

# Nicola J Mulder

## List of Publications by Year in descending order

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175  
papers

31,807  
citations

71102

41  
h-index

5120

166  
g-index

269  
all docs

269  
docs citations

269  
times ranked

38597  
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	27.8	21,074
2	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009, 37, D211-D215.	14.5	1,712
3	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	14.5	921
4	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003, 31, 315-318.	14.5	640
5	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2004, 33, D201-D205.	14.5	478
6	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007, 35, D224-D228.	14.5	444
7	Enabling the genomic revolution in Africa. <i>Science</i> , 2014, 344, 1346-1348.	12.6	361
8	InterPro and InterProScan. <i>Methods in Molecular Biology</i> , 2007, 396, 59-70.	0.9	339
9	The Gene Ontology Annotation (GOA) Project: Implementation of GO in SWISS-PROT, TrEMBL, and InterPro. <i>Genome Research</i> , 2003, 13, 662-672.	5.5	297
10	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	5.6	290
11	The minimum information required for reporting a molecular interaction experiment (MIMIx). <i>Nature Biotechnology</i> , 2007, 25, 894-898.	17.5	274
12	Genome Sequence of the Tsetse Fly ( <i>Glossina morsitans</i> ): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	12.6	254
13	Curated genome annotation of <i>Oryza sativa</i> ssp. <i>japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	5.5	218
14	High-depth African genomes inform human migration and health. <i>Nature</i> , 2020, 586, 741-748.	27.8	197
15	Genome-wide association study of ancestry-specific TB risk in the South African Coloured population. <i>Human Molecular Genetics</i> , 2014, 23, 796-809.	2.9	162
16	InterPro: An integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002, 3, 225-235.	6.5	155
17	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	12.6	144
18	Microbial Composition Predicts Genital Tract Inflammation and Persistent Bacterial Vaginosis in South African Adolescent Females. <i>Infection and Immunity</i> , 2018, 86, .	2.2	136

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19	Disruption of maternal gut microbiota during gestation alters offspring microbiota and immunity. <i>Microbiome</i> , 2018, 6, 124.	11.1	109
20	Manual GO annotation of predictive protein signatures: the InterPro approach to GO curation. <i>Database: the Journal of Biological Databases and Curation</i> , 2012, 2012, bar068-bar068.	3.0	108
21	H3Africa: current perspectives. <i>Pharmacogenomics and Personalized Medicine</i> , 2018, Volume 11, 59-66.	0.7	101
22	H3ABioNet, a sustainable pan-African bioinformatics network for human heredity and health in Africa. <i>Genome Research</i> , 2016, 26, 271-277.	5.5	94
23	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	6.5	94
24	Function Prediction and Analysis of Mycobacterium tuberculosis Hypothetical Proteins. <i>International Journal of Molecular Sciences</i> , 2012, 13, 7283-7302.	4.1	88
25	Whole-genome sequencing for an enhanced understanding of genetic variation among South Africans. <i>Nature Communications</i> , 2017, 8, 2062.	12.8	88
26	Four simple recommendations to encourage best practices in research software. <i>F1000Research</i> , 2017, 6, 876.	1.6	88
27	The development and application of bioinformatics core competencies to improve bioinformatics training and education. <i>PLoS Computational Biology</i> , 2018, 14, e1005772.	3.2	84
28	Host and Microbiome Genome-Wide Association Studies: Current State and Challenges. <i>Frontiers in Genetics</i> , 2018, 9, 637.	2.3	71
29	The InterPro Database and Tools for Protein Domain Analysis. <i>Current Protocols in Bioinformatics</i> , 2008, 21, Unit 2.7.	25.8	69
30	The H3Africa policy framework: negotiating fairness in genomics. <i>Trends in Genetics</i> , 2015, 31, 117-119.	6.7	65
31	The Proteome Analysis database: a tool for the in silico analysis of whole proteomes. <i>Nucleic Acids Research</i> , 2003, 31, 414-417.	14.5	64
32	From sets to graphs: towards a realistic enrichment analysis of transcriptomic systems. <i>Bioinformatics</i> , 2011, 27, i366-i373.	4.1	64
33	Gene Ontology semantic similarity tools: survey on features and challenges for biological knowledge discovery. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw067.	6.5	63
34	Machine Learning and Network Analyses Reveal Disease Subtypes of Pancreatic Cancer and their Molecular Characteristics. <i>Scientific Reports</i> , 2020, 10, 1212.	3.3	62
35	Bioinformatics Education–Perspectives and Challenges out of Africa. <i>Briefings in Bioinformatics</i> , 2015, 16, 355-364.	6.5	61
36	The European Bioinformatics Institute's data resources. <i>Nucleic Acids Research</i> , 2003, 31, 43-50.	14.5	56

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37	Metabolic gene alterations impact the clinical aggressiveness and drug responses of 32 human cancers. <i>Communications Biology</i> , 2019, 2, 414.	4.4	55
38	Applications of InterPro in protein annotation and genome analysis. <i>Briefings in Bioinformatics</i> , 2002, 3, 285-295.	6.5	54
39	GOBLET: The Global Organisation for Bioinformatics Learning, Education and Training. <i>PLoS Computational Biology</i> , 2015, 11, e1004143.	3.2	52
40	Best practices in bioinformatics training for life scientists. <i>Briefings in Bioinformatics</i> , 2013, 14, 528-537.	6.5	51
41	Modelling the risk of airborne infectious disease using exhaled air. <i>Journal of Theoretical Biology</i> , 2015, 372, 100-106.	1.7	51
42	Development of Bioinformatics Infrastructure for Genomics Research. <i>Global Heart</i> , 2017, 12, 91.	2.3	47
43	A Topology-Based Metric for Measuring Term Similarity in the Gene Ontology. <i>Advances in Bioinformatics</i> , 2012, 2012, 1-17.	5.7	44
44	Information Content-Based Gene Ontology Semantic Similarity Approaches: Toward a Unified Framework Theory. <i>BioMed Research International</i> , 2013, 2013, 1-11.	1.9	43
45	Using biological networks to improve our understanding of infectious diseases. <i>Computational and Structural Biotechnology Journal</i> , 2014, 11, 1-10.	4.1	43
46	Ten simple rules for organizing a webinar series. <i>PLoS Computational Biology</i> , 2019, 15, e1006671.	3.2	43
47	Determining Ancestry Proportions in Complex Admixture Scenarios in South Africa Using a Novel Proxy Ancestry Selection Method. <i>PLoS ONE</i> , 2013, 8, e73971.	2.5	42
48	A Genomic Portrait of Haplotype Diversity and Signatures of Selection in Indigenous Southern African Populations. <i>PLoS Genetics</i> , 2015, 11, e1005052.	3.5	42
49	Profiling the malaria genome: a gene survey of three species of malaria parasite with comparison to other apicomplexan species. <i>Molecular and Biochemical Parasitology</i> , 2001, 118, 201-210.	1.1	40
50	Population-specific common SNPs reflect demographic histories and highlight regions of genomic plasticity with functional relevance. <i>BMC Genomics</i> , 2014, 15, 437.	2.8	40
51	Real-Time Investigation of Tuberculosis Transmission: Developing the Respiratory Aerosol Sampling Chamber (RASC). <i>PLoS ONE</i> , 2016, 11, e0146658.	2.5	40
52	Leveraging crowdsourcing to accelerate global health solutions. <i>Nature Biotechnology</i> , 2019, 37, 848-850.	17.5	36
53	Recent advances in predicting gene-disease associations. <i>F1000Research</i> , 2017, 6, 578.	1.6	36
54	A review of clinical pharmacogenetics Studies in African populations. <i>Personalized Medicine</i> , 2020, 17, 155-170.	1.5	35

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55	Identification of Quantitative Proteomic Differences between Mycobacterium tuberculosis Lineages with Altered Virulence. <i>Frontiers in Microbiology</i> , 2016, 7, 813.	3.5	34
56	Does having a mobile phone matter? Linking phone access among women to health in India: An exploratory analysis of the National Family Health Survey. <i>PLoS ONE</i> , 2020, 15, e0236078.	2.5	34
57	Predicting and Analyzing Interactions between Mycobacterium tuberculosis and Its Human Host. <i>PLoS ONE</i> , 2013, 8, e67472.	2.5	34
58	DaGO-Fun: tool for Gene Ontology-based functional analysis using term information content measures. <i>BMC Bioinformatics</i> , 2013, 14, 284.	2.6	33
59	Information Content-Based Gene Ontology Functional Similarity Measures: Which One to Use for a Given Biological Data Type?. <i>PLoS ONE</i> , 2014, 9, e113859.	2.5	33
60	Developing reproducible bioinformatics analysis workflows for heterogeneous computing environments to support African genomics. <i>BMC Bioinformatics</i> , 2018, 19, 457.	2.6	33
61	Integrated molecular characterisation of the MAPK pathways in human cancers reveals pharmacologically vulnerable mutations and gene dependencies. <i>Communications Biology</i> , 2021, 4, 9.	4.4	32
62	Feeding-Related Gut Microbial Composition Associates With Peripheral T-Cell Activation and Mucosal Gene Expression in African Infants. <i>Clinical Infectious Diseases</i> , 2018, 67, 1237-1246.	5.8	31
63	Hackathons as a means of accelerating scientific discoveries and knowledge transfer. <i>Genome Research</i> , 2018, 28, 759-765.	5.5	31
64	The Data Use Ontology to streamline responsible access to human biomedical datasets. <i>Cell Genomics</i> , 2021, 1, 100028.	6.5	31
65	Designing a course model for distance-based online bioinformatics training in Africa: The H3ABioNet experience. <i>PLoS Computational Biology</i> , 2017, 13, e1005715.	3.2	29
66	A comprehensive survey of models for dissecting local ancestry deconvolution in human genome. <i>Briefings in Bioinformatics</i> , 2019, 20, 1709-1724.	6.5	29
67	Generation and Analysis of Large-Scale Data-Driven <i>Mycobacterium tuberculosis</i> Functional Networks for Drug Target Identification. <i>Advances in Bioinformatics</i> , 2011, 2011, 1-14.	5.7	28
68	A-DaGO-Fun: an adaptable Gene Ontology semantic similarity-based functional analysis tool. <i>Bioinformatics</i> , 2016, 32, 477-479.	4.1	28
69	HIV-exposure, early life feeding practices and delivery mode impacts on faecal bacterial profiles in a South African birth cohort. <i>Scientific Reports</i> , 2018, 8, 5078.	3.3	28
70	Latent Tuberculosis: Models, Computational Efforts and the Pathogen's Regulatory Mechanisms during Dormancy. <i>Frontiers in Bioengineering and Biotechnology</i> , 2013, 1, 4.	4.1	27
71	Proteogenomic Analysis of Mycobacterium smegmatis Using High Resolution Mass Spectrometry. <i>Frontiers in Microbiology</i> , 2016, 7, 427.	3.5	27
72	The Influence of HIV on the Evolution of Mycobacterium tuberculosis. <i>Molecular Biology and Evolution</i> , 2017, 34, 1654-1668.	8.9	27

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73	The African Genomic Medicine Training Initiative (AGMT): Showcasing a Community and Framework Driven Genomic Medicine Training for Nurses in Africa. <i>Frontiers in Genetics</i> , 2019, 10, 1209.	2.3	26
74	A mathematical representation of the development of <i>Mycobacterium tuberculosis</i> active, latent and dormant stages. <i>Journal of Theoretical Biology</i> , 2012, 292, 44-59.	1.7	24
75	Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum) <i>Tj ETQq1 1 0.784314 rgBT /Over</i>	3.2	24
76	Genome-Wide Association Study of Brain Connectivity Changes for Alzheimer's Disease. <i>Scientific Reports</i> , 2020, 10, 1433.	3.3	24
77	Scoring Protein Relationships in Functional Interaction Networks Predicted from Sequence Data. <i>PLoS ONE</i> , 2011, 6, e18607.	2.5	24
78	Tools and resources for identifying protein families, domains and motifs. <i>Genome Biology</i> , 2001, 3, reviews2001.1.	9.6	23
79	Co-infection with <i>Mycobacterium tuberculosis</i> and human immunodeficiency virus: an overview and motivation for systems approaches. <i>Pathogens and Disease</i> , 2013, 69, 101-113.	2.0	23
80	Microbial function and genital inflammation in young South African women at high risk of HIV infection. <i>Microbiome</i> , 2020, 8, 165.	11.1	23
81	A Quick Guide for Building a Successful Bioinformatics Community. <i>PLoS Computational Biology</i> , 2015, 11, e1003972.	3.2	23
82	A web-based protein interaction network visualizer. <i>BMC Bioinformatics</i> , 2014, 15, 129.	2.6	21
83	ancGWAS: a post genome-wide association study method for interaction, pathway and ancestry analysis in homogeneous and admixed populations. <i>Bioinformatics</i> , 2016, 32, 549-556.	4.1	21
84	Genetic modifiers of long-term survival in sickle cell anemia. <i>Clinical and Translational Medicine</i> , 2020, 10, e152.	4.0	21
85	Genomic Research Data Generation, Analysis and Sharing – Challenges in the African Setting. <i>Data Science Journal</i> , 2017, 16, .	1.3	21
86	A broad survey of DNA sequence data simulation tools. <i>Briefings in Functional Genomics</i> , 2020, 19, 49-59.	2.7	20
87	Using the underlying biological organization of the <i>Mycobacterium tuberculosis</i> functional network for protein function prediction. <i>Infection, Genetics and Evolution</i> , 2012, 12, 922-932.	2.3	19
88	Association of Novel Locus With Rheumatic Heart Disease in Black African Individuals. <i>JAMA Cardiology</i> , 2021, 6, 1000.	6.1	18
89	Ensuring best practice in genomics education and evaluation: reporting item standards for education and its evaluation in genomics (RISE2 Genomics). <i>Genetics in Medicine</i> , 2021, 23, 1356-1365.	2.4	17
90	A Genomic and Protein-Protein Interaction Analyses of Nonsyndromic Hearing Impairment in Cameroon Using Targeted Genomic Enrichment and Massively Parallel Sequencing. <i>OMICS A Journal of Integrative Biology</i> , 2017, 21, 90-99.	2.0	16

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91	Development to enable precision medicine in Africa. <i>Personalized Medicine</i> , 2017, 14, 467-470.	1.5	16
92	Accessing Biospecimens from the H3Africa Consortium. <i>Biopreservation and Biobanking</i> , 2017, 15, 95-98.	1.0	15
93	Integrative landscape of dysregulated signaling pathways of clinically distinct pancreatic cancer subtypes. <i>Oncotarget</i> , 2018, 9, 29123-29139.	1.8	15
94	Dasty3, a WEB framework for DAS. <i>Bioinformatics</i> , 2011, 27, 2616-2617.	4.1	14
95	The Sickle Cell Disease Ontology: enabling universal sickle cell-based knowledge representation. <i>Database: the Journal of Biological Databases and Curation</i> , 2019, 2019, .	3.0	14
96	Contribution of microarray data to the advancement of knowledge on the Mycobacterium tuberculosis interactome: Use of the random partial least squares approach. <i>Infection, Genetics and Evolution</i> , 2011, 11, 181-189.	2.3	13
97	Human OMICs and Computational Biology Research in Africa: Current Challenges and Prospects. <i>OMICS A Journal of Integrative Biology</i> , 2021, 25, 213-233.	2.0	13
98	The Development of Computational Biology in South Africa: Successes Achieved and Lessons Learnt. <i>PLoS Computational Biology</i> , 2016, 12, e1004395.	3.2	12
99	A common molecular signature of patients with sickle cell disease revealed by microarray meta-analysis and a genome-wide association study. <i>PLoS ONE</i> , 2018, 13, e0199461.	2.5	12
100	Using Whole Genome Sequencing in an African Subphenotype of Myasthenia Gravis to Generate a Pathogenetic Hypothesis. <i>Frontiers in Genetics</i> , 2019, 10, 136.	2.3	12
101	Contribution of microarray data to the advancement of knowledge on the Mycobacterium tuberculosis interactome: Use of the random partial least squares approach. <i>Infection, Genetics and Evolution</i> , 2011, 11, 725-733.	2.3	11
102	Understanding TB latency using computational and dynamic modelling procedures. <i>Infection, Genetics and Evolution</i> , 2013, 13, 267-283.	2.3	11
103	A Quantitative Approach to Analyzing Genome Reductive Evolution Using Protein-Protein Interaction Networks: A Case Study of Mycobacterium leprae. <i>Frontiers in Genetics</i> , 2016, 7, 39.	2.3	11
104	Sickle cell disease: tipping the balance of genomic research to catalyse discoveries in Africa. <i>Lancet, The</i> , 2017, 389, 2355-2358.	13.7	11
105	Organizing and running bioinformatics hackathons within Africa: The H3ABioNet cloud computing experience. <i>AAS Open Research</i> , 2018, 1, 9.	1.5	11
106	Organizing and running bioinformatics hackathons within Africa: The H3ABioNet cloud computing experience. <i>AAS Open Research</i> , 2018, 1, 9.	1.5	11
107	A systems-level analysis of drug-target-disease associations for drug repositioning. <i>Briefings in Functional Genomics</i> , 2018, 17, 34-41.	2.7	10
108	Using a multiple-delivery-mode training approach to develop local capacity and infrastructure for advanced bioinformatics in Africa. <i>PLoS Computational Biology</i> , 2021, 17, e1008640.	3.2	10

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109	Protein Function Microarrays: Design, Use and Bioinformatic Analysis in Cancer Biomarker Discovery and Quantitation. Translational Bioinformatics, 2013, , 39-74.	0.0	10
110	H3ABioNet: Developing Sustainable Bioinformatics Capacity in Africa. EMBnet Journal, 2017, 23, 886.	0.6	10
111	Revealing the Mutational Spectrum in Southern Africans With Amyotrophic Lateral Sclerosis. Neurology: Genetics, 2022, 8, e654.	1.9	10
112	InterPro. , 2005, , .		9
113	Assessing computational genomics skills: Our experience in the H3ABioNet African bioinformatics network. PLoS Computational Biology, 2017, 13, e1005419.	3.2	9
114	Environmental and social factors impacting on epidemic and endemic tuberculosis: a modelling analysis. Royal Society Open Science, 2018, 5, 170726.	2.4	9
115	Multi-stage Association Analysis of Glioblastoma Gene Expressions with Texture and Spatial Patterns. Lecture Notes in Computer Science, 2019, 11383, 239-250.	1.3	9
116	PPI layouts: BioJS components for the display of Protein-Protein Interactions. F1000Research, 2014, 3, 50.	1.6	9
117	Large-scale data-driven integrative framework for extracting essential targets and processes from disease-associated gene data sets. Briefings in Bioinformatics, 2018, 19, 1141-1152.	6.5	8
118	Assessing exposure to Kilkari: a big data analysis of a large maternal mobile messaging service across 13 states in India. BMJ Global Health, 2021, 6, e005213.	4.7	8
119	The Mycobacterium tuberculosis mysB gene product is a functional equivalent of the Escherichia coli sigma factor, KatF. Gene, 1999, 240, 361-370.	2.2	7
120	IHP-PING“generating integrated human protein“protein interaction networks on-the-fly. Briefings in Bioinformatics, 2021, 22, .	6.5	7
121	H3ABioNet genomic medicine and microbiome data portals hackathon proceedings. Database: the Journal of Biological Databases and Curation, 2021, 2021, .	3.0	7
122	Ten simple rules for forming a scientific professional society. PLoS Computational Biology, 2017, 13, e1005226.	3.2	7
123	iAnn: an event sharing platform for the life sciences. Bioinformatics, 2013, 29, 1919-1921.	4.1	6
124	The use of semantic similarity measures for optimally integrating heterogeneous Gene Ontology data from large scale annotation pipelines. Frontiers in Genetics, 2014, 5, 264.	2.3	6
125	Strategies and opportunities for promoting bioinformatics in Zimbabwe. PLoS Computational Biology, 2018, 14, e1006480.	3.2	6
126	The Hearing Impairment Ontology: A Tool for Unifying Hearing Impairment Knowledge to Enhance Collaborative Research. Genes, 2019, 10, 960.	2.4	6



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127	The H3ABioNet helpdesk: an online bioinformatics resource, enhancing Africa's capacity for genomics research. BMC Bioinformatics, 2019, 20, 741.	2.6	6
128	Hypothalamicâ€‘pituitaryâ€‘adrenal axis suppression in asthma: A glucocorticoid receptor polymorphism may protect. Pediatric Allergy and Immunology, 2021, 32, 273-279.	2.6	6
129	Repeats expansions in ATXN2, NOP56, NIPA1 and ATXN1 are not associated with ALS in Africans. IBRO Neuroscience Reports, 2021, 10, 130-135.	1.6	6
130	Data Management Plans in the genomics research revolution of Africa: Challenges and recommendations. Journal of Biomedical Informatics, 2021, 122, 103900.	4.3	6
131	ANIMA: Association network integration for multiscale analysis. Wellcome Open Research, 2018, 3, 27.	1.8	6
132	Relating Global and Local Connectome Changes to Dementia and Targeted Gene Expression in Alzheimer's Disease. Frontiers in Human Neuroscience, 2021, 15, 761424.	2.0	6
133	Comparative analysis of microbial genomes to study unique and expanded gene families in Mycobacterium tuberculosis. Infection, Genetics and Evolution, 2009, 9, 314-321.	2.3	5
134	myKaryoView: A Light-Weight Client for Visualization of Genomic Data. PLoS ONE, 2011, 6, e26345.	2.5	5
135	A multi-scenario genome-wide medical population genetics simulation framework. Bioinformatics, 2017, 33, 2995-3002.	4.1	5
136	Challenges and Considerations for Delivering Bioinformatics Training in LMICs: Perspectives From Pan-African and Latin American Bioinformatics Networks. Frontiers in Education, 2021, 6, .	2.1	5
137	Ethical and practical issues to consider in the governance of genomic and human research data and data sharing in South Africa: a meeting report. AAS Open Research, 2019, 2, 15.	1.5	5
138	ANIMA: Association network integration for multiscale analysis. Wellcome Open Research, 2018, 3, 27.	1.8	5
139	The Sickle Cell Disease Ontology: recent development and expansion of the universal sickle cell knowledge representation. Database: the Journal of Biological Databases and Curation, 2022, 2022, .	3.0	5
140	Polygenic risk scores for CARDINAL study. Nature Genetics, 2022, 54, 527-530.	21.4	5
141	The InterPro Database and Tools for Protein Domain Analysis. Current Protocols in Bioinformatics, 2003, 2, 2.7.1.	25.8	4
142	DAS Writeback: A Collaborative Annotation System. BMC Bioinformatics, 2011, 12, 143.	2.6	4
143	GenGraph: a python module for the simple generation and manipulation of genome graphs. BMC Bioinformatics, 2019, 20, 519.	2.6	4
144	Reviewing and assessing existing meta-analysis models and tools. Briefings in Bioinformatics, 2021, 22, .	6.5	4

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145	Ten simple rules for organizing a bioinformatics training course in low- and middle-income countries. PLoS Computational Biology, 2021, 17, e1009218.	3.2	4
146	Projection of gene-protein networks to the functional space of the proteome and its application to analysis of organism complexity. BMC Genomics, 2010, 11, S4.	2.8	3
147	FRANC: a unified framework for multi-way local ancestry deconvolution with high density SNP data. Briefings in Bioinformatics, 2020, 21, 1837-1845.	6.5	3
148	Simulation of African and non-African low and high coverage whole genome sequence data to assess variant calling approaches. Briefings in Bioinformatics, 2020, 22, .	6.5	3
149	African Global Representation in Biomedical Sciences. Annual Review of Biomedical Data Science, 2021, 4, 57-81.	6.5	3
150	The Development of a Sustainable Bioinformatics Training Environment Within the H3Africa Bioinformatics Network (H3ABioNet). Frontiers in Education, 2021, 6, .	2.1	3
151	Building Infrastructure for African Human Genomic Data Management. Data Science Journal, 2019, 18, .	1.3	3
152	Protein Domain Architectures. Methods in Molecular Biology, 2010, 609, 83-95.	0.9	2
153	Data acquisition and data/knowledge sharing in global genomic studies. Applied & Translational Genomics, 2014, 3, 109-110.	2.1	2
154	H3ABioNet computational metagenomics workshop in Mauritius: training to analyse microbial diversity for Africa. Standards in Genomic Sciences, 2015, 10, .	1.5	2
155	Accumulation of Splice Variants and Transcripts in Response to PI3K Inhibition in T Cells. PLoS ONE, 2013, 8, e50695.	2.5	2
156	MyDas, an Extensible Java DAS Server. PLoS ONE, 2012, 7, e44180.	2.5	2
157	Ten simple rules for developing bioinformatics capacity at an academic institution. PLoS Computational Biology, 2021, 17, e1009592.	3.2	2
158	Investigating the effect of paralogs on microarray gene-set analysis. BMC Bioinformatics, 2011, 12, 29.	2.6	1
159	Knowing Whom We Are trying to Protect: An Assessment of HIV Risk in South African Adolescent Females. AIDS Research and Human Retroviruses, 2014, 30, A131-A131.	1.1	1
160	Proposed minimum information guideline for kidney diseaseâ€”research and clinical data reporting: a cross-sectional study. BMJ Open, 2019, 9, e029539.	1.9	1
161	Impact of effective contact rate and post treatment immune status on population tuberculosis infection and disease using a mathematical model. F1000Research, 0, 6, 1817.	1.6	1
162	ANIMA: Association network integration for multiscale analysis. Wellcome Open Research, 0, 3, 27.	1.8	1

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163	Proposed Guideline for Minimum Information Stroke Research and Clinical Data Reporting. Data Science Journal, 2019, 18, 26.	1.3	1
164	Geografiese ligging beïnvloed vaginale mikrobiële profile in Suid-Afrikaanse vroue. South African Journal of Science and Technology, 2020, 38, 41-49.	0.1	1
165	Getting the most out of protein family classification resources. , 2005, , .		0
166	Classification of proteins into families. , 2005, , .		0
167	Analysis of Duplicate Gene Families in Microbial Genomes and Application to the Study of Gene Duplication in M. tuberculosis. , 2011, , .		0
168	Biotechnology Innovators To Convene in Cape Town, South Africa: Pharmacogenetics and Precision Medicine Conference (April 7-9, 2016). OMICS A Journal of Integrative Biology, 2015, 19, 731-732.	2.0	0
169	A19- The impact of HIV-1 on the evolution of Mycobacterium tuberculosis. Virus Evolution, 2018, 4, .	4.9	0
170	Editorial: The Genetic and Environmental Basis for Diseases in Understudied Populations. Frontiers in Genetics, 2020, 11, 559956.	2.3	0
171	Identification of All Exact and Approximate Inverted Repeats in Regular and Weighted Sequences. Communications in Computer and Information Science, 2013, , 11-19.	0.5	0
172	High rates of bacterial vaginosis and Chlamydia in a low-income, high-population-density community in Cape Town. South African Journal of Science and Technology, 2017, 36, .	0.1	0
173	Hoër voorkomskoe van bakteriële vaginose en Chlamydia in 'n lae-inkomste, hoër-bevolkingsdigtheid gemeenskap in Kaapstad. South African Journal of Science and Technology, 2017, 36, .	0.1	0
174	Advancing the international data science workforce through shared training and education. F1000Research, 0, 8, 251.	1.6	0
175	African Genomic Medicine Portal: A Web Portal for Biomedical Applications. Journal of Personalized Medicine, 2022, 12, 265.	2.5	0