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	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
2	An explainable artificial intelligence approach for predicting cardiovascular outcomes using electronic health records. , 2022, 1, e0000004.		13
3	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
4	Common Variation in Cytoskeletal Genes Is Associated with Conotruncal Heart Defects. Genes, 2021, 12, 655.	2.4	2
5	The genomic basis of evolutionary differentiation among honey bees. Genome Research, 2021, 31, 1203-1215.	5.5	17
6	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
7	Two Genomic Loci Control Three Eye Colors in the Domestic Pigeon (Columba livia). Molecular Biology and Evolution, 2021, 38, 5376-5390.	8.9	11
8	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
9	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
10	A ROR2 coding variant is associated with craniofacial variation in domestic pigeons. Current Biology, 2021, 31, 5069-5076.e5.	3.9	14
11	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
12	The history and geographic distribution of a KCNQ1 atrial fibrillation risk allele. Nature Communications, 2021, 12, 6442.	12.8	7
13	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
14	Curses or Cures: A Review of the Numerous Benefits Versus the Biosecurity Concerns of Conotoxin Research. Biomedicines, 2020, 8, 235.	3.2	27
15	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
16	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
17	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
18	Comprehensive Analysis of AR Alterations in Circulating Tumor DNA from Patients with Advanced Prostate Cancer. Oncologist, 2020, 25, 327-333.	3.7	27

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19	Pulmonary Eosinophilic Granulomatosis with Polyangiitis Has IgG4 Plasma Cells and Immunoregulatory Features. American Journal of Pathology, 2020, 190, 1438-1448.	3.8	7
20	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
21	De novo and recessive forms of congenital heart disease have distinct genetic and phenotypic landscapes. Nature Communications, 2019, 10, 4722.	12.8	58
22	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
23	Improved Genome Assembly and Annotation for the Rock Pigeon (Columba livia). G3: Genes, Genomes, Genetics, 2018, 8, 1391-1398.	1.8	62
24	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
25	The sea lamprey germline genome provides insights into programmed genome rearrangement and vertebrate evolution. Nature Genetics, 2018, 50, 270-277.	21.4	262
26	XPAT: a toolkit to conduct cross-platform association studies with heterogeneous sequencing datasets. Nucleic Acids Research, 2018, 46, e32-e32.	14.5	6
27	Discovery of Novel Conotoxin Candidates Using Machine Learning. Toxins, 2018, 10, 503.	3.4	20
28	Introgression of regulatory alleles and a missense coding mutation drive plumage pattern diversity in the rock pigeon. ELife, 2018, 7, .	6.0	66
29	The VAAST Variant Prioritizer (VVP): ultrafast, easy to use whole genome variant prioritization tool. BMC Bioinformatics, 2018, 19, 57.	2.6	29
30	Regulatory Divergence in Wound-Responsive Gene Expression between Domesticated and Wild Tomato. Plant Cell, 2018, 30, 1445-1460.	6.6	23
31	Hormone-like peptides in the venoms of marine cone snails. General and Comparative Endocrinology, 2017, 244, 11-18.	1.8	63
32	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
33	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
34	Human Bocavirus Capsid Messenger RNA Detection in Children With Pneumonia. Journal of Infectious Diseases, 2017, 216, 688-696.	4.0	22
35	The Douglas-Fir Genome Sequence Reveals Specialization of the Photosynthetic Apparatus in Pinaceae. G3: Genes, Genomes, Genetics, 2017, 7, 3157-3167.	1.8	103
36	Settling the score: variant prioritization and Mendelian disease. Nature Reviews Genetics, 2017, 18, 599-612.	16.3	213

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37	The Venom Repertoire of Conus gloriamaris (Chemnitz, 1777), the Glory of the Sea. Marine Drugs, 2017, 15, 145.	4.6	27
38	Divergence of the Venom Exogene Repertoire in Two Sister Species of Turriconus. Genome Biology and Evolution, 2017, 9, 2211-2225.	2.5	30
39	Molecular shifts in limb identity underlie development of feathered feet in two domestic avian species. ELife, 2016, 5, e12115.	6.0	64
40	Antimicrobial Functions of Lactoferrin Promote Genetic Conflicts in Ancient Primates and Modern Humans. PLoS Genetics, 2016, 12, e1006063.	3.5	32
41	VARPRISM: incorporating variant prioritization in tests of de novo mutation association. Genome Medicine, 2016, 8, 91.	8.2	7
42	The draft genome sequence and annotation of the desert woodrat Neotoma lepida. Genomics Data, 2016, 9, 58-59.	1.3	9
43	Venom Insulins of Cone Snails Diversify Rapidly and Track Prey Taxa. Molecular Biology and Evolution, 2016, 33, 2924-2934.	8.9	44
44	Taxonomer: an interactive metagenomics analysis portal for universal pathogen detection and host mRNA expression profiling. Genome Biology, 2016, 17, 111.	8.8	152
45	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
46	The spotted gar genome illuminates vertebrate evolution and facilitates human-teleost comparisons. Nature Genetics, 2016, 48, 427-437.	21.4	545
47	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
48	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
49	An Introduction to Genome Annotation. Current Protocols in Bioinformatics, 2015, 52, 4.1.1-4.1.17.	25.8	4
50	Wham: Identifying Structural Variants of Biological Consequence. PLoS Computational Biology, 2015, 11, e1004572.	3.2	105
51	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
52	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
53	Muscle stem cells contribute to myofibres in sedentary adult mice. Nature Communications, 2015, 6, 7087.	12.8	222
54	Genomic signatures of evolutionary transitions from solitary to group living. Science, 2015, 348, 1139-1143.	12.6	357

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55	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
56	Coordinated control of senescence by lncRNA and a novel T-box3 co-repressor complex. ELife, 2014, 3, .	6.0	81
57	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
58	TBX3 Regulates Splicing In Vivo: A Novel Molecular Mechanism for Ulnar-Mammary Syndrome. PLoS Genetics, 2014, 10, e1004247.	3.5	31
59	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
60	Transposable element islands facilitate adaptation to novel environments in an invasive species. Nature Communications, 2014, 5, 5495.	12.8	183
61	DisAp-dependent striated fiber elongation is required to organize ciliary arrays. Journal of Cell Biology, 2014, 207, 705-715.	5.2	43
62	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
63	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
64	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
65	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
66	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
67	Epistatic and Combinatorial Effects of Pigmentary Gene Mutations in the Domestic Pigeon. Current Biology, 2014, 24, 459-464.	3.9	75
68	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
69	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
70	A beginner's guide to eukaryotic genome annotation. Nature Reviews Genetics, 2012, 13, 329-342.	16.3	553
71	A probabilistic disease-gene finder for personal genomes. Genome Research, 2011, 21, 1529-1542.	5.5	182
72	MAKER2: an annotation pipeline and genome-database management tool for second-generation genome projects. BMC Bioinformatics, 2011, 12, 491.	2.6	1,654

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73	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