

Matthew I Bellgard

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

128
papers

6,299
citations

35
h-index

77
g-index

134
ext. papers

7,828
ext. citations

4.8
avg, IF

4.93
L-index

#	Paper	IF	Citations
128	Immunomic Investigation of Holocyclotoxins to Produce the First Protective Anti-Venom Vaccine Against the Australian Paralysis Tick,. <i>Frontiers in Immunology</i> , 2021 , 12, 744795	8.4	2
127	MiNDAUS partnership: a roadmap for the cure and management of motor Neurone disease. <i>Amyotrophic Lateral Sclerosis and Frontotemporal Degeneration</i> , 2021 , 1-8	3.6	0
126	Design, development and deployment of a web-based patient registry for rare genetic lipid disorders. <i>Pathology</i> , 2020 , 52, 447-452	1.6	1
125	BarleyVarDB: a database of barley genomic variation. <i>Database: the Journal of Biological Databases and Curation</i> , 2020 , 2020,	5	7
124	ERDMAS: An exemplar-driven institutional research data management and analysis strategy. <i>International Journal of Information Management</i> , 2020 , 50, 337-340	16.4	5
123	Trial Refresh: A Case for an Adaptive Platform Trial for Pulmonary Exacerbations of Cystic Fibrosis. <i>Frontiers in Pharmacology</i> , 2019 , 10, 301	5.6	3
122	RD-RAP: beyond rare disease patient registries, devising a comprehensive data and analytic framework. <i>Orphanet Journal of Rare Diseases</i> , 2019 , 14, 176	4.2	10
121	A web-based registry for rare genetic lipid disorders. <i>Pathology</i> , 2019 , 51, S108	1.6	
120	Characterization of genome-wide variations induced by gamma-ray radiation in barley using RNA-Seq. <i>BMC Genomics</i> , 2019 , 20, 783	4.5	2
119	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	2.6	11
118	The role of patient registries for rare genetic lipid disorders. <i>Current Opinion in Lipidology</i> , 2018 , 29, 156-162	4.2	15
117	Research protocol: The initiation, design and establishment of the Global Angelman Syndrome Registry. <i>Journal of Intellectual Disability Research</i> , 2018 , 62, 431-443	3.2	6
116	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	2.1	14
115	Transcriptome and toxin family analysis of the paralysis tick, Ixodes holocyclus. <i>International Journal for Parasitology</i> , 2018 , 48, 71-82	4.3	22
114	The Expressed Portion of the Barley Genome. <i>Compendium of Plant Genomes</i> , 2018 , 89-107	0.8	
113	Differentially expressed genes in response to amitraz treatment suggests a proposed model of resistance to amitraz in R. decoloratus ticks. <i>International Journal for Parasitology: Drugs and Drug Resistance</i> , 2018 , 8, 361-371	4	10
112	A Web-Based Registry for Familial Hypercholesterolaemia. <i>Heart Lung and Circulation</i> , 2017 , 26, 635-639	1.8	14

111	MASTR-MS: a web-based collaborative laboratory information management system (LIMS) for metabolomics. <i>Metabolomics</i> , 2017 , 13, 14	4.7	12
110	An internet-based bioinformatics toolkit for plant biosecurity diagnosis and surveillance of viruses and viroids. <i>BMC Bioinformatics</i> , 2017 , 18, 26	3.6	37
109	A chromosome conformation capture ordered sequence of the barley genome. <i>Nature</i> , 2017 , 544, 427-433	33.4	822
108	Construction of a map-based reference genome sequence for barley, <i>Hordeum vulgare</i> L. <i>Scientific Data</i> , 2017 , 4, 170044	8.2	93
107	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	4.3	35
106	A web-based, patient driven registry for Angelman syndrome: the global Angelman syndrome registry. <i>Orphanet Journal of Rare Diseases</i> , 2017 , 12, 134	4.2	10
105	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	4	23
104	Plant Proteogenomics: Improvements to the Grapevine Genome Annotation. <i>Proteomics</i> , 2017 , 17, 1700197	1.7	16
103	Rare disease registries: a call to action. <i>Internal Medicine Journal</i> , 2017 , 47, 1075-1079	1.6	22
102	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	5	84
101	Translational development of splice-modifying antisense oligomers. <i>Expert Opinion on Biological Therapy</i> , 2017 , 17, 15-30	5.4	16
100	Comprehending the Health Informatics Spectrum: Grappling with System Entropy and Advancing Quality Clinical Research. <i>Frontiers in Public Health</i> , 2017 , 5, 224	6	2
99	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	3.6	13
98	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	4.7	27
97	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, 135-41	3.8	23
96	Phenotyping: targeting genotype's rich cousin for diagnosis. <i>Journal of Paediatrics and Child Health</i> , 2015 , 51, 381-6	1.3	26
95	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	4.9	67
94	Differential gene expression analysis in early and late erythroid progenitor cells in β -thalassaemia. <i>British Journal of Haematology</i> , 2015 , 170, 257-67	4.5	7

93	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	3.7	22
92	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, 3027-40	2.4	8
91	Pseudoexon activation increases phenotype severity in a Becker muscular dystrophy patient. <i>Molecular Genetics & Genomic Medicine</i> , 2015 , 3, 320-6	2.3	18
90	Shoot transcriptome of the giant reed, <i>Arundo donax</i> . <i>Data in Brief</i> , 2015 , 3, 1-6	1.2	15
89	The TREAT-NMD DMD Global Database: analysis of more than 7,000 Duchenne muscular dystrophy mutations. <i>Human Mutation</i> , 2015 , 36, 395-402	4.7	338
88	A Registry Framework Enabling Patient-Centred Care. <i>Studies in Health Technology and Informatics</i> , 2015 , 214, 8-14	0.5	10
87	Genome sequencing and analysis of the paclitaxel-producing endophytic fungus <i>Penicillium aurantiogriseum</i> NRRL 62431. <i>BMC Genomics</i> , 2014 , 15, 69	4.5	85
86	High-throughput parallel proteogenomics: a bacterial case study. <i>Proteomics</i> , 2014 , 14, 2780-9	4.8	20
85	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	4.8	8
84	Second generation registry framework. <i>Source Code for Biology and Medicine</i> , 2014 , 9, 14	1.9	22
83	A chromosome-based draft sequence of the hexaploid bread wheat (<i>Triticum aestivum</i>) genome. <i>Science</i> , 2014 , 345, 1251788	33.3	1129
82	Ancient hybridizations among the ancestral genomes of bread wheat. <i>Science</i> , 2014 , 345, 1250092	33.3	419
81	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,		1
80	Classification of fish samples via an integrated proteomics and bioinformatics approach. <i>Proteomics</i> , 2013 , 13, 3124-30	4.8	3
79	Dispelling myths about rare disease registry system development. <i>Source Code for Biology and Medicine</i> , 2013 , 8, 21	1.9	41
78	Role of international registries in enhancing the care of familial hypercholesterolaemia. <i>International Journal of Evidence-Based Healthcare</i> , 2013 , 11, 134-9	2.6	26
77	<i>Rhipicephalus microplus</i> 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, 739-52	4.3	19
76	Plant proteogenomics: from protein extraction to improved gene predictions. <i>Methods in Molecular Biology</i> , 2013 , 1002, 267-94	1.4	13

75	Wheat Grain Proteomics for the Food Industry 2013 , 341-377		
74	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	3.8	12
73	Genome sequences of six wheat-infecting fusarium species isolates. <i>Genome Announcements</i> , 2013 , 1,		23
72	Scrapheap challenge: a novel bulk-bone metabarcoding method to investigate ancient DNA in faunal assemblages. <i>Scientific Reports</i> , 2013 , 3, 3371	4.9	53
71	Objective monitoring of mTOR inhibitor therapy by three-dimensional facial analysis. <i>Twin Research and Human Genetics</i> , 2013 , 16, 840-4	2.2	13
70	Metabarcoding avian diets at airports: implications for birdstrike hazard management planning. <i>Investigative Genetics</i> , 2013 , 4, 27		22
69	CattleTickBase: an integrated Internet-based bioinformatics resource for Rhipicephalus (Boophilus) microplus. <i>International Journal for Parasitology</i> , 2012 , 42, 161-9	4.3	51
68	Bread matters: a national initiative to profile the genetic diversity of Australian wheat. <i>Plant Biotechnology Journal</i> , 2012 , 10, 703-8	11.6	39
67	A Bioinformatics Framework for plant pathologists to deliver global food security outcomes. <i>Australasian Plant Pathology</i> , 2012 , 41, 113-124	1.4	5
66	Yabi: An online research environment for grid, high performance and cloud computing. <i>Source Code for Biology and Medicine</i> , 2012 , 7, 1	1.9	75
65	High-throughput sequencing of ancient plant and mammal DNA preserved in herbivore middens. <i>Quaternary Science Reviews</i> , 2012 , 58, 135-145	3.9	34
64	Genome-level identification of cell wall invertase genes in wheat for the study of drought tolerance. <i>Functional Plant Biology</i> , 2012 , 39, 569-579	2.7	14
63	The New Zealand Neuromuscular Disease Registry. <i>Journal of Clinical Neuroscience</i> , 2012 , 19, 1749-50	2.2	17
62	The genetics of symbiotic nitrogen fixation: comparative genomics of 14 rhizobia strains by resolution of protein clusters. <i>Genes</i> , 2012 , 3, 138-66	4.2	61
61	Comparative genomics of Brachyspira pilosicoli strains: genome rearrangements, reductions and correlation of genetic compliment with phenotypic diversity. <i>BMC Genomics</i> , 2012 , 13, 454	4.5	31
60	A modular approach to disease registry design: successful adoption of an internet-based rare disease registry. <i>Human Mutation</i> , 2012 , 33, E2356-66	4.7	27
59	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	6	180
58	An Open Framework for Extensible Multi-stage Bioinformatics Software. <i>Lecture Notes in Computer Science</i> , 2012 , 106-117	0.9	

57	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	2.3	6
56	Evidence that the 36 kb plasmid of <i>Brachyspira hyodysenteriae</i> contributes to virulence. <i>Veterinary Microbiology</i> , 2011 , 153, 150-5	3.3	18
55	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, 1001-14	4.3	26
54	Diverse approaches to achieving grain yield in wheat. <i>Functional and Integrative Genomics</i> , 2011 , 11, 37-48	3.8	32
53	Genome studies at the PAG 2011 conference. <i>Functional and Integrative Genomics</i> , 2011 , 11, 1-11	3.8	2
52	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	4.5	31
51	De novo assembly of <i>Euphorbia fischeriana</i> root transcriptome identifies prostratin pathway related genes. <i>BMC Genomics</i> , 2011 , 12, 600	4.5	57
50	ThalInd, a β -thalassemia and hemoglobinopathies database for India: defining a model country-specific and disease-centric bioinformatics resource. <i>Human Mutation</i> , 2011 , 32, 887-93	4.7	9
49	DNA-based faecal dietary analysis: a comparison of qPCR and high throughput sequencing approaches. <i>PLoS ONE</i> , 2011 , 6, e25776	3.7	87
48	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	4.5	71
47	The transcript repeat element: the human Alu sequence as a component of gene networks influencing cancer. <i>Functional and Integrative Genomics</i> , 2010 , 10, 307-19	3.8	14
46	Germin-like proteins (GLPs) in cereal genomes: gene clustering and dynamic roles in plant defence. <i>Functional and Integrative Genomics</i> , 2010 , 10, 463-76	3.8	54
45	A descriptive profile of β -thalassaemia mutations in India, Pakistan and Sri Lanka. <i>Journal of Community Genetics</i> , 2010 , 1, 149-57	2.5	25
44	Reassociation kinetics-based approach for partial genome sequencing of the cattle tick, <i>Rhipicephalus (Boophilus) microplus</i> . <i>BMC Genomics</i> , 2010 , 11, 374	4.5	27
43	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	4.5	39
42	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	5.3	11
41	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	5.3	11
40	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, 304-20	2.8	29

39	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	3.7	48
38	Genomic analysis of <i>Campylobacter fetus</i> subspecies: identification of candidate virulence determinants and diagnostic assay targets. <i>BMC Microbiology</i> , 2009 , 9, 86	4.5	40
37	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, 340-5	3.3	34
36	A reverse vaccinology approach to swine dysentery vaccine development. <i>Veterinary Microbiology</i> , 2009 , 137, 111-9	3.3	25
35	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, 330-8	3.3	45
34	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		50
33	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	4.5	50
32	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	3.7	84
31	Classification of Information About Proteins 2009 , 243-258		
30	Current Trends in Biomedical Data and Applications. <i>Studies in Computational Intelligence</i> , 2009 , 1-9	0.8	
29	Protein Data Integration Problem. <i>Studies in Computational Intelligence</i> , 2009 , 55-69	0.8	
28	BAC-derived markers for assaying the stem rust resistance gene, Sr2, in wheat breeding programs. <i>Molecular Breeding</i> , 2008 , 22, 15-24	3.4	32
27	The H-Invitational Database (H-InvDB), a comprehensive annotation resource for human genes and transcripts. <i>Nucleic Acids Research</i> , 2008 , 36, D793-9	20.1	52
26	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		11
25	A Bioinformatics Reference Model: Towards a Framework for Developing and Organising Bioinformatic Resources. <i>AIP Conference Proceedings</i> , 2007 ,	0	3
24	A promoter with bidirectional activity is located between TLX1/HOX11 and a divergently transcribed novel human gene. <i>Gene</i> , 2007 , 391, 223-32	3.8	6
23	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, 225-38	6	106
22	Ten years of bacterial genome sequencing: comparative-genomics-based discoveries. <i>Functional and Integrative Genomics</i> , 2006 , 6, 165-85	3.8	120

21	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, 964-75	5.5	50
20	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, 364-72	2.2	20
19	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, 1421-8	7.2	11
18	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
17	Integrative annotation of 21,037 human genes validated by full-length cDNA clones. <i>PLoS Biology</i> , 2004 , 2, e162	9.7	255
16	Genes controlling seed dormancy and pre-harvest sprouting in a rice-wheat-barley comparison. <i>Functional and Integrative Genomics</i> , 2004 , 4, 84-93	3.8	113
15	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, 118-30	3.8	26
14	MASV--Multiple (BLAST) Annotation System Viewer. <i>Bioinformatics</i> , 2003 , 19, 2313-5	7.2	5
13	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	3.1	43
12	Microarray analysis using bioinformatics analysis audit trails (BAATs). <i>Comptes Rendus - Biologies</i> , 2003 , 326, 1083-7	1.4	4
11	Intragenic variation of synonymous substitution rates is caused by nonrandom mutations at methylated CpG. <i>Journal of Molecular Evolution</i> , 2001 , 53, 456-64	3.1	13
10	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, 465-8	3.1	28
9	Dynamic evolution of genomes and the concept of genome space. <i>Annals of the New York Academy of Sciences</i> , 1999 , 870, 293-300	6.5	15
8	Inferring the direction of evolutionary changes of genomic base composition. <i>Trends in Genetics</i> , 1999 , 15, 254-6	8.5	6
7	Structure and polymorphism of two stress-activated protein kinase genes centromeric of the MHC: SAPK2a and SAPK4. <i>DNA Sequence</i> , 1999 , 10, 229-43		4
6	Significant differences between the G+C content of synonymous codons in orthologous genes and the genomic G+C content. <i>Gene</i> , 1999 , 238, 33-7	3.8	15
5	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	3.8	9
4	The evolution of MHC diversity by segmental duplication and transposition of retroelements. <i>Journal of Molecular Evolution</i> , 1998 , 46, 734	3.1	5

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| 3 | MHC haplotype analysis by artificial neural networks. <i>Human Immunology</i> , 1998 , 59, 56-62 | 2.3 | 9 |
| 2 | The evolution of MHC diversity by segmental duplication and transposition of retroelements. <i>Journal of Molecular Evolution</i> , 1997 , 45, 599-609 | 3.1 | 49 |
| 1 | Harmonizing Music the Boltzmann Way. <i>Connection Science</i> , 1994 , 6, 281-297 | 2.8 | 8 |