Mark Yandell

List of Publications by Year
in descending order

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73 papers	7,187 citations	109321 35 h-index	79698 73 g-index
82 all docs	82 docs citations	82 times ranked	14441 citing authors

#	Article	IF	Citations
1	MAKER2: an annotation pipeline and genome-database management tool for second-generation genome projects. BMC Bioinformatics, 2011, 12, 491.	2.6	1,654
2	A beginner's guide to eukaryotic genome annotation. Nature Reviews Genetics, 2012, 13, 329-342.	16.3	553
3	The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. Nature Genetics, 2016, 48, 427-437.	21.4	545
4	Genomic signatures of evolutionary transitions from solitary to group living. Science, 2015, 348, 1139-1143.	12.6	357
5	The sea lamprey germline genome provides insights into programmed genome rearrangement and vertebrate evolution. Nature Genetics, 2018, 50, 270-277.	21.4	262
6	Using VAAST to Identify an X-Linked Disorder Resulting in Lethality in Male Infants Due to N-Terminal Acetyltransferase Deficiency. American Journal of Human Genetics, 2011, 89, 28-43.	6.2	222
7	Muscle stem cells contribute to myofibres in sedentary adult mice. Nature Communications, 2015, 6, 7087.	12.8	222
8	Settling the score: variant prioritization and Mendelian disease. Nature Reviews Genetics, 2017, 18, 599-612.	16.3	213
9	Transposable element islands facilitate adaptation to novel environments in an invasive species. Nature Communications, 2014, 5, 5495.	12.8	183
10	A probabilistic disease-gene finder for personal genomes. Genome Research, 2011, 21, 1529-1542.	5.5	182
11	Unbiased Detection of Respiratory Viruses by Use of RNA Sequencing-Based Metagenomics: a Systematic Comparison to a Commercial PCR Panel. Journal of Clinical Microbiology, 2016, 54, 1000-1007.	3.9	177
12	Phevor Combines Multiple Biomedical Ontologies for Accurate Identification of Disease-Causing Alleles in Single Individuals and Small Nuclear Families. American Journal of Human Genetics, 2014, 94, 599-610.	6.2	175
13	Taxonomer: an interactive metagenomics analysis portal for universal pathogen detection and host mRNA expression profiling. Genome Biology, 2016, 17, 111.	8.8	152
14	Evidence for extensive horizontal gene transfer from the draft genome of a tardigrade. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 15976-15981.	7.1	145
15	Specialized insulin is used for chemical warfare by fish-hunting cone snails. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 1743-1748.	7.1	134
16	VAAST 2.0: Improved Variant Classification and Diseaseâ€Gene Identification Using a Conservationâ€Controlled Amino Acid Substitution Matrix. Genetic Epidemiology, 2013, 37, 622-634.	1.3	128
17	Wham: Identifying Structural Variants of Biological Consequence. PLoS Computational Biology, 2015, 11, e1004572.	3.2	105
18	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. G3: Genes, Genomes, Genetics, 2017, 7, 3157-3167.	1.8	103

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19	A unified test of linkage analysis and rare-variant association for analysis of pedigree sequence data. Nature Biotechnology, 2014, 32, 663-669.	17.5	93
20	Viral Pathogen Detection by Metagenomics and Pan-Viral Group Polymerase Chain Reaction in Children With Pneumonia Lacking Identifiable Etiology. Journal of Infectious Diseases, 2017, 215, 1407-1415.	4.0	85
21	Coordinated control of senescence by lncRNA and a novel T-box3 co-repressor complex. ELife, 2014, 3, .	6.0	81
22	Transiently Active Wnt/Î²-Catenin Signaling Is Not Required but Must Be Silenced for Stem Cell Function during Muscle Regeneration. Stem Cell Reports, 2014, 3, 475-488.	4.8	76
23	Epistatic and Combinatorial Effects of Pigmentary Gene Mutations in the Domestic Pigeon. Current Biology, 2014, 24, 459-464.	3.9	75
24	Introgression of regulatory alleles and a missense coding mutation drive plumage pattern diversity in the rock pigeon. ELife, 2018, 7, .	6.0	66
25	Molecular shifts in limb identity underlie development of feathered feet in two domestic avian species. ELife, 2016, 5, e12115.	6.0	64
26	Hormone-like peptides in the venoms of marine cone snails. General and Comparative Endocrinology, 2017, 244, 11-18.	1.8	63
27	Improved Genome Assembly and Annotation for the Rock Pigeon (Columba livia). G3: Genes, Genomes, Genetics, 2018, 8, 1391-1398.	1.8	62
28	De novo and recessive forms of congenital heart disease have distinct genetic and phenotypic landscapes. Nature Communications, 2019, 10, 4722.	12.8	58
29	Identification of Polycystic Kidney Disease 1 Like 1 Gene Variants in Children With Biliary Atresia Splenic Malformation Syndrome. Hepatology, 2019, 70, 899-910.	7.3	58
30	Autoimmunity due to RAG deficiency and estimated disease incidence in RAG1/2 mutations. Journal of Allergy and Clinical Immunology, 2014, 133, 880-882.e10.	2.9	54
31	Automated Update, Revision, and Quality Control of the Maize Genome Annotations Using MAKER-P Improves the B73 RefGen_v3 Gene Models and Identifies New Genes Â. Plant Physiology, 2014, 167, 25-39.	4.8	53
32	Primary Ovarian Insufficiency and Azoospermia in Carriers of a Homozygous PSMC3IP Stop Gain Mutation. Journal of Clinical Endocrinology and Metabolism, 2018, 103, 555-563.	3.6	45
33	Venom Insulins of Cone Snails Diversify Rapidly and Track Prey Taxa. Molecular Biology and Evolution, 2016, 33, 2924-2934.	8.9	44
34	DisAp-dependent striated fiber elongation is required to organize ciliary arrays. Journal of Cell Biology, 2014, 207, 705-715.	5.2	43
35	Rapid expansion of the protein disulfide isomerase gene family facilitates the folding of venom peptides. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3227-3232.	7.1	39
36	Emergence of a Viral RNA Polymerase Variant during Gene Copy Number Amplification Promotes Rapid Evolution of Vaccinia Virus. Journal of Virology, 2017, 91, .	3.4	36

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37	A copy number variant is associated with a spectrum of pigmentation patterns in the rock pigeon (Columba livia). PLoS Genetics, 2020, 16, e1008274.	3.5	34
38	Antimicrobial Functions of Lactoferrin Promote Genetic Conflicts in Ancient Primates and Modern Humans. PLoS Genetics, 2016, 12, e1006063.	3.5	32
39	TBX3 Regulates Splicing In Vivo: A Novel Molecular Mechanism for Ulnar-Mammary Syndrome. PLoS Genetics, 2014, 10, e1004247.	3.5	31
40	Divergence of the Venom Exogene Repertoire in Two Sister Species of Turriconus. Genome Biology and Evolution, 2017, 9, 2211-2225.	2.5	30
41	The VAAST Variant Prioritizer (VVP): ultrafast, easy to use whole genome variant prioritization tool. BMC Bioinformatics, 2018, 19, 57.	2.6	29
42	The Venom Repertoire of Conus gloriamaris (Chemnitz, 1777), the Glory of the Sea. Marine Drugs, 2017, 15, 145.	4.6	27
43	Curses or Cures: A Review of the Numerous Benefits Versus the Biosecurity Concerns of Conotoxin Research. Biomedicines, 2020, 8, 235.	3.2	27
44	Comprehensive Analysis of AR Alterations in Circulating Tumor DNA from Patients with Advanced Prostate Cancer. Oncologist, 2020, 25, 327-333.	3.7	27
45	Pharmacogenomics of 17-alpha hydroxyprogesterone caproate for recurrent preterm birth prevention. American Journal of Obstetrics and Gynecology, 2014, 210, 321.e1-321.e21.	1.3	23
46	Regulatory Divergence in Wound-Responsive Gene Expression between Domesticated and Wild Tomato. Plant Cell, 2018, 30, 1445-1460.	6.6	23
47	Human Bocavirus Capsid Messenger RNA Detection in Children With Pneumonia. Journal of Infectious Diseases, 2017, 216, 688-696.	4.0	22
48	Using VAAST to Identify Diseaseâ€Associated Variants in Nextâ€Generation Sequencing Data. Current Protocols in Human Genetics, 2014, 81, 6.14.1-25.	3.5	21
49	Discovery of Novel Conotoxin Candidates Using Machine Learning. Toxins, 2018, 10, 503.	3.4	20
50	Clinical and molecular epidemiology of invasive Staphylococcus aureus infection in Utah children; continued dominance of MSSA over MRSA. PLoS ONE, 2020, 15, e0238991.	2.5	20
51	Exome analysis of a family with Wolffâ€“Parkinsonâ€“White syndrome identifies a novel disease locus. American Journal of Medical Genetics, Part A, 2015, 167, 2975-2984.	1.2	17
52	Transcriptomic Profiling Reveals Extraordinary Diversity of Venom Peptides in Unexplored Predatory Gastropods of the Genus Clavus. Genome Biology and Evolution, 2020, 12, 684-700.	2.5	17
53	The genomic basis of evolutionary differentiation among honey bees. Genome Research, 2021, 31, 1203-1215.	5.5	17
54	Shared Segment Analysis and Next-Generation Sequencing Implicates the Retinoic Acid Signaling Pathway in Total Anomalous Pulmonary Venous Return (TAPVR). PLoS ONE, 2015, 10, e0131514.	2.5	16

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55	A ROR2 coding variant is associated with craniofacial variation in domestic pigeons. Current Biology, 2021, 31, 5069-5076.e5.	3.9	14
56	Causal and Candidate Gene Variants in a Large Cohort of Women With Primary Ovarian Insufficiency. Journal of Clinical Endocrinology and Metabolism, 2022, 107, 685-714.	3.6	13
57	An explainable artificial intelligence approach for predicting cardiovascular outcomes using electronic health records. , 2022, 1, e0000004.		13
58	Two Genomic Loci Control Three Eye Colors in the Domestic Pigeon (Columba livia). Molecular Biology and Evolution, 2021, 38, 5376-5390.	8.9	11
59	The draft genome sequence and annotation of the desert woodrat Neotoma lepida. Genomics Data, 2016, 9, 58-59.	1.3	9
60	Identification of Somatic Gene Signatures in Circulating <scp>Cell-Free DNA</scp> Associated with Disease Progression in Metastatic Prostate Cancer by a Novel Machine Learning Platform. Oncologist, 2021, 26, 751-760.	3.7	9
61	VARPRISM: incorporating variant prioritization in tests of de novo mutation association. Genome Medicine, 2016, 8, 91.	8.2	7
62	Pulmonary Eosinophilic Granulomatosis with Polyangiitis Has IgG4 Plasma Cells and Immunoregulatory Features. American Journal of Pathology, 2020, 190, 1438-1448.	3.8	7
63	The history and geographic distribution of a KCNQ1 atrial fibrillation risk allele. Nature Communications, 2021, 12, 6442.	12.8	7
64	XPAT: a toolkit to conduct cross-platform association studies with heterogeneous sequencing datasets. Nucleic Acids Research, 2018, 46, e32-e32.	14.5	6
65	A Poisson binomial-based statistical testing framework for comorbidity discovery across electronic health record datasets. Nature Computational Science, 2021, 1, 694-702.	8.0	6
66	Comprehensive variant calling from wholeâ€genome sequencing identifies a complex inversion that disrupts <scp>ZFPM2</scp> in familial congenital diaphragmatic hernia. Molecular Genetics & Genomic Medicine, 2022, 10, e1888.	1.2	6
67	Deep whole-genome sequencing of multiple proband tissues and parental blood reveals the complex genetic etiology of congenital diaphragmatic hernias. Human Genetics and Genomics Advances, 2020, 1, 100008.	1.7	5
68	An Introduction to Genome Annotation. Current Protocols in Bioinformatics, 2015, 52, 4.1.1-4.1.17.	25.8	4
69	Noncoding sequence variants define a novel regulatory element in the first intron of the N â€acetylglutamate synthase gene. Human Mutation, 2021, 42, 1624-1636.	2.5	3
70	Development of a Portable Tool to Identify Patients With Atrial Fibrillation Using Clinical Notes From the Electronic Medical Record. Circulation: Cardiovascular Quality and Outcomes, 2020, 13, e006516.	2.2	2
71	Common Variation in Cytoskeletal Genes Is Associated with Conotruncal Heart Defects. Genes, 2021, 12, 655.	2.4	2
72	Addressing Ethical and Laboratory Challenges for Initiation of a Rapid Whole Genome Sequencing Program. Journal of Clinical and Translational Science, 2021, 5, 1-13.	0.6	2

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73	Next Generation Sequencing to Delineate the Mutational Landscape of Chronic Myelomonocytic Leukemia (CMML): Novel Disease Genes and Correlations with Survival. Blood, 2014, 124, 4637-4637.	1.4	0