

Matthew I Bellgard

List of Publications by Year in descending order

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131
papers

8,617
citations

81743

39
h-index

48187

88
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134
all docs

134
docs citations

134
times ranked

12128
citing authors

#	ARTICLE	IF	CITATIONS
1	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014, 345, 1251788.	6.0	1,479
2	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017, 544, 427-433.	13.7	1,365
3	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014, 345, 1250092.	6.0	629
4	The TREAT-NMD DMD Global Database: Analysis of More than 7,000 Duchenne Muscular Dystrophy Mutations. <i>Human Mutation</i> , 2015, 36, 395-402.	1.1	507
5	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	2.6	290
6	Deep Sequencing of Plant and Animal DNA Contained within Traditional Chinese Medicines Reveals Legality Issues and Health Safety Concerns. <i>PLoS Genetics</i> , 2012, 8, e1002657.	1.5	245
7	Genes controlling seed dormancy and pre-harvest sprouting in a rice-wheat-barley comparison. <i>Functional and Integrative Genomics</i> , 2004, 4, 84-93.	1.4	157
8	Ten years of bacterial genome sequencing: comparative-genomics-based discoveries. <i>Functional and Integrative Genomics</i> , 2006, 6, 165-185.	1.4	156
9	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L.. <i>Scientific Data</i> , 2017, 4, 170044.	2.4	130
10	Genome sequencing and analysis of the paclitaxel-producing endophytic fungus <i>Penicillium aurantiogriseum</i> NRRL 62431. <i>BMC Genomics</i> , 2014, 15, 69.	1.2	125
11	Clinical Outcomes in Duchenne Muscular Dystrophy: A Study of 5345 Patients from the TREAT-NMD DMD Global Database. <i>Journal of Neuromuscular Diseases</i> , 2017, 4, 293-306.	1.1	125
12	DNA-Based Faecal Dietary Analysis: A Comparison of qPCR and High Throughput Sequencing Approaches. <i>PLoS ONE</i> , 2011, 6, e25776.	1.1	124
13	The first gene-based map of <i>Lupinus angustifolius</i> L.-location of domestication genes and conserved synteny with <i>Medicago truncatula</i> . <i>Theoretical and Applied Genetics</i> , 2006, 113, 225-238.	1.8	116
14	Genome Sequence of the Pathogenic Intestinal Spirochete <i>Brachyspira hyodysenteriae</i> Reveals Adaptations to Its Lifestyle in the Porcine Large Intestine. <i>PLoS ONE</i> , 2009, 4, e4641.	1.1	107
15	Combined DNA, toxicological and heavy metal analyses provides an auditing toolkit to improve pharmacovigilance of traditional Chinese medicine (TCM). <i>Scientific Reports</i> , 2015, 5, 17475.	1.6	99
16	Yabi: An online research environment for grid, high performance and cloud computing. <i>Source Code for Biology and Medicine</i> , 2012, 7, 1.	1.7	98
17	The Genetics of Symbiotic Nitrogen Fixation: Comparative Genomics of 14 Rhizobia Strains by Resolution of Protein Clusters. <i>Genes</i> , 2012, 3, 138-166.	1.0	94
18	De novo assembly of <i>Euphorbia fischeriana</i> root transcriptome identifies prostratin pathway related genes. <i>BMC Genomics</i> , 2011, 12, 600.	1.2	75

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19	Aligning a New Reference Genetic Map of <i>Lupinus angustifolius</i> with the Genome Sequence of the Model Legume, <i>Lotus japonicus</i> . <i>DNA Research</i> , 2010, 17, 73-83.	1.5	73
20	The Evolution of MHC Diversity by Segmental Duplication and Transposition of Retroelements. <i>Journal of Molecular Evolution</i> , 1997, 45, 599-609.	0.8	72
21	Scrapheap Challenge: A novel bulk-bone metabarcoding method to investigate ancient DNA in faunal assemblages. <i>Scientific Reports</i> , 2013, 3, 3371.	1.6	72
22	Germin-like proteins (GLPs) in cereal genomes: gene clustering and dynamic roles in plant defence. <i>Functional and Integrative Genomics</i> , 2010, 10, 463-476.	1.4	70
23	Profiling β -thalassaemia mutations in India at state and regional levels: implications for genetic education, screening and counselling programmes. <i>The HUGO Journal</i> , 2009, 3, 51-62.	4.1	68
24	Gene expression profiling of Japanese psoriatic skin reveals an increased activity in molecular stress and immune response signals. <i>Journal of Molecular Medicine</i> , 2005, 83, 964-975.	1.7	62
25	Evidence of a tick RNAi pathway by comparative genomics and reverse genetics screen of targets with known loss-of-function phenotypes in <i>Drosophila</i> . <i>BMC Molecular Biology</i> , 2009, 10, 26.	3.0	61
26	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2007, 36, D793-D799.	6.5	57
27	Multilocus sequence typing as a tool for studying the molecular epidemiology and population structure of <i>Brachyspira hyodysenteriae</i> . <i>Veterinary Microbiology</i> , 2009, 138, 330-338.	0.8	57
28	CattleTickBase: An integrated Internet-based bioinformatics resource for <i>Rhipicephalus (Boophilus) microplus</i> . <i>International Journal for Parasitology</i> , 2012, 42, 161-169.	1.3	55
29	The Complete Genome Sequence of the Pathogenic Intestinal Spirochete <i>Brachyspira pilosicoli</i> and Comparison with Other <i>Brachyspira</i> Genomes. <i>PLoS ONE</i> , 2010, 5, e11455.	1.1	54
30	An internet-based bioinformatics toolkit for plant biosecurity diagnosis and surveillance of viruses and viroids. <i>BMC Bioinformatics</i> , 2017, 18, 26.	1.2	52
31	Genomic analysis of <i>Campylobacter fetus</i> subspecies: identification of candidate virulence determinants and diagnostic assay targets. <i>BMC Microbiology</i> , 2009, 9, 86.	1.3	51
32	Editorial: Precision Public Health. <i>Frontiers in Public Health</i> , 2018, 6, 121.	1.3	50
33	Genomic and Phylogenetic Analysis of the S100A7 (Psoriasin) Gene Duplications Within the Region of the S100 Gene Cluster on Human Chromosome 1q21. <i>Journal of Molecular Evolution</i> , 2003, 56, 397-406.	0.8	49
34	Dispelling myths about rare disease registry system development. <i>Source Code for Biology and Medicine</i> , 2013, 8, 21.	1.7	49
35	Comparative microarray analysis of <i>Rhipicephalus (Boophilus) microplus</i> expression profiles of larvae pre-attachment and feeding adult female stages on <i>Bos indicus</i> and <i>Bos taurus</i> cattle. <i>BMC Genomics</i> , 2010, 11, 437.	1.2	48
36	Gene-enriched draft genome of the cattle tick <i>Rhipicephalus microplus</i> : assembly by the hybrid Pacific Biosciences/Illumina approach enabled analysis of the highly repetitive genome. <i>International Journal for Parasitology</i> , 2017, 47, 569-583.	1.3	48

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37	Bread matters: a national initiative to profile the genetic diversity of Australian wheat. <i>Plant Biotechnology Journal</i> , 2012, 10, 703-708.	4.1	45
38	Early Detection of G + C Differences in Bacterial Species Inferred from the Comparative Analysis of the Two Completely Sequenced <i>Helicobacter pylori</i> Strains. <i>Journal of Molecular Evolution</i> , 2001, 53, 465-468.	0.8	41
39	Identification of genes associated with prophage-like gene transfer agents in the pathogenic intestinal spirochaetes <i>Brachyspira hyodysenteriae</i> , <i>Brachyspira pilosicoli</i> and <i>Brachyspira intermedia</i> . <i>Veterinary Microbiology</i> , 2009, 134, 340-345.	0.8	41
40	High-throughput sequencing of ancient plant and mammal DNA preserved in herbivore middens. <i>Quaternary Science Reviews</i> , 2012, 58, 135-145.	1.4	40
41	Comparative genomics of <i>Brachyspira pilosicoli</i> strains: genome rearrangements, reductions and correlation of genetic complement with phenotypic diversity. <i>BMC Genomics</i> , 2012, 13, 454.	1.2	38
42	Genome Sequences of Six Wheat-Infecting <i>Fusarium</i> Species Isolates. <i>Genome Announcements</i> , 2013, 1, .	0.8	38
43	The mitochondrial genome of a Texas outbreak strain of the cattle tick, <i>Rhipicephalus (Boophilus) microplus</i> , derived from whole genome sequencing Pacific Biosciences and Illumina reads. <i>Gene</i> , 2015, 571, 135-141.	1.0	37
44	BAC-derived markers for assaying the stem rust resistance gene, Sr2, in wheat breeding programs. <i>Molecular Breeding</i> , 2008, 22, 15-24.	1.0	36
45	Suppressive subtractive hybridization analysis of <i>Rhipicephalus (Boophilus) microplus</i> larval and adult transcript expression during attachment and feeding. <i>Veterinary Parasitology</i> , 2010, 167, 304-320.	0.7	36
46	Analysis of Multiple <i>Brachyspira hyodysenteriae</i> Genomes Confirms That the Species Is Relatively Conserved but Has Potentially Important Strain Variation. <i>PLoS ONE</i> , 2015, 10, e0131050.	1.1	36
47	A descriptive profile of β -thalassaemia mutations in India, Pakistan and Sri Lanka. <i>Journal of Community Genetics</i> , 2010, 1, 149-157.	0.5	35
48	Diverse approaches to achieving grain yield in wheat. <i>Functional and Integrative Genomics</i> , 2011, 11, 37-48.	1.4	35
49	Gene expression evidence for off-target effects caused by RNA interference-mediated gene silencing of Ubiquitin-63E in the cattle tick <i>Rhipicephalus microplus</i> . <i>International Journal for Parasitology</i> , 2011, 41, 1001-1014.	1.3	33
50	Evolutionary conserved microRNAs are ubiquitously expressed compared to tick-specific miRNAs in the cattle tick <i>Rhipicephalus (Boophilus) microplus</i> . <i>BMC Genomics</i> , 2011, 12, 328.	1.2	33
51	Rare disease registries: a call to action. <i>Internal Medicine Journal</i> , 2017, 47, 1075-1079.	0.5	33
52	Transcriptome and toxin family analysis of the paralysis tick, <i>Ixodes holocyclus</i> . <i>International Journal for Parasitology</i> , 2018, 48, 71-82.	1.3	33
53	A reverse vaccinology approach to swine dysentery vaccine development. <i>Veterinary Microbiology</i> , 2009, 137, 111-119.	0.8	32
54	Reassociation kinetics-based approach for partial genome sequencing of the cattle tick, <i>Rhipicephalus (Boophilus) microplus</i> . <i>BMC Genomics</i> , 2010, 11, 374.	1.2	31

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55	A modular approach to disease registry design: Successful adoption of an internet-based rare disease registry. <i>Human Mutation</i> , 2012, 33, E2356-E2366.	1.1	31
56	Comparative organization of wheat homoeologous group 3S and 7L using wheat-rice synteny and identification of potential markers for genes controlling xanthophyll content in wheat. <i>Functional and Integrative Genomics</i> , 2004, 4, 118-130.	1.4	30
57	Phenotyping: Targeting genotype's rich cousin for diagnosis. <i>Journal of Paediatrics and Child Health</i> , 2015, 51, 381-386.	0.4	29
58	Design of the Familial Hypercholesterolaemia Australasia Network Registry: Creating Opportunities for Greater International Collaboration. <i>Journal of Atherosclerosis and Thrombosis</i> , 2017, 24, 1075-1084.	0.9	29
59	The transcript repeat element: the human Alu sequence as a component of gene networks influencing cancer. <i>Functional and Integrative Genomics</i> , 2010, 10, 307-319.	1.4	28
60	Role of international registries in enhancing the care of familial hypercholesterolaemia. <i>International Journal of Evidence-Based Healthcare</i> , 2013, 11, 134-139.	0.1	28
61	How to Identify Pathogenic Mutations among All Those Variations: Variant Annotation and Filtration in the Genome Sequencing Era. <i>Human Mutation</i> , 2016, 37, 1272-1282.	1.1	28
62	Metabarcoding avian diets at airports: implications for birdstrike hazard management planning. <i>Investigative Genetics</i> , 2013, 4, 27.	3.3	25
63	Second generation registry framework. <i>Source Code for Biology and Medicine</i> , 2014, 9, 14.	1.7	25
64	Rhipicephalus microplus lipocalins (LRMs): Genomic identification and analysis of the bovine immune response using in silico predicted B and T cell epitopes. <i>International Journal for Parasitology</i> , 2013, 43, 739-752.	1.3	24
65	Pseudoxon activation increases phenotype severity in a Becker muscular dystrophy patient. <i>Molecular Genetics & Genomic Medicine</i> , 2015, 3, 320-326.	0.6	23
66	De novo assembly of honey bee RNA viral genomes by tapping into the innate insect antiviral response pathway. <i>Journal of Invertebrate Pathology</i> , 2018, 152, 38-47.	1.5	23
67	Plant Proteogenomics: Improvements to the Grapevine Genome Annotation. <i>Proteomics</i> , 2017, 17, 1700197.	1.3	22
68	RD-RAP: beyond rare disease patient registries, devising a comprehensive data and analytic framework. <i>Orphanet Journal of Rare Diseases</i> , 2019, 14, 176.	1.2	22
69	Polymorphic Alu Insertions and their Associations with MHC Class I Alleles and Haplotypes in the Northeastern Thais. <i>Annals of Human Genetics</i> , 2005, 69, 364-372.	0.3	21
70	High-throughput parallel proteogenomics: A bacterial case study. <i>Proteomics</i> , 2014, 14, 2780-2789.	1.3	21
71	Evidence that the 36 kb plasmid of <i>Brachyspira hyodysenteriae</i> contributes to virulence. <i>Veterinary Microbiology</i> , 2011, 153, 150-155.	0.8	20
72	The New Zealand Neuromuscular Disease Registry. <i>Journal of Clinical Neuroscience</i> , 2012, 19, 1749-1750.	0.8	20

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73	Prediction of G protein-coupled receptor encoding sequences from the synganglion transcriptome of the cattle tick, <i>Rhipicephalus microplus</i> . <i>Ticks and Tick-borne Diseases</i> , 2016, 7, 670-677.	1.1	20
74	The role of patient registries for rare genetic lipid disorders. <i>Current Opinion in Lipidology</i> , 2018, 29, 156-162.	1.2	20
75	Translational development of splice-modifying antisense oligomers. <i>Expert Opinion on Biological Therapy</i> , 2017, 17, 15-30.	1.4	19
76	Dynamic Evolution of Genomes and the Concept of Genome Space. <i>Annals of the New York Academy of Sciences</i> , 1999, 870, 293-300.	1.8	18
77	Genome-level identification of cell wall invertase genes in wheat for the study of drought tolerance. <i>Functional Plant Biology</i> , 2012, 39, 569.	1.1	18
78	Wheat beta-expansin (EXPB11) genes: Identification of the expressed gene on chromosome 3BS carrying a pollen allergen domain. <i>BMC Plant Biology</i> , 2010, 10, 99.	1.6	17
79	Shoot transcriptome of the giant reed, <i>Arundo donax</i> . <i>Data in Brief</i> , 2015, 3, 1-6.	0.5	17
80	Design of a framework for the deployment of collaborative independent rare disease-centric registries: Gaucher disease registry model. <i>Blood Cells, Molecules, and Diseases</i> , 2018, 68, 232-238.	0.6	17
81	Significant differences between the G+C content of synonymous codons in orthologous genes and the genomic G+C content. <i>Gene</i> , 1999, 238, 33-37.	1.0	16
82	A highly conserved gene island of three genes on chromosome 3B of hexaploid wheat: diverse gene function and genomic structure maintained in a tightly linked block. <i>BMC Plant Biology</i> , 2010, 10, 98.	1.6	16
83	A Web-Based Registry for Familial Hypercholesterolaemia. <i>Heart Lung and Circulation</i> , 2017, 26, 635-639.	0.2	16
84	MASTR-MS: a web-based collaborative laboratory information management system (LIMS) for metabolomics. <i>Metabolomics</i> , 2017, 13, 14.	1.4	16
85	Differentially expressed genes in response to amitraz treatment suggests a proposed model of resistance to amitraz in <i>R. decoloratus</i> ticks. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2018, 8, 361-371.	1.4	16
86	Intragenic Variation of Synonymous Substitution Rates Is Caused by Nonrandom Mutations at Methylated CpG. <i>Journal of Molecular Evolution</i> , 2001, 53, 456-464.	0.8	15
87	A web-based, patient driven registry for Angelman syndrome: the global Angelman syndrome registry. <i>Orphanet Journal of Rare Diseases</i> , 2017, 12, 134.	1.2	15
88	Research protocol: The initiation, design and establishment of the Global Angelman Syndrome Registry. <i>Journal of Intellectual Disability Research</i> , 2018, 62, 431-443.	1.2	15
89	Plant Proteogenomics: From Protein Extraction to Improved Gene Predictions. <i>Methods in Molecular Biology</i> , 2013, 1002, 267-294.	0.4	14
90	Objective Monitoring of mTOR Inhibitor Therapy by Three-Dimensional Facial Analysis. <i>Twin Research and Human Genetics</i> , 2013, 16, 840-844.	0.3	14

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91	Harmonizing Music the Boltzmann Way. <i>Connection Science</i> , 1994, 6, 281-297.	1.8	13
92	BarleyVarDB: a database of barley genomic variation. <i>Database: the Journal of Biological Databases and Curation</i> , 2020, 2020, .	1.4	13
93	Statistical evaluation and comparison of a pairwise alignment algorithm that a priori assigns the number of gaps rather than employing gap penalties. <i>Bioinformatics</i> , 2005, 21, 1421-1428.	1.8	12
94	Wheat genome structure and function: genome sequence data and the International Wheat Genome Sequencing Consortium. <i>Australian Journal of Agricultural Research</i> , 2007, 58, 470.	1.5	12
95	Advances in biotechnology and informatics to link variation in the genome to phenotypes in plants and animals. <i>Functional and Integrative Genomics</i> , 2013, 13, 1-9.	1.4	12
96	Thalassaemia and hemoglobinopathies database for India: defining a model country-specific and disease-centric bioinformatics resource. <i>Human Mutation</i> , 2011, 32, 887-893.	1.1	11
97	Acetylcholinesterase 1 in populations of organophosphate-resistant North American strains of the cattle tick, <i>Rhipicephalus microplus</i> (Acari: Ixodidae). <i>Parasitology Research</i> , 2015, 114, 3027-3040.	0.6	11
98	A Registry Framework Enabling Patient-Centred Care. <i>Studies in Health Technology and Informatics</i> , 2015, 214, 8-14.	0.2	11
99	MHC Haplotype Analysis by Artificial Neural Networks. <i>Human Immunology</i> , 1998, 59, 56-62.	1.2	10
100	Identification of a ribonuclease H gene in both <i>Mycoplasma genitalium</i> and <i>Mycoplasma pneumoniae</i> by a new method for exhaustive identification of ORFs in the complete genome sequences. <i>FEBS Letters</i> , 1999, 445, 6-8.	1.3	10
101	Differential gene expression analysis in early and late erythroid progenitor cells in thalassaemia. <i>British Journal of Haematology</i> , 2015, 170, 257-267.	1.2	10
102	Rare Disease Research Roadmap: Navigating the bioinformatics and translational challenges for improved patient health outcomes. <i>Health Policy and Technology</i> , 2014, 3, 325-335.	1.3	9
103	Characterization of genome-wide variations induced by gamma-ray radiation in barley using RNA-Seq. <i>BMC Genomics</i> , 2019, 20, 783.	1.2	9
104	ERDMAS: An exemplar-driven institutional research data management and analysis strategy. <i>International Journal of Information Management</i> , 2020, 50, 337-340.	10.5	9
105	Inferring the direction of evolutionary changes of genomic base composition. <i>Trends in Genetics</i> , 1999, 15, 254-256.	2.9	8
106	Structure and Polymorphism of two Stress-Activated Protein Kinase Genes Centromeric of the MHC: SAPK2a and SAPK4. <i>DNA Sequence</i> , 1999, 10, 229-243.	0.7	7
107	A promoter with bidirectional activity is located between TLX1/HOX11 and a divergently transcribed novel human gene. <i>Gene</i> , 2007, 391, 223-232.	1.0	7
108	Trial Refresh: A Case for an Adaptive Platform Trial for Pulmonary Exacerbations of Cystic Fibrosis. <i>Frontiers in Pharmacology</i> , 2019, 10, 301.	1.6	7

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109	The complexity of <i>Rhipicephalus (Boophilus) microplus</i> genome characterised through detailed analysis of two BAC clones. <i>BMC Research Notes</i> , 2011, 4, 254.	0.6	6
110	A Bioinformatics Framework for plant pathologists to deliver global food security outcomes. <i>Australasian Plant Pathology</i> , 2012, 41, 113-124.	0.5	6
111	Immunoic Investigation of Holocyclotoxins to Produce the First Protective Anti-Venom Vaccine Against the Australian Paralysis Tick, <i>Ixodes holocyclus</i> . <i>Frontiers in Immunology</i> , 2021, 12, 744795.	2.2	6
112	The Evolution of MHC Diversity by Segmental Duplication and Transposition of Retroelements. <i>Journal of Molecular Evolution</i> , 1998, 46, 734-734.	0.8	5
113	MASV–Multiple (BLAST) Annotation System Viewer. <i>Bioinformatics</i> , 2003, 19, 2313-2315.	1.8	5
114	Microarray analysis using bioinformatics analysis audit trails (BAATs). <i>Comptes Rendus - Biologies</i> , 2003, 326, 1083-1087.	0.1	4
115	MiNDAUS partnership: a roadmap for the cure and management of motor Neurone disease. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2022, 23, 321-328.	1.1	4
116	A Bioinformatics Reference Model: Towards a Framework for Developing and Organising Bioinformatic Resources. <i>AIP Conference Proceedings</i> , 2007, , .	0.3	3
117	Genome studies at the PAC 2011 conference. <i>Functional and Integrative Genomics</i> , 2011, 11, 1-11.	1.4	3
118	Classification of fish samples via an integrated proteomics and bioinformatics approach. <i>Proteomics</i> , 2013, 13, 3124-3130.	1.3	3
119	Design, development and deployment of a web-based patient registry for rare genetic lipid disorders. <i>Pathology</i> , 2020, 52, 447-452.	0.3	3
120	Comprehending the Health Informatics Spectrum: Grappling with System Entropy and Advancing Quality Clinical Research. <i>Frontiers in Public Health</i> , 2017, 5, 224.	1.3	2
121	Looking through genomics: concepts and technologies for plant and animal genomics. <i>Functional and Integrative Genomics</i> , 2004, 4, 71-73.	1.4	1
122	Wheat Grain Proteomics for the Food Industry. , 2013, , 341-377.		1
123	Draft Genome Sequences of <i>Campylobacter fetus</i> subsp. <i>venerealis</i> bv. <i>venerealis</i> Strain B6 and bv. <i>intermedius</i> Strain 642-21. <i>Genome Announcements</i> , 2014, 2, .	0.8	1
124	Comparative genomic analysis of non-coding sequences and the application of RNA interference tools for bovine functional genomics. <i>Australian Journal of Experimental Agriculture</i> , 2005, 45, 995.	1.0	1
125	Looking through genomics?from the editors. <i>Functional and Integrative Genomics</i> , 2005, 5, 1-3.	1.4	0
126	The Expressed Portion of the Barley Genome. <i>Compendium of Plant Genomes</i> , 2018, , 89-107.	0.3	0

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127	A web-based registry for rare genetic lipid disorders. Pathology, 2019, 51, S108.	0.3	0
128	Classification of Information About Proteins. , 2009, , 243-258.		0
129	Current Trends in Biomedical Data and Applications. Studies in Computational Intelligence, 2009, , 1-9.	0.7	0
130	Protein Data Integration Problem. Studies in Computational Intelligence, 2009, , 55-69.	0.7	0
131	An Open Framework for Extensible Multi-stage Bioinformatics Software. Lecture Notes in Computer Science, 2012, , 106-117.	1.0	0