Morris A Swertz

List of Publications by Year
in descending order

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	The FAIR Guiding Principles for scientific data management and stewardship. Scientific Data, 2016, 3, 160018.	5.3	8,670
2	Genetic studies of body mass index yield new insights for obesity biology. Nature, 2015, 518, 197-206.	27.8	3,823
3	A reference panel of 64,976 haplotypes for genotype imputation. Nature Genetics, 2016, 48, 1279-1283.	21.4	2,421
4	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
5	Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity. Science, 2016, 352, 565-569.	12.6	1,398
6	New genetic loci link adipose and insulin biology to body fat distribution. Nature, 2015, 518, 187-196.	27.8	1,328
7	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
8	The effect of host genetics on the gut microbiome. Nature Genetics, 2016, 48, 1407-1412.	21.4	672
9	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
10	Cohort Profile: LifeLines, a three-generation cohort study and biobank. International Journal of Epidemiology, 2015, 44, 1172-1180.	1.9	578
11	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
12	Disease variants alter transcription factor levels and methylation of their binding sites. Nature Genetics, 2017, 49, 131-138.	21.4	390
13	Genome-wide patterns and properties of de novo mutations in humans. Nature Genetics, 2015, 47, 822-826.	21.4	384
14	Host and Environmental Factors Influencing Individual Human Cytokine Responses. Cell, 2016, 167, 1111-1124.e13.	28.9	364
15	Identification of context-dependent expression quantitative trait loci in whole blood. Nature Genetics, 2017, 49, 139-145.	21.4	363
16	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
17	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
18	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

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19	Single-cell RNA sequencing identifies celltype-specific cis-eQTLs and co-expression QTLs. Nature Genetics, 2018, 50, 493-497.	21.4	289
20	Genome-wide analysis identifies 12 loci influencing human reproductive behavior. Nature Genetics, 2016, 48, 1462-1472.	21.4	284
21	A Functional Genomics Approach to Understand Variation in Cytokine Production in Humans. Cell, 2016, 167, 1099-1110.e14.	28.9	275
22	The Genome of the Netherlands: design, and project goals. European Journal of Human Genetics, 2014, 22, 221-227.	2.8	246
23	Environmental factors shaping the gut microbiome in a Dutch population. Nature, 2022, 604, 732-739.	27.8	239
24	Mutation update on the CHD7 gene involved in CHARGE syndrome. Human Mutation, 2012, 33, 1149-1160.	2.5	224
25	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
26	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
27	Differential Effects of Environmental and Genetic Factors on T and B Cell Immune Traits. Cell Reports, 2016, 17, 2474-2487.	6.4	154
28	DNA Methylation Analysis Identifies Loci for Blood Pressure Regulation. American Journal of Human Genetics, 2017, 101, 888-902.	6.2	154
29	Inter-individual variability and genetic influences on cytokine responses to bacteria and fungi. Nature Medicine, 2016, 22, 952-960.	30.7	148
30	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
31	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
32	Genotype harmonizer: automatic strand alignment and format conversion for genotype data integration. BMC Research Notes, 2014, 7, 901.	1.4	122
33	Mutations in potassium channel *kcnd3* cause spinocerebellar ataxia type 19. Annals of Neurology, 2012, 72, 870-880.	5.3	121
34	Age-related accrual of methylomic variability is linked to fundamental ageing mechanisms. Genome Biology, 2016, 17, 191.	8.8	120
35	New workflow for classification of genetic variants' 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
36	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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37	Characteristics of de novo structural changes in the human genome. Genome Research, 2015, 25, 792-801.	5.5	115
38	Improving the diagnostic yield of exome- sequencing by predicting gene–phenotype associations using large-scale gene expression analysis. Nature Communications, 2019, 10, 2837.	12.8	107
39	The MOLGENIS toolkit: rapid prototyping of biosoftware at the push of a button. BMC Bioinformatics, 2010, 11, S12.	2.6	102
40	A high-quality human reference panel reveals the complexity and distribution of genomic structural variants. Nature Communications, 2016, 7, 12989.	12.8	99
41	Rapid Targeted Genomics in Critically Ill Newborns. Pediatrics, 2017, 140, .	2.1	99
42	1000 Genomes-based meta-analysis identifies 10 novel loci for kidney function. Scientific Reports, 2017, 7, 45040.	3.3	98
43	Improved imputation quality of low-frequency and rare variants in European samples using the 'Genome of The Netherlands'. European Journal of Human Genetics, 2014, 22, 1321-1326.	2.8	92
44	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
45	Diagnostic interpretation of array data using public databases and internet sources. Human Mutation, 2012, 33, 930-940.	2.5	87
46	Complex nature of SNP genotype effects on gene expression in primary human leucocytes. BMC Medical Genomics, 2009, 2, 1.	1.5	86
47	Population-specific genotype imputations using minimac or IMPUTE2. Nature Protocols, 2015, 10, 1285-1296.	12.0	84
48	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
49	Associations of autozygosity with a broad range of human phenotypes. Nature Communications, 2019, 10, 4957.	12.8	84
50	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
51	CoNVaDING: Single Exon Variation Detection in Targeted NGS Data. Human Mutation, 2016, 37, 457-464.	2.5	79
52	The ARVD/C Genetic Variants Database: 2014 Update. Human Mutation, 2015, 36, 403-410.	2.5	77
53	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
54	A principal component meta-analysis on multiple anthropometric traits identifies novel loci for body shape. Nature Communications, 2016, 7, 13357.	12.8	74

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55	Neurodegenerative diseases: Lessons from genome‑wide screens in small model organisms. EMBO Molecular Medicine, 2009, 1, 360-370.	6.9	72
56	Leveraging European infrastructures to access 1 million human genomes by 2022. Nature Reviews Genetics, 2019, 20, 693-701.	16.3	69
57	BBMRI-ERIC Directory: 515 Biobanks with Over 60 Million Biological Samples. Biopreservation and Biobanking, 2016, 14, 559-562.	1.0	68
58	The 1000IBD project: multi-omics data of 1000 inflammatory bowel disease patients; data release 1. BMC Gastroenterology, 2019, 19, 5.	2.0	68
59	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
60	Discovery and refinement of genetic loci associated with cardiometabolic risk using dense imputation maps. Nature Genetics, 2016, 48, 1303-1312.	21.4	66
61	Toward Global Biobank Integration by Implementation of the Minimum Information About Blobank Data Sharing (MIABIS 2.0 Core). Biopreservation and Biobanking, 2016, 14, 298-306.	1.0	66
62	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
63	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
64	CNV-association meta-analysis in 191,161 European adults reveals new loci associated with anthropometric traits. Nature Communications, 2017, 8, 744.	12.8	64
65	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
66	Understanding human immune function using the resources from the Human Functional Genomics Project. Nature Medicine, 2016, 22, 831-833.	30.7	63
67	An Overview and Online Registry of Microvillus Inclusion Disease Patients and their *MYO5B* Mutations. Human Mutation, 2013, 34, 1597-1605.	2.5	62
68	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
69	MOLGENIS research: advanced bioinformatics data software for non-bioinformaticians. Bioinformatics, 2019, 35, 1076-1078.	4.1	58
70	Interoperability and FAIRness through a novel combination of Web technologies. PeerJ Computer Science, 0, 3, e110.	4.5	58
71	Beyond standardization: dynamic software infrastructures for systems biology. Nature Reviews Genetics, 2007, 8, 235-243.	16.3	55
72	Global Genetic Robustness of the Alternative Splicing Machinery in *Caenorhabditis elegans*. Genetics, 2010, 186, 405-410.	2.9	55

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73	RNA Sequencing Analysis of Intracranial Aneurysm Walls Reveals Involvement of Lysosomes and Immunoglobulins in Rupture. Stroke, 2016, 47, 1286-1293.	2.0	55
74	GAVIN: Gene-Aware Variant INterpretation for medical sequencing. Genome Biology, 2017, 18, 6.	8.8	55
75	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
76	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
77	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
78	*MYO5B*, *STX3*, and *STXBP2* mutations 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
79	Epigenome-wide Association Study of Attention-Deficit/Hyperactivity Disorder Symptoms in Adults. Biological Psychiatry, 2019, 86, 599-607.	1.3	47
80	Genome of the Netherlands population-specific imputations identify an ABCA6 variant associated with cholesterol levels. Nature Communications, 2015, 6, 6065.	12.8	45
81	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
82	Meta-analysis uncovers genome-wide significant variants for rapid kidney function decline. Kidney International, 2021, 99, 926-939.	5.2	42
83	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
84	Deconvolution of bulk blood eQTL effects into immune cell subpopulations. BMC Bioinformatics, 2020, 21, 243.	2.6	38
85	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
86	Meta-analysis of 49â€¦549 individuals imputed with the 1000 Genomes Project reveals an exonic damaging variant in *ANGPTL4* determining fasting TG levels. Journal of Medical Genetics, 2016, 53, 441-449.	3.2	34
87	WormQTLâ€"public archive and analysis web portal for natural variation data in Caenorhabditis spp. Nucleic Acids Research, 2012, 41, D738-D743.	14.5	33
88	Fine mapping of the celiac disease-associated LPP locus reveals a potential functional variant. Human Molecular Genetics, 2014, 23, 2481-2489.	2.9	32
89	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
90	Dutch genome diagnostic laboratories accelerated and improved variant interpretation and increased accuracy by sharing data. Human Mutation, 2019, 40, 2230-2238.	2.5	32

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91	Running‑wheel activity delays mitochondrial respiratory flux decline in aging mouse muscle via a post‑transcriptional mechanism. Aging Cell, 2018, 17, e12700.	6.7	31
92	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
93	The Data Use Ontology to streamline responsible access to human biomedical datasets. Cell Genomics, 2021, 1, 100028.	6.5	31
94	MetaNetwork: a computational protocol for the genetic study of metabolic networks. Nature Protocols, 2007, 2, 685-694.	12.0	30
95	OntoCAT -- simple ontology search and integration in Java, R and REST/JavaScript. BMC Bioinformatics, 2011, 12, 218.	2.6	30
96	CAPICE: a computational method for Consequence-Agnostic Pathogenicity Interpretation of Clinical Exome variations. Genome Medicine, 2020, 12, 75.	8.2	30
97	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
98	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
99	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
100	reGenotyper: Detecting mislabeled samples in genetic data. PLoS ONE, 2017, 12, e0171324.	2.5	25
101	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
102	The EU Child Cohort Network'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
103	Advancing tools for human early lifecourse exposome research and translation (ATHLETE). Environmental Epidemiology, 2021, 5, e166.	3.0	24
104	Molecular Genetics Information System (MOLGENIS): alternatives in developing local experimental genomics databases. Bioinformatics, 2004, 20, 2075-2083.	4.1	23
105	Solutions for data integration in functional genomics: a critical assessment and case study. Briefings in Bioinformatics, 2008, 9, 532-544.	6.5	23
106	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
107	RNA-Sequencing Highlights Inflammation and Impaired Integrity of the Vascular Wall in Brain Arteriovenous Malformations. Stroke, 2020, 51, 268-274.	2.0	22
108	Associations of early-life pet ownership with asthma and allergic sensitization: A meta-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

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109	XGAP: a uniform and extensible data model and software platform for genotype and phenotype experiments. Genome Biology, 2010, 11, R27.	9.6	20
110	WormQTLHD—a web database for linking human disease to natural variation data in C. elegans. Nucleic Acids Research, 2014, 42, D794-D801.	14.5	20
111	Estimation of Genetic Relationships Between Individuals Across Cohorts and Platforms: Application to Childhood Height. Behavior Genetics, 2015, 45, 514-528.	2.1	20
112	Modifiers of mutant huntingtin aggregationfunctional conservation of C. elegans-modifiers of polyglutamine aggregation. PLOS Currents, 2011, 3, RRN1255.	1.4	20
113	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
114	VarioML framework for comprehensive variation data representation and exchange. BMC Bioinformatics, 2012, 13, 254.	2.6	17
115	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
116	BBMRI-ERIC's contributions to research and knowledge exchange on COVID-19. European Journal of Human Genetics, 2020, 28, 728-731.	2.8	17
117	xQTL workbench: a scalable web environment for multi-level QTL analysis. Bioinformatics, 2012, 28, 1042-1044.	4.1	16
118	State-of-the-Art and Future Challenges in the Integration of Biobank Catalogues. Lecture Notes in Computer Science, 2015, , 261-273.	1.3	16
119	Novel Algorithms for Improved Sensitivity in Non-Invasive Prenatal Testing. Scientific Reports, 2017, 7, 1838.	3.3	14
120	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
121	Combining microarrays and genetic analysis. Briefings in Bioinformatics, 2005, 6, 135-145.	6.5	12
122	MOLGENIS/connect: a system for semi-automatic integration of heterogeneous phenotype data with applications in biobanks. Bioinformatics, 2016, 32, 2176-2183.	4.1	12
123	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
124	Worm variation made accessible. Worm, 2014, 3, e28357.	1.0	11
125	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
126	designGG: an R-package and web tool for the optimal design of genetical genomics experiments. BMC Bioinformatics, 2009, 10, 188.	2.6	10

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127	Consensus and conflict cards for metabolic pathway databases. BMC Systems Biology, 2013, 7, 50.	3.0	10
128	NIPTRIC: an online tool for clinical interpretation of non-invasive prenatal testing (NIPT) results. Scientific Reports, 2016, 6, 38359.	3.3	10
129	<tt>ontoCAT</tt>: an R package for ontology traversal and search. Bioinformatics, 2011, 27, 2468-2470.	4.1	9
130	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
131	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
132	Molgenis-impute: imputation pipeline in a box. BMC Research Notes, 2015, 8, 359.	1.4	8
133	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
134	IRF7 and RNH1 are modifying factors of HIV-1 reservoirs: a genome-wide association analysis. BMC Medicine, 2021, 19, 282.	5.5	8
135	FAIR Genomes metadata schema promoting Next Generation Sequencing data reuse in Dutch healthcare and research. Scientific Data, 2022, 9, 169.	5.3	8
136	NIPTeR: an R package for fast and accurate trisomy prediction in non-invasive prenatal testing. BMC Bioinformatics, 2018, 19, 531.	2.6	7
137	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
138	Strategies in Rapid Genetic Diagnostics of Critically Ill Children: Experiences From a Dutch University Hospital. Frontiers in Pediatrics, 2021, 9, 600556.	1.9	6
139	LongITools: Dynamic longitudinal exposome trajectories in cardiovascular and metabolic noncommunicable diseases. Environmental Epidemiology, 2022, 6, e184.	3.0	6
140	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
141	The ELIXIR Human Copy Number Variations Community: building bioinformatics infrastructure for research. F1000Research, 2020, 9, 1229.	1.6	5
142	Towards a MOLGENIS Based Computational Framework. , 2011, , .		4
143	Feasibility of predicting allele specific expression from DNA sequencing using machine learning. Scientific Reports, 2021, 11, 10606.	3.3	4
144	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

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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	PyPedia: using the wiki paradigm as crowd sourcing environment for bioinformatics protocols. Source Code for Biology and Medicine, 2015, 10, 14.	1.7	3
147	Target and (Astro-)WISE technologies Data federations and its applications. Proceedings of the International Astronomical Union, 2016, 12, 333-340.	0.0	3
148	BiobankUniverse: automatic matchmaking between datasets for biobank data discovery and integration. Bioinformatics, 2017, 33, 3627-3634.	4.1	3
149	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
150	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
151	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
152	Towards dynamic database infrastructures for mouse genetics. , 2008, , .		1
153	The Hybrid Synthetic Microdata Platform: A Method for Statistical Disclosure Control. Biopreservation and Biobanking, 2015, 13, 178-182.	1.0	1
154	Creating Transparent and Reproducible Pipelines: Best Practices for Tools, Data, and Workflow Management Systems. , 2018, , 15-43.		1
155	OntoCAT â€" a simpler way to access ontology resources. Nature Precedings, 0, , .	0.1	1
156	Next-Gen Databasing Links Mutations with Prognosis and Clinical Outcome. Human Mutation, 2010, 31, v-v.	2.5	0
157	OntoCAT - an integrated programming toolkit for common ontology application tasks. Nature Precedings, 2011, , .	0.1	0
158	FAIRification of data: Great but how?. ISEE Conference Abstracts, 2021, 2021, .	0.0	0