	XGAP: a uniform and extensible data model and software platform for genotype and phenotype experiments. Genome Biology, 2010, 11, R27.	9.6	20
148	designGG: an R-package and web tool for the optimal design of genetical genomics experiments. BMC Bioinformatics, 2009, 10, 188.	2.6	10
149	Neurodegenerative diseases: Lessons from genomeâ€wide screens in small model organisms. EMBO Molecular Medicine, 2009, 1, 360-370.	6.9	72
150	Complex nature of SNP genotype effects on gene expression in primary human leucocytes. BMC Medical Genomics, 2009, 2, 1.	1.5	86
151	Solutions for data integration in functional genomics: a critical assessment and case study. Briefings in Bioinformatics, 2008, 9, 532-544.	6.5	23
152	Towards dynamic database infrastructures for mouse genetics. , 2008, , .		1
153	MetaNetwork: a computational protocol for the genetic study of metabolic networks. Nature Protocols, 2007, 2, 685-694.	12.0	30
154	Beyond standardization: dynamic software infrastructures for systems biology. Nature Reviews Genetics, 2007, 8, 235-243.	16.3	55
155	Combining microarrays and genetic analysis. Briefings in Bioinformatics, 2005, 6, 135-145.	6.5	12
156	Molecular Genetics Information System (MOLGENIS): alternatives in developing local experimental genomics databases. Bioinformatics, 2004, 20, 2075-2083.	4.1	23
157	OntoCAT â€“ a simpler way to access ontology resources. Nature Precedings, 0, , .	0.1	1
158	Interoperability and FAIRness through a novel combination of Web technologies. PeerJ Computer Science, 0, 3, e110.	4.5	58