

Nicola J Mulder

List of Publications by Year in descending order

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Version: 2024-02-01

175
papers

31,807
citations

70961

41
h-index

5101

166
g-index

269
all docs

269
docs citations

269
times ranked

38597
citing authors

#	ARTICLE	IF	CITATIONS
1	Revealing the Mutational Spectrum in Southern Africans With Amyotrophic Lateral Sclerosis. <i>Neurology: Genetics</i> , 2022, 8, e654.	0.9	10
2	The Sickle Cell Disease Ontology: recent development and expansion of the universal sickle cell knowledge representation. <i>Database: the Journal of Biological Databases and Curation</i> , 2022, 2022, .	1.4	5
3	African Genomic Medicine Portal: A Web Portal for Biomedical Applications. <i>Journal of Personalized Medicine</i> , 2022, 12, 265.	1.1	0
4	Polygenic risk scores for CARDINAL study. <i>Nature Genetics</i> , 2022, 54, 527-530.	9.4	5
5	IHP-PINGâ€”generating integrated human proteinâ€”protein interaction networks on-the-fly. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	7
6	Hypothalamicâ€”pituitaryâ€”adrenal axis suppression in asthma: A glucocorticoid receptor polymorphism may protect. <i>Pediatric Allergy and Immunology</i> , 2021, 32, 273-279.	1.1	6
7	Integrated molecular characterisation of the MAPK pathways in human cancers reveals pharmacologically vulnerable mutations and gene dependencies. <i>Communications Biology</i> , 2021, 4, 9.	2.0	32
8	H3ABioNet genomic medicine and microbiome data portals hackathon proceedings. <i>Database: the Journal of Biological Databases and Curation</i> , 2021, 2021, .	1.4	7
9	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.	1.5	10
10	Human OMICs and Computational Biology Research in Africa: Current Challenges and Prospects. <i>OMICS A Journal of Integrative Biology</i> , 2021, 25, 213-233.	1.0	13
11	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.	1.1	17
12	Repeats expansions in ATXN2, NOP56, NIPA1 and ATXN1 are not associated with ALS in Africans. <i>IBRO Neuroscience Reports</i> , 2021, 10, 130-135.	0.7	6
13	Challenges and Considerations for Delivering Bioinformatics Training in LMICs: Perspectives From Pan-African and Latin American Bioinformatics Networks. <i>Frontiers in Education</i> , 2021, 6, .	1.2	5
14	African Global Representation in Biomedical Sciences. <i>Annual Review of Biomedical Data Science</i> , 2021, 4, 57-81.	2.8	3
15	Assessing exposure to Kikari: a big data analysis of a large maternal mobile messaging service across 13 states in India. <i>BMJ Global Health</i> , 2021, 6, e005213.	2.0	8
16	Reviewing and assessing existing meta-analysis models and tools. <i>Briefings in Bioinformatics</i> , 2021, 22, .	3.2	4
17	Ten simple rules for organizing a bioinformatics training course in low- and middle-income countries. <i>PLoS Computational Biology</i> , 2021, 17, e1009218.	1.5	4
18	Association of Novel Locus With Rheumatic Heart Disease in Black African Individuals. <i>JAMA Cardiology</i> , 2021, 6, 1000.	3.0	18

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19	The Development of a Sustainable Bioinformatics Training Environment Within the H3Africa Bioinformatics Network (H3ABioNet). <i>Frontiers in Education</i> , 2021, 6, .	1.2	3
20	Data Management Plans in the genomics research revolution of Africa: Challenges and recommendations. <i>Journal of Biomedical Informatics</i> , 2021, 122, 103900.	2.5	6
21	A year of genomic surveillance reveals how the SARS-CoV-2 pandemic unfolded in Africa. <i>Science</i> , 2021, 374, 423-431.	6.0	144
22	The Data Use Ontology to streamline responsible access to human biomedical datasets. <i>Cell Genomics</i> , 2021, 1, 100028.	3.0	31
23	GA4GH: International policies and standards for data sharing across genomic research and healthcare. <i>Cell Genomics</i> , 2021, 1, 100029.	3.0	94
24	Relating Global and Local Connectome Changes to Dementia and Targeted Gene Expression in Alzheimer's Disease. <i>Frontiers in Human Neuroscience</i> , 2021, 15, 761424.	1.0	6
25	Ten simple rules for developing bioinformatics capacity at an academic institution. <i>PLoS Computational Biology</i> , 2021, 17, e1009592.	1.5	2
26	A broad survey of DNA sequence data simulation tools. <i>Briefings in Functional Genomics</i> , 2020, 19, 49-59.	1.3	20
27	FRANC: a unified framework for multi-way local ancestry deconvolution with high density SNP data. <i>Briefings in Bioinformatics</i> , 2020, 21, 1837-1845.	3.2	3
28	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.	1.1	34
29	Microbial function and genital inflammation in young South African women at high risk of HIV infection. <i>Microbiome</i> , 2020, 8, 165.	4.9	23
30	High-depth African genomes inform human migration and health. <i>Nature</i> , 2020, 586, 741-748.	13.7	197
31	Genetic modifiers of long-term survival in sickle cell anemia. <i>Clinical and Translational Medicine</i> , 2020, 10, e152.	1.7	21
32	Simulation of African and non-African low and high coverage whole genome sequence data to assess variant calling approaches. <i>Briefings in Bioinformatics</i> , 2020, 22, .	3.2	3
33	Editorial: The Genetic and Environmental Basis for Diseases in Understudied Populations. <i>Frontiers in Genetics</i> , 2020, 11, 559956.	1.1	0
34	A review of clinical pharmacogenetics Studies in African populations. <i>Personalized Medicine</i> , 2020, 17, 155-170.	0.8	35
35	Machine Learning and Network Analyses Reveal Disease Subtypes of Pancreatic Cancer and their Molecular Characteristics. <i>Scientific Reports</i> , 2020, 10, 1212.	1.6	62
36	Genome-Wide Association Study of Brain Connectivity Changes for Alzheimer's Disease. <i>Scientific Reports</i> , 2020, 10, 1433.	1.6	24

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37	Geografiese ligging beïnvloed vaginale mikrobiële profiele in Suid-Afrikaanse vrou. South African Journal of Science and Technology, 2020, 38, 41-49.	0.1	1
38	A comprehensive survey of models for dissecting local ancestry deconvolution in human genome. Briefings in Bioinformatics, 2019, 20, 1709-1724.	3.2	29
39	Leveraging crowdsourcing to accelerate global health solutions. Nature Biotechnology, 2019, 37, 848-850.	9.4	36
40	GenGraph: a python module for the simple generation and manipulation of genome graphs. BMC Bioinformatics, 2019, 20, 519.	1.2	4
41	Using Whole Genome Sequencing in an African Subphenotype of Myasthenia Gravis to Generate a Pathogenetic Hypothesis. Frontiers in Genetics, 2019, 10, 136.	1.1	12
42	Multi-stage Association Analysis of Glioblastoma Gene Expressions with Texture and Spatial Patterns. Lecture Notes in Computer Science, 2019, 11383, 239-250.	1.0	9
43	Ten simple rules for organizing a webinar series. PLoS Computational Biology, 2019, 15, e1006671.	1.5	43
44	Proposed minimum information guideline for kidney disease research and clinical data reporting: a cross-sectional study. BMJ Open, 2019, 9, e029539.	0.8	1
45	The African Genomic Medicine Training Initiative (AGMT): Showcasing a Community and Framework Driven Genomic Medicine Training for Nurses in Africa. Frontiers in Genetics, 2019, 10, 1209.	1.1	26
46	Metabolic gene alterations impact the clinical aggressiveness and drug responses of 32 human cancers. Communications Biology, 2019, 2, 414.	2.0	55
47	The Sickle Cell Disease Ontology: enabling universal sickle cell-based knowledge representation. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	14
48	The Hearing Impairment Ontology: A Tool for Unifying Hearing Impairment Knowledge to Enhance Collaborative Research. Genes, 2019, 10, 960.	1.0	6
49	The H3ABioNet helpdesk: an online bioinformatics resource, enhancing Africa's capacity for genomics research. BMC Bioinformatics, 2019, 20, 741.	1.2	6
50	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
51	Building Infrastructure for African Human Genomic Data Management. Data Science Journal, 2019, 18, .	0.6	3
52	Proposed Guideline for Minimum Information Stroke Research and Clinical Data Reporting. Data Science Journal, 2019, 18, 26.	0.6	1
53	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.	3.2	8
54	HIV-exposure, early life feeding practices and delivery mode impacts on faecal bacterial profiles in a South African birth cohort. Scientific Reports, 2018, 8, 5078.	1.6	28

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55	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.	2.9	31
56	Hackathons as a means of accelerating scientific discoveries and knowledge transfer. <i>Genome Research</i> , 2018, 28, 759-765.	2.4	31
57	Microbial Composition Predicts Genital Tract Inflammation and Persistent Bacterial Vaginosis in South African Adolescent Females. <i>Infection and Immunity</i> , 2018, 86, .	1.0	136
58	A systems-level analysis of drugâ€“targetâ€“disease associations for drug repositioning. <i>Briefings in Functional Genomics</i> , 2018, 17, 34-41.	1.3	10
59	Developing reproducible bioinformatics analysis workflows for heterogeneous computing environments to support African genomics. <i>BMC Bioinformatics</i> , 2018, 19, 457.	1.2	33
60	Strategies and opportunities for promoting bioinformatics in Zimbabwe. <i>PLoS Computational Biology</i> , 2018, 14, e1006480.	1.5	6
61	A19â€“,The impact of HIV-1 on the evolution of <i>Mycobacterium tuberculosis</i> . <i>Virus Evolution</i> , 2018, 4, .	2.2	0
62	H3Africa: current perspectives. <i>Pharmacogenomics and Personalized Medicine</i> , 2018, Volume 11, 59-66.	0.4	101
63	Environmental and social factors impacting on epidemic and endemic tuberculosis: a modelling analysis. <i>Royal Society Open Science</i> , 2018, 5, 170726.	1.1	9
64	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.	1.1	12
65	Disruption of maternal gut microbiota during gestation alters offspring microbiota and immunity. <i>Microbiome</i> , 2018, 6, 124.	4.9	109
66	Host and Microbiome Genome-Wide Association Studies: Current State and Challenges. <i>Frontiers in Genetics</i> , 2018, 9, 637.	1.1	71
67	Organizing and running bioinformatics hackathons within Africa: The H3ABioNet cloud computing experience. <i>AAS Open Research</i> , 2018, 1, 9.	1.5	11
68	ANIMA: Association network integration for multiscale analysis. <i>Wellcome Open Research</i> , 2018, 3, 27.	0.9	6
69	The development and application of bioinformatics core competencies to improve bioinformatics training and education. <i>PLoS Computational Biology</i> , 2018, 14, e1005772.	1.5	84
70	Integrative landscape of dysregulated signaling pathways of clinically distinct pancreatic cancer subtypes. <i>Oncotarget</i> , 2018, 9, 29123-29139.	0.8	15
71	ANIMA: Association network integration for multiscale analysis. <i>Wellcome Open Research</i> , 2018, 3, 27.	0.9	5
72	Organizing and running bioinformatics hackathons within Africa: The H3ABioNet cloud computing experience. <i>AAS Open Research</i> , 2018, 1, 9.	1.5	11

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73	Gene Ontology semantic similarity tools: survey on features and challenges for biological knowledge discovery. <i>Briefings in Bioinformatics</i> , 2017, 18, bbw067.	3.2	63
74	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.	1.0	16
75	Accessing Biospecimens from the H3Africa Consortium. <i>Biopreservation and Biobanking</i> , 2017, 15, 95-98.	0.5	15
76	Sickle cell disease: tipping the balance of genomic research to catalyse discoveries in Africa. <i>Lancet, The</i> , 2017, 389, 2355-2358.	6.3	11
77	The Influence of HIV on the Evolution of <i>Mycobacterium tuberculosis</i> . <i>Molecular Biology and Evolution</i> , 2017, 34, 1654-1668.	3.5	27
78	Development to enable precision medicine in Africa. <i>Personalized Medicine</i> , 2017, 14, 467-470.	0.8	16
79	A multi-scenario genome-wide medical population genetics simulation framework. <i>Bioinformatics</i> , 2017, 33, 2995-3002.	1.8	5
80	Whole-genome sequencing for an enhanced understanding of genetic variation among South Africans. <i>Nature Communications</i> , 2017, 8, 2062.	5.8	88
81	Assessing computational genomics skills: Our experience in the H3ABioNet African bioinformatics network. <i>PLoS Computational Biology</i> , 2017, 13, e1005419.	1.5	9
82	Designing a course model for distance-based online bioinformatics training in Africa: The H3ABioNet experience. <i>PLoS Computational Biology</i> , 2017, 13, e1005715.	1.5	29
83	Four simple recommendations to encourage best practices in research software. <i>F1000Research</i> , 2017, 6, 876.	0.8	88
84	Development of Bioinformatics Infrastructure for Genomics Research. <i>Global Heart</i> , 2017, 12, 91.	0.9	47
85	Recent advances in predicting gene-disease associations. <i>F1000Research</i> , 2017, 6, 578.	0.8	36
86	Ten simple rules for forming a scientific professional society. <i>PLoS Computational Biology</i> , 2017, 13, e1005226.	1.5	7
87	H3ABioNet: Developing Sustainable Bioinformatics Capacity in Africa. <i>EMBnet Journal</i> , 2017, 23, 886.	0.2	10
88	Genomic Research Data Generation, Analysis and Sharing - Challenges in the African Setting. <i>Data Science Journal</i> , 2017, 16, .	0.6	21
89	High rates of bacterial vaginosis and Chlamydia in a low-income, high-population-density community in Cape Town. <i>South African Journal of Science and Technology</i> , 2017, 36, .	0.1	0
90	Hoër voorkomskoeers van bakteriële vaginose en Chlamydia in 'n lae-inkomste, hoër-bevolkingsdigtheid gemeenskap in Kaapstad. <i>South African Journal of Science and Technology</i> , 2017, 36, .	0.1	0

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91	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.	1.1	11
92	Proteogenomic Analysis of Mycobacterium smegmatis Using High Resolution Mass Spectrometry. <i>Frontiers in Microbiology</i> , 2016, 7, 427.	1.5	27
93	Identification of Quantitative Proteomic Differences between Mycobacterium tuberculosis Lineages with Altered Virulence. <i>Frontiers in Microbiology</i> , 2016, 7, 813.	1.5	34
94	The Development of Computational Biology in South Africa: Successes Achieved and Lessons Learnt. <i>PLoS Computational Biology</i> , 2016, 12, e1004395.	1.5	12
95	Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum) Tj ETQq1 1 0.784314, rgBT /Over	1.5	24
96	H3ABioNet, a sustainable pan-African bioinformatics network for human heredity and health in Africa. <i>Genome Research</i> , 2016, 26, 271-277.	2.4	94
97	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.	1.8	21
98	A-DaGO-Fun: an adaptable Gene Ontology semantic similarity-based functional analysis tool. <i>Bioinformatics</i> , 2016, 32, 477-479.	1.8	28
99	Real-Time Investigation of Tuberculosis Transmission: Developing the Respiratory Aerosol Sampling Chamber (RASC). <i>PLoS ONE</i> , 2016, 11, e0146658.	1.1	40
100	Biotechnology Innovators To Convene in Cape Town, South Africa: Pharmacogenetics and Precision Medicine Conference (April 7-9, 2016). <i>OMICS A Journal of Integrative Biology</i> , 2015, 19, 731-732.	1.0	0
101	H3ABioNet computational metagenomics workshop in Mauritius: training to analyse microbial diversity for Africa. <i>Standards in Genomic Sciences</i> , 2015, 10, .	1.5	2
102	Bioinformatics Education-Perspectives and Challenges out of Africa. <i>Briefings in Bioinformatics</i> , 2015, 16, 355-364.	3.2	61
103	A Genomic Portrait of Haplotype Diversity and Signatures of Selection in Indigenous Southern African Populations. <i>PLoS Genetics</i> , 2015, 11, e1005052.	1.5	42
104	The H3Africa policy framework: negotiating fairness in genomics. <i>Trends in Genetics</i> , 2015, 31, 117-119.	2.9	65
105	GOBLET: The Global Organisation for Bioinformatics Learning, Education and Training. <i>PLoS Computational Biology</i> , 2015, 11, e1004143.	1.5	52
106	Modelling the risk of airborne infectious disease using exhaled air. <i>Journal of Theoretical Biology</i> , 2015, 372, 100-106.	0.8	51
107	A Quick Guide for Building a Successful Bioinformatics Community. <i>PLoS Computational Biology</i> , 2015, 11, e1003972.	1.5	23
108	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.	1.1	33

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109	The use of semantic similarity measures for optimally integrating heterogeneous Gene Ontology data from large scale annotation pipelines. <i>Frontiers in Genetics</i> , 2014, 5, 264.	1.1	6
110	Using biological networks to improve our understanding of infectious diseases. <i>Computational and Structural Biotechnology Journal</i> , 2014, 11, 1-10.	1.9	43
111	Knowing Whom We Are trying to Protect: An Assessment of HIV Risk in South African Adolescent Females. <i>AIDS Research and Human Retroviruses</i> , 2014, 30, A131-A131.	0.5	1
112	Genome Sequence of the Tsetse Fly (<i>Glossina morsitans</i>): Vector of African Trypanosomiasis. <i>Science</i> , 2014, 344, 380-386.	6.0	254
113	Genome-wide association study of ancestry-specific TB risk in the South African Coloured population. <i>Human Molecular Genetics</i> , 2014, 23, 796-809.	1.4	162
114	Enabling the genomic revolution in Africa. <i>Science</i> , 2014, 344, 1346-1348.	6.0	361
115	Population-specific common SNPs reflect demographic histories and highlight regions of genomic plasticity with functional relevance. <i>BMC Genomics</i> , 2014, 15, 437.	1.2	40
116	A web-based protein interaction network visualizer. <i>BMC Bioinformatics</i> , 2014, 15, 129.	1.2	21
117	Data acquisition and data/knowledge sharing in global genomic studies. <i>Applied & Translational Genomics</i> , 2014, 3, 109-110.	2.1	2
118	PPI layouts: BioJS components for the display of Protein-Protein Interactions. <i>F1000Research</i> , 2014, 3, 50.	0.8	9
119	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.	0.8	23
120	Understanding TB latency using computational and dynamic modelling procedures. <i>Infection, Genetics and Evolution</i> , 2013, 13, 267-283.	1.0	11
121	DaGO-Fun: tool for Gene Ontology-based functional analysis using term information content measures. <i>BMC Bioinformatics</i> , 2013, 14, 284.	1.2	33
122	Best practices in bioinformatics training for life scientists. <i>Briefings in Bioinformatics</i> , 2013, 14, 528-537.	3.2	51
123	iAnn: an event sharing platform for the life sciences. <i>Bioinformatics</i> , 2013, 29, 1919-1921.	1.8	6
124	Information Content-Based Gene Ontology Semantic Similarity Approaches: Toward a Unified Framework Theory. <i>BioMed Research International</i> , 2013, 2013, 1-11.	0.9	43
125	Determining Ancestry Proportions in Complex Admixture Scenarios in South Africa Using a Novel Proxy Ancestry Selection Method. <i>PLoS ONE</i> , 2013, 8, e73971.	1.1	42
126	Latent Tuberculosis: Models, Computational Efforts and the Pathogen's Regulatory Mechanisms during Dormancy. <i>Frontiers in Bioengineering and Biotechnology</i> , 2013, 1, 4.	2.0	27

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127	Protein Function Microarrays: Design, Use and Bioinformatic Analysis in Cancer Biomarker Discovery and Quantitation. <i>Translational Bioinformatics</i> , 2013, , 39-74.	0.0	10
128	Accumulation of Splice Variants and Transcripts in Response to PI3K Inhibition in T Cells. <i>PLoS ONE</i> , 2013, 8, e50695.	1.1	2
129	Predicting and Analyzing Interactions between <i>Mycobacterium tuberculosis</i> and Its Human Host. <i>PLoS ONE</i> , 2013, 8, e67472.	1.1	34
130	Identification of All Exact and Approximate Inverted Repeats in Regular and Weighted Sequences. <i>Communications in Computer and Information Science</i> , 2013, , 11-19.	0.4	0
131	Manual GO annotation of predictive protein signatures: the InterPro approach to GO curation. Database: the <i>Journal of Biological Databases and Curation</i> , 2012, 2012, bar068-bar068.	1.4	108
132	InterPro in 2011: new developments in the family and domain prediction database. <i>Nucleic Acids Research</i> , 2012, 40, D306-D312.	6.5	921
133	Function Prediction and Analysis of <i>Mycobacterium tuberculosis</i> Hypothetical Proteins. <i>International Journal of Molecular Sciences</i> , 2012, 13, 7283-7302.	1.8	88
134	A Topology-Based Metric for Measuring Term Similarity in the Gene Ontology. <i>Advances in Bioinformatics</i> , 2012, 2012, 1-17.	5.7	44
135	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.	0.8	24
136	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.	1.0	19
137	MyDas, an Extensible Java DAS Server. <i>PLoS ONE</i> , 2012, 7, e44180.	1.1	2
138	Analysis of Duplicate Gene Families in Microbial Genomes and Application to the Study of Gene Duplication in <i>M. tuberculosis</i> . , 2011, , .		0
139	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
140	myKaryoView: A Light-Weight Client for Visualization of Genomic Data. <i>PLoS ONE</i> , 2011, 6, e26345.	1.1	5
141	DAS Writeback: A Collaborative Annotation System. <i>BMC Bioinformatics</i> , 2011, 12, 143.	1.2	4
142	Investigating the effect of paralogs on microarray gene-set analysis. <i>BMC Bioinformatics</i> , 2011, 12, 29.	1.2	1
143	Contribution of microarray data to the advancement of knowledge on the <i>Mycobacterium tuberculosis</i> interactome: Use of the random partial least squares approach. <i>Infection, Genetics and Evolution</i> , 2011, 11, 181-189.	1.0	13
144	Contribution of microarray data to the advancement of knowledge on the <i>Mycobacterium tuberculosis</i> interactome: Use of the random partial least squares approach. <i>Infection, Genetics and Evolution</i> , 2011, 11, 725-733.	1.0	11

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145	Dasty3, a WEB framework for DAS. <i>Bioinformatics</i> , 2011, 27, 2616-2617.	1.8	14
146	From sets to graphs: towards a realistic enrichment analysis of transcriptomic systems. <i>Bioinformatics</i> , 2011, 27, i366-i373.	1.8	64
147	Scoring Protein Relationships in Functional Interaction Networks Predicted from Sequence Data. <i>PLoS ONE</i> , 2011, 6, e18607.	1.1	24
148	Protein Domain Architectures. <i>Methods in Molecular Biology</i> , 2010, 609, 83-95.	0.4	2
149	Projection of gene-protein networks to the functional space of the proteome and its application to analysis of organism complexity. <i>BMC Genomics</i> , 2010, 11, S4.	1.2	3
150	InterPro: the integrative protein signature database. <i>Nucleic Acids Research</i> , 2009, 37, D211-D215.	6.5	1,712
151	Comparative analysis of microbial genomes to study unique and expanded gene families in <i>Mycobacterium tuberculosis</i> . <i>Infection, Genetics and Evolution</i> , 2009, 9, 314-321.	1.0	5
152	The InterPro Database and Tools for Protein Domain Analysis. <i>Current Protocols in Bioinformatics</i> , 2008, 21, Unit 2.7.	25.8	69
153	New developments in the InterPro database. <i>Nucleic Acids Research</i> , 2007, 35, D224-D228.	6.5	444
154	Curated genome annotation of <i>Oryza sativa ssp. japonica</i> and comparative genome analysis with <i>Arabidopsis thaliana</i> . <i>Genome Research</i> , 2007, 17, 175-183.	2.4	218
155	InterPro and InterProScan. <i>Methods in Molecular Biology</i> , 2007, 396, 59-70.	0.4	339
156	The minimum information required for reporting a molecular interaction experiment (MIMix). <i>Nature Biotechnology</i> , 2007, 25, 894-898.	9.4	274
157	InterPro. , 2005, , .		9
158	Getting the most out of protein family classification resources. , 2005, , .		0
159	Classification of proteins into families. , 2005, , .		0
160	InterPro, progress and status in 2005. <i>Nucleic Acids Research</i> , 2004, 33, D201-D205.	6.5	478
161	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	2.6	290
162	The Gene Ontology Annotation (GOA) Project: Implementation of GO in SWISS-PROT, TrEMBL, and InterPro. <i>Genome Research</i> , 2003, 13, 662-672.	2.4	297

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163	The Proteome Analysis database: a tool for the in silico analysis of whole proteomes. <i>Nucleic Acids Research</i> , 2003, 31, 414-417.	6.5	64
164	The European Bioinformatics Institute's data resources. <i>Nucleic Acids Research</i> , 2003, 31, 43-50.	6.5	56
165	The InterPro Database, 2003 brings increased coverage and new features. <i>Nucleic Acids Research</i> , 2003, 31, 315-318.	6.5	640
166	The InterPro Database and Tools for Protein Domain Analysis. <i>Current Protocols in Bioinformatics</i> , 2003, 2, 2.7.1.	25.8	4
167	InterPro: An integrated documentation resource for protein families, domains and functional sites. <i>Briefings in Bioinformatics</i> , 2002, 3, 225-235.	3.2	155
168	Applications of InterPro in protein annotation and genome analysis. <i>Briefings in Bioinformatics</i> , 2002, 3, 285-295.	3.2	54
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