

# Jane Grimwood

## List of Publications by Year in descending order

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131  
papers

64,044  
citations

8180

76  
h-index

12944

131  
g-index

139  
all docs

139  
docs citations

139  
times ranked

61555  
citing authors

#	ARTICLE	IF	CITATIONS
1	Initial sequencing and analysis of the human genome. <i>Nature</i> , 2001, 409, 860-921.	27.8	21,074
2	Genome sequence of the palaeopolyploid soybean. <i>Nature</i> , 2010, 463, 178-183.	27.8	3,854
3	The <i>Sorghum bicolor</i> genome and the diversification of grasses. <i>Nature</i> , 2009, 457, 551-556.	27.8	2,642
4	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. <i>Science</i> , 2007, 318, 245-250.	12.6	2,354
5	Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 16899-16903.	7.1	1,610
6	The genomic basis of adaptive evolution in threespine sticklebacks. <i>Nature</i> , 2012, 484, 55-61.	27.8	1,600
7	The <i>Phaeodactylum</i> genome reveals the evolutionary history of diatom genomes. <i>Nature</i> , 2008, 456, 239-244.	27.8	1,458
8	Widespread Parallel Evolution in Sticklebacks by Repeated Fixation of Ectodysplasin Alleles. <i>Science</i> , 2005, 307, 1928-1933.	12.6	1,299
9	Repeated polyploidization of <i>Gossypium</i> genomes and the evolution of spinnable cotton fibres. <i>Nature</i> , 2012, 492, 423-427.	27.8	1,204
10	A reference genome for common bean and genome-wide analysis of dual domestications. <i>Nature Genetics</i> , 2014, 46, 707-713.	21.4	1,159
11	The high-quality draft genome of peach ( <i>Prunus persica</i> ) identifies unique patterns of genetic diversity, domestication and genome evolution. <i>Nature Genetics</i> , 2013, 45, 487-494.	21.4	1,031
12	Insights into Land Plant Evolution Garnered from the <i>Marchantia polymorpha</i> Genome. <i>Cell</i> , 2017, 171, 287-304.e15.	28.9	973
13	Adaptive Evolution of Pelvic Reduction in Sticklebacks by Recurrent Deletion of a <i>Pitx1</i> Enhancer. <i>Science</i> , 2010, 327, 302-305.	12.6	901
14	Reference genome sequence of the model plant <i>Setaria</i> . <i>Nature Biotechnology</i> , 2012, 30, 555-561.	17.5	864
15	Genome evolution in the allotetraploid frog <i>Xenopus laevis</i> . <i>Nature</i> , 2016, 538, 336-343.	27.8	849
16	The <i>Arabidopsis lyrata</i> genome sequence and the basis of rapid genome size change. <i>Nature Genetics</i> , 2011, 43, 476-481.	21.4	814
17	The <i>Trichoplax</i> genome and the nature of placozoans. <i>Nature</i> , 2008, 454, 955-960.	27.8	801
18	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	27.8	725

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19	The Genome of the Western Clawed Frog <i>Xenopus tropicalis</i> . <i>Science</i> , 2010, 328, 633-636.	12.6	708
20	Comparative genomes of <i>Chlamydia pneumoniae</i> and <i>C. trachomatis</i> . <i>Nature Genetics</i> , 1999, 21, 385-389.	21.4	636
21	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 2009, 324, 268-272.	12.6	591
22	Sequencing of diverse mandarin, pummelo and orange genomes reveals complex history of admixture during citrus domestication. <i>Nature Biotechnology</i> , 2014, 32, 656-662.	17.5	572
23	Insights into bilaterian evolution from three spiralian genomes. <i>Nature</i> , 2013, 493, 526-531.	27.8	564
24	The tiny eukaryote <i>Ostreococcus</i> provides genomic insights into the paradox of plankton speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7705-7710.	7.1	563
25	Genomic Analysis of Organismal Complexity in the Multicellular Green Alga <i>Volvox carteri</i> . <i>Science</i> , 2010, 329, 223-226.	12.6	536
26	Finished Genome of the Fungal Wheat Pathogen <i>Mycosphaerella graminicola</i> Reveals Dispersome Structure, Chromosome Plasticity, and Stealth Pathogenesis. <i>PLoS Genetics</i> , 2011, 7, e1002070.	3.5	532
27	The Status, Quality, and Expansion of the NIH Full-Length cDNA Project: The Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2004, 14, 2121-2127.	5.5	486
28	The genome of the seagrass <i>Zostera marina</i> reveals angiosperm adaptation to the sea. <i>Nature</i> , 2016, 530, 331-335.	27.8	460
29	Coding potential of laboratory and clinical strains of human cytomegalovirus. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 14976-14981.	7.1	450
30	Genome sequence of the lignocellulose-bioconverting and xylose-fermenting yeast <i>Pichia stipitis</i> . <i>Nature Biotechnology</i> , 2007, 25, 319-326.	17.5	449
31	The genome sequence of segmental allotetraploid peanut <i>Arachis hypogaea</i> . <i>Nature Genetics</i> , 2019, 51, 877-884.	21.4	439
32	The <i>Sorghum bicolor</i> reference genome: improved assembly, gene annotations, a transcriptome atlas, and signatures of genome organization. <i>Plant Journal</i> , 2018, 93, 338-354.	5.7	431
33	Comparative genomic analysis of the thermophilic biomass-degrading fungi <i>Myceliophthora thermophila</i> and <i>Thielavia terrestris</i> . <i>Nature Biotechnology</i> , 2011, 29, 922-927.	17.5	428
34	The <i>Physcomitrella patens</i> chromosome-scale assembly reveals moss genome structure and evolution. <i>Plant Journal</i> , 2018, 93, 515-533.	5.7	406
35	The Genome of <i>Nectria haematococca</i> : Contribution of Supernumerary Chromosomes to Gene Expansion. <i>PLoS Genetics</i> , 2009, 5, e1000618.	3.5	402
36	Algal genomes reveal evolutionary mosaicism and the fate of nucleomorphs. <i>Nature</i> , 2012, 492, 59-65.	27.8	377

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37	The <i>Capsella rubella</i> genome and the genomic consequences of rapid mating system evolution. <i>Nature Genetics</i> , 2013, 45, 831-835.	21.4	374
38	Longitudinal serum concentrations of placental growth factor: Evidence for abnormal placental angiogenesis in pathologic pregnancies. <i>American Journal of Obstetrics and Gynecology</i> , 2003, 188, 177-182.	1.3	373
39	The Master Sex-Determination Locus in Threespine Sticklebacks Is on a Nascent Y Chromosome. <i>Current Biology</i> , 2004, 14, 1416-1424.	3.9	367
40	Genome sequence of the button mushroom <i>Agaricus bisporus</i> reveals mechanisms governing adaptation to a humic-rich ecological niche. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 17501-17506.	7.1	359
41	Sequencing wild and cultivated cassava and related species reveals extensive interspecific hybridization and genetic diversity. <i>Nature Biotechnology</i> , 2016, 34, 562-570.	17.5	340
42	Comparative genomics of citric-acid-producing <i>Aspergillus niger</i> ATCC 1015 versus enzyme-producing CBS 513.88. <i>Genome Research</i> , 2011, 21, 885-897.	5.5	329
43	A role for a neo-sex chromosome in stickleback speciation. <i>Nature</i> , 2009, 461, 1079-1083.	27.8	327
44	The barley pan-genome reveals the hidden legacy of mutation breeding. <i>Nature</i> , 2020, 588, 284-289.	27.8	314
45	The DNA sequence and biology of human chromosome 19. <i>Nature</i> , 2004, 428, 529-535.	27.8	298
46	On the origin and evolutionary consequences of gene body DNA methylation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 9111-9116.	7.1	260
47	Genomic diversifications of five <i>Gossypium</i> allopolyploid species and their impact on cotton improvement. <i>Nature Genetics</i> , 2020, 52, 525-533.	21.4	249
48	Insights into the red algae and eukaryotic evolution from the genome of <i>Porphyra umbilicalis</i> (Bangiophyceae, Rhodophyta). <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E6361-E6370.	7.1	233
49	Comparative Genome Structure, Secondary Metabolite, and Effector Coding Capacity across <i>Cochliobolus</i> Pathogens. <i>PLoS Genetics</i> , 2013, 9, e1003233.	3.5	232
50	Comparative DNA Sequence Analysis of Mouse and Human Protocadherin Gene Clusters. <i>Genome Research</i> , 2001, 11, 389-404.	5.5	224
51	A Genome-wide SNP Genotyping Array Reveals Patterns of Global and Repeated Species-Pair Divergence in Sticklebacks. <i>Current Biology</i> , 2012, 22, 83-90.	3.9	212
52	Insight into trade-off between wood decay and parasitism from the genome of a fungal forest pathogen. <i>New Phytologist</i> , 2012, 194, 1001-1013.	7.3	210
53	The Reference Genome of the Halophytic Plant <i>Eutrema salsugineum</i> . <i>Frontiers in Plant Science</i> , 2013, 4, 46.	3.6	198
54	Long-read sequence assembly: a technical evaluation in barley. <i>Plant Cell</i> , 2021, 33, 1888-1906.	6.6	180

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55	Transposable Elements versus the Fungal Genome: Impact on Whole-Genome Architecture and Transcriptional Profiles. <i>PLoS Genetics</i> , 2016, 12, e1006108.	3.5	177
56	Expansion of Signal Transduction Pathways in Fungi by Extensive Genome Duplication. <i>Current Biology</i> , 2016, 26, 1577-1584.	3.9	175
57	Quality assessment of the human genome sequence. <i>Nature</i> , 2004, 429, 365-368.	27.8	172
58	Evolution of an Expanded Sex-Determining Locus in <i>Volvox</i> . <i>Science</i> , 2010, 328, 351-354.	12.6	159
59	The sequence and analysis of duplication-rich human chromosome 16. <i>Nature</i> , 2004, 432, 988-994.	27.8	156
60	The Chlamydomonas genome project: a decade on. <i>Trends in Plant Science</i> , 2014, 19, 672-680.	8.8	145
61	Genomic mechanisms of climate adaptation in polyploid bioenergy switchgrass. <i>Nature</i> , 2021, 590, 438-444.	27.8	144
62	Evolving New Skeletal Traits by cis-Regulatory Changes in Bone Morphogenetic Proteins. <i>Cell</i> , 2016, 164, 45-56.	28.9	132
63	The completion of the Mammalian Gene Collection (MGC). <i>Genome Research</i> , 2009, 19, 2324-2333.	5.5	125
64	The <i>Aquilegia</i> genome provides insight into adaptive radiation and reveals an extraordinarily polymorphic chromosome with a unique history. <i>ELife</i> , 2018, 7, .	6.0	120
65	The <i>Physcomitrella patens</i> gene atlas project: large-scale RNA-seq based expression data. <i>Plant Journal</i> , 2018, 95, 168-182.	5.7	115
66	Construction and comparison of three reference-quality genome assemblies for soybean. <i>Plant Journal</i> , 2019, 100, 1066-1082.	5.7	113
67	<i>Toxoplasma gondii</i> : the role of parasite surface and secreted proteins in host cell invasion. <i>International Journal for Parasitology</i> , 1996, 26, 169-173.	3.1	104
68	A genome resource for green millet <i>Setaria viridis</i> enables discovery of agronomically valuable loci. <i>Nature Biotechnology</i> , 2020, 38, 1203-1210.	17.5	103
69	The DNA sequence and comparative analysis of human chromosome 5. <i>Nature</i> , 2004, 431, 268-274.	27.8	102
70	The genomic landscape of molecular responses to natural drought stress in <i>Panicum hallii</i> . <i>Nature Communications</i> , 2018, 9, 5213.	12.8	101
71	Gene Conversion and the Evolution of Protocadherin Gene Cluster Diversity. <i>Genome Research</i> , 2004, 14, 354-366.	5.5	100
72	<i>Toxoplasma gondii</i> : The role of a 30-kDa surface protein in host cell invasion. <i>Experimental Parasitology</i> , 1992, 74, 106-111.	1.2	98

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73	Genetic analysis of <i>Physcomitrella patens</i> identifies ABSCISIC ACID NON-RESPONSIVE (ANR), a regulator of ABA responses unique to basal land plants and required for desiccation tolerance. <i>Plant Cell</i> , 2016, 28, tpc.00091.2016.	6.6	98
74	Computational Analysis of the Polymorphic Membrane Protein Superfamily of <i>Chlamydia trachomatis</i> and <i>Chlamydia pneumoniae</i> . <i>Microbial &amp; Comparative Genomics</i> , 1999, 4, 187-201.	0.4	95
75	A Hypervariable Invertebrate Allodeterminant. <i>Current Biology</i> , 2009, 19, 583-589.	3.9	95
76	A Comparative Epigenomic Analysis of Polyploidy-Derived Genes in Soybean and Common Bean. <i>Plant Physiology</i> , 2015, 168, 1433-1447.	4.8	88
77	Empty Niches after Extinctions Increase Population Sizes of Modern Corals. <i>Current Biology</i> , 2016, 26, 3190-3194.	3.9	79
78	Divergent cytosine DNA methylation patterns in single-cell, soybean root hairs. <i>New Phytologist</i> , 2017, 214, 808-819.	7.3	75
79	PEATmoss ( <i>Physcomitrella</i> Expression Atlas Tool): a unified gene expression atlas for the model plant <i>Physcomitrella patens</i> . <i>Plant Journal</i> , 2020, 102, 165-177.	5.7	74
80	Sequencing and analysis of 10,967 full-length cDNA clones from <i>Xenopus laevis</i> and <i>Xenopus tropicalis</i> reveals post-tetraploidization transcriptome remodeling. <i>Genome Research</i> , 2006, 16, 796-803.	5.5	73
81	Coelacanth genome sequence reveals the evolutionary history of vertebrate genes. <i>Genome Research</i> , 2004, 14, 2397-2405.	5.5	70
82	A physical map of the highly heterozygous <i>Populus</i> genome: integration with the genome sequence and genetic map and analysis of haplotype variation. <i>Plant Journal</i> , 2007, 50, 1063-1078.	5.7	70
83	Development of an integrated transcript sequence database and a gene expression atlas for gene discovery and analysis in switchgrass ( <i>Panicum virgatum</i> L.). <i>Plant Journal</i> , 2013, 74, 160-173.	5.7	70
84	A genome assembly and the somatic genetic and epigenetic mutation rate in a wild long-lived perennial <i>Populus trichocarpa</i> . <i>Genome Biology</i> , 2020, 21, 259.	8.8	68
85	Genome biology of the paleotetraploid perennial biomass crop <i>Miscanthus</i> . <i>Nature Communications</i> , 2020, 11, 5442.	12.8	67
86	Expression of <i>Chlamydia pneumoniae</i> Polymorphic Membrane Protein Family Genes. <i>Infection and Immunity</i> , 2001, 69, 2383-2389.	2.2	66
87	Complete HOX cluster characterization of the coelacanth provides further evidence for slow evolution of its genome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 3622-3627.	7.1	65
88	New Genomic Tools for Molecular Studies of Evolutionary Change in Threespine Sticklebacks. <i>Behaviour</i> , 2004, 141, 1331-1344.	0.8	64
89	Hydractinia Allodeterminant alr1 Resides in an Immunoglobulin Superfamily-like Gene Complex. <i>Current Biology</i> , 2010, 20, 1122-1127.	3.9	61
90	Genome sequence of the model rice variety KitaakeX. <i>BMC Genomics</i> , 2019, 20, 905.	2.8	59

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91	Gene-rich UV sex chromosomes harbor conserved regulators of sexual development. <i>Science Advances</i> , 2021, 7, .	10.3	53
92	The GC-Rich Mitochondrial and Plastid Genomes of the Green Alga <i>Coccomyxa</i> Give Insight into the Evolution of Organelle DNA Nucleotide Landscape. <i>PLoS ONE</i> , 2011, 6, e23624.	2.5	53
93	Extensive Linkage Disequilibrium, a Common 16.7-Kilobase Deletion, and Evidence of Balancing Selection in the Human Protocadherin $\hat{\pm}$ Cluster. <i>American Journal of Human Genetics</i> , 2003, 72, 621-635.	6.2	51
94	Comprehensive analysis of Hox gene expression in the amphipod crustacean <i>Parhyale hawaiiensis</i> . <i>Developmental Biology</i> , 2016, 409, 297-309.	2.0	51
95	A Genome-Wide Survey of Switchgrass Genome Structure and Organization. <i>PLoS ONE</i> , 2012, 7, e33892.	2.5	50
96	Hardwood Tree Genomics: Unlocking Woody Plant Biology. <i>Frontiers in Plant Science</i> , 2018, 9, 1799.	3.6	50
97	Four chromosome scale genomes and a pan-genome annotation to accelerate pecan tree breeding. <i>Nature Communications</i> , 2021, 12, 4125.	12.8	49
98	Closing the Gaps on Human Chromosome 19 Revealed Genes With a High Density of Repetitive Tandemly Arrayed Elements. <i>Genome Research</i> , 2004, 14, 239-246.	5.5	47
99	A chromosome-scale genome assembly and dense genetic map for <i>Xenopus tropicalis</i> . <i>Developmental Biology</i> , 2019, 452, 8-20.	2.0	43
100	The tepary bean genome provides insight into evolution and domestication under heat stress. <i>Nature Communications</i> , 2021, 12, 2638.	12.8	43
101	Genome Analysis of Planctomycetes Inhabiting Blades of the Red Alga <i>Porphyra umbilicalis</i> . <i>PLoS ONE</i> , 2016, 11, e0151883.	2.5	39
102	Toward a Reference Sequence of the Soybean Genome: A Multiagency Effort. <i>Crop Science</i> , 2006, 46, S-55.	1.8	37
103	Sequencing of 15,622 gene-bearing BAC s clarifies the gene-dense regions of the barley genome. <i>Plant Journal</i> , 2015, 84, 216-227.	5.7	36
104	Genome Sequence of the Chestnut Blight Fungus <i>Cryphonectria parasitica</i> EP155: A Fundamental Resource for an Archetypical Invasive Plant Pathogen. <i>Phytopathology</i> , 2020, 110, 1180-1188.	2.2	34
105	Genome mapping of quantitative trait loci (QTL) controlling domestication traits of intermediate wheatgrass ( <i>Thinopyrum intermedium</i> ). <i>Theoretical and Applied Genetics</i> , 2019, 132, 2325-2351.	3.6	30
106	Widespread polycistronic gene expression in green algae. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	30
107	Complete Plastome Sequences from <i>Glycine syndetika</i> and Six Additional Perennial Wild Relatives of Soybean. <i>G3: Genes, Genomes, Genetics</i> , 2014, 4, 2023-2033.	1.8	26
108	Phylogenomics of the genus <i>Glycine</i> sheds light on polyploid evolution and life-strategy transition. <i>Nature Plants</i> , 2022, 8, 233-244.	9.3	26

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109	Novel metabolic interactions and environmental conditions mediate the boreal peatmoss-cyanobacteria mutualism. <i>ISME Journal</i> , 2022, 16, 1074-1085.	9.8	25
110	Fowl sequence. <i>Nature</i> , 2004, 432, 679-680.	27.8	24
111	Sub genome anchored physical frameworks of the allotetraploid Upland cotton ( <i>Gossypium hirsutum</i> ) Tj ETQq1 1 0.784314 rgBT /Ov... 7, 15274.	3.3	23
112	Pests, diseases, and aridity have shaped the genome of <i>Corymbia citriodora</i> . <i>Communications Biology</i> , 2021, 4, 537.	4.4	21
113	Legacy genetics of <i>Arachis cardenasii</i> in the peanut crop shows the profound benefits of international seed exchange. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	18
114	Multiplex knockout of trichome-regulating MYB duplicates in hybrid poplar using a single gRNA. <i>Plant Physiology</i> , 2022, 189, 516-526.	4.8	18
115	Habitat-adapted microbial communities mediate <i>Sphagnum</i> peatmoss resilience to warming. <i>New Phytologist</i> , 2022, 234, 2111-2125.	7.3	18
116	Genomic variation within the maize stiff-stalk heterotic germplasm pool. <i>Plant Genome</i> , 2021, 14, e20114.	2.8	14
117	Exploring the loblolly pine ( <i>Pinus taeda</i> L.) genome by BAC sequencing and Cot analysis. <i>Gene</i> , 2018, 663, 165-177.	2.2	13
118	Targeted Switchgrass BAC Library Screening and Sequence Analysis Identifies Predicted Biomass and Stress Response-Related Genes. <i>Bioenergy Research</i> , 2016, 9, 109-122.	3.9	10
119	Comparative Transcriptomics of Non-Embryogenic and Embryogenic Callus in Semi-Recalcitrant and Non-Recalcitrant Upland Cotton Lines. <i>Plants</i> , 2021, 10, 1775.	3.5	10
120	Chloroplast genome sequences of <i>Carya illinoensis</i> from two distinct geographic populations. <i>Tree Genetics and Genomes</i> , 2020, 16, 1.	1.6	9
121	The recent evolutionary rescue of a staple crop depended on over half a century of global germplasm exchange. <i>Science Advances</i> , 2022, 8, eabj4633.	10.3	9
122	Kinetics of the growth and variation in infectivity of <i>Toxoplasma gondii</i> in mice. <i>Annals of Tropical Medicine and Parasitology</i> , 1991, 85, 659-661.	1.6	8
123	Six is seventh. <i>Nature</i> , 2003, 425, 775-776.	27.8	8
124	LCM and RNA-seq analyses revealed roles of cell cycle and translational regulation and homoeolog expression bias in cotton fiber cell initiation. <i>BMC Genomics</i> , 2021, 22, 309.	2.8	7
125	The Common Bean V Gene Encodes Flavonoid 3-Hydroxylase: A Major Mutational Target for Flavonoid Diversity in Angiosperms. <i>Frontiers in Plant Science</i> , 2022, 13, 869582.	3.6	7
126	Gene disruption by structural mutations drives selection in US rice breeding over the last century. <i>PLoS Genetics</i> , 2021, 17, e1009389.	3.5	6



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127	A draft genome provides hypotheses on drought tolerance in a keystone plant species in Western North America threatened by climate change. <i>Ecology and Evolution</i> , 2021, 11, 15417-15429.	1.9	6
128	Attachment of <i>Toxoplasma gondii</i> to a Specific Membrane Fraction of CHO Cells. <i>Infection and Immunity</i> , 2000, 68, 7198-7201.	2.2	5
129	A generalistâ€“specialist trade-off between switchgrass cytotypes impacts climate adaptation and geographic range. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2118879119.	7.1	5
130	Genome organization of the <i>vg1</i> and <i>nodal3</i> gene clusters in the allotetraploid frog <i>Xenopus laevis</i> . <i>Developmental Biology</i> , 2017, 426, 236-244.	2.0	4
131	eP144: Long-read genome sequencing secondary processing pipelines provide variant call accuracy that exceeds current clinical standards for short-read genome sequencing. <i>Genetics in Medicine</i> , 2022, 24, S89.	2.4	0