Sequencing depth and coverage: key considerations in g

Nature Reviews Genetics 15, 121-132 DOI: 10.1038/nrg3642

Citation Report

#	Article	IF	CITATIONS
1	Direct Chloroplast Sequencing: Comparison of Sequencing Platforms and Analysis Tools for Whole Chloroplast Barcoding. PLoS ONE, 2014, 9, e110387.	1.1	22
2	Next Generation Sequencing for Disorders of Sex Development. Endocrine Development, 2014, 27, 53-62.	1.3	14
3	Exploring the Transcriptome of Mycorrhizal Interactions. Advances in Botanical Research, 2014, 70, 53-78.	0.5	8
4	New gene models and alternative splicing in the maize pathogen Colletotrichum graminicola revealed by RNA-Seq analysis. BMC Genomics, 2014, 15, 842.	1.2	59
5	Quantitative assessment of the robustness of next-generation sequencing of antibody variable gene repertoires from immunized mice. BMC Immunology, 2014, 15, 40.	0.9	61
6	The Groucho Co-repressor Is Primarily Recruited to Local Target Sites in Active Chromatin to Attenuate Transcription. PLoS Genetics, 2014, 10, e1004595.	1.5	29
7	Next maSigPro: updating maSigPro bioconductor package for RNA-seq time series. Bioinformatics, 2014, 30, 2598-2602.	1.8	315
8	High throughput exome coverage of clinically relevant cardiac genes. BMC Medical Genomics, 2014, 7, 67.	0.7	9
9	The genomic landscape of polymorphic human nuclear mitochondrial insertions. Nucleic Acids Research, 2014, 42, 12640-12649.	6.5	168
10	Old Cell, New Trick? Cnidocytes as a Model for the Evolution of Novelty. Integrative and Comparative Biology, 2014, 54, 714-722.	0.9	25
11	Advances and limits of using population genetics to understand local adaptation. Trends in Ecology and Evolution, 2014, 29, 673-680.	4.2	329
12	Epigenetics reloaded: the single-cell revolution. Trends in Cell Biology, 2014, 24, 712-723.	3.6	59
13	An efficient quantitation method of next-generation sequencing libraries by using MiSeq sequencer. Analytical Biochemistry, 2014, 466, 27-29.	1.1	47
14	Low-coverage single-cell mRNA sequencing reveals cellular heterogeneity and activated signaling pathways in developing cerebral cortex. Nature Biotechnology, 2014, 32, 1053-1058.	9.4	850
15	Modeling genome coverage in single-cell sequencing. Bioinformatics, 2014, 30, 3159-3165.	1.8	53
16	Variant detection sensitivity and biases in whole genome and exome sequencing. BMC Bioinformatics, 2014, 15, 247.	1.2	197
17	Patterns of sequencing coverage bias revealed by ultra-deep sequencing of vertebrate mitochondria. BMC Genomics, 2014, 15, 467.	1.2	55
18	A field guide to wholeâ€genome sequencing, assembly and annotation. Evolutionary Applications, 2014, 7, 1026-1042.	1.5	296

#	Article	IF	CITATIONS
19	Copy number variation detection using next generation sequencing read counts. BMC Bioinformatics, 2014, 15, 109.	1.2	75
20	The thrills and agonies of using next-generation sequencing for somatic mutation detection in cancer. Personalized Medicine, 2014, 11, 369-371.	0.8	0
21	A presenilin 1 mutation in the first case of Alzheimer's disease: Revisited. Alzheimer's and Dementia, 2014, 10, 869-872.	0.4	22
22	Application of Massively Parallel Sequencing in the Clinical Diagnostic Testing of Inherited Cardiac Conditions. Medical Sciences (Basel, Switzerland), 2014, 2, 98-126.	1.3	2
23	Accurate genetic diagnosis of Finnish pulmonary arterial hypertension patients using oligonucleotideâ€selective sequencing. Molecular Genetics & Genomic Medicine, 2015, 3, 354-362.	0.6	5
24	Estimating copy numbers of alleles from population-scale high-throughput sequencing data. BMC Bioinformatics, 2015, 16, S4.	1.2	0
25	Comparison among three variant callers and assessment of the accuracy of imputation from SNP array data to whole-genome sequence level in chicken. BMC Genomics, 2015, 16, 824.	1.2	20
26	cFinder: definition and quantification of multiple haplotypes in a mixed sample. BMC Research Notes, 2015, 8, 422.	0.6	8
27	Choice of reference-guided sequence assembler and SNP caller for analysis of Listeria monocytogenes short-read sequence data greatly influences rates of error. BMC Research Notes, 2015, 8, 748.	0.6	31
28	Pediatric asthma and autism—genomic perspectives. Clinical and Translational Medicine, 2015, 4, 37.	1.7	6
29	Utility and limitations of exome sequencing as a genetic diagnostic tool for conditions associated with pediatric sudden cardiac arrest/sudden cardiac death. Human Genomics, 2015, 9, 15.	1.4	5
30	Effects of subsampling on characteristics of RNA-seq data from triple-negative breast cancer patients. Chinese Journal of Cancer, 2015, 34, 427-38.	4.9	4
31	Severe lethal phenotype of a Japanese case of Netherton syndrome with homozygous founder mutations ofSPINK5c.375_376delAT. Journal of Dermatology, 2015, 42, 1212-1214.	0.6	10
32	Kennewick Man: coming to closure. Antiquity, 2015, 89, 1485-1493.	0.5	25
33	Maxillary carcinosarcoma: Identification of a novel <i>MET</i> mutation in both carcinomatous and sarcomatous components through next generation sequencing. Head and Neck, 2015, 37, E179-85.	0.9	10
34	Psoralen Inactivation of Viruses: A Process for the Safe Manipulation of Viral Antigen and Nucleic Acid. Viruses, 2015, 7, 5875-5888.	1.5	27
35	Next Generation Sequencing in Non-Small Cell Lung Cancer: New Avenues Toward the Personalized Medicine. Current Drug Targets, 2015, 16, 47-59.	1.0	38
36	Challenges and opportunities in understanding microbial communities with metagenome assembly (accompanied by IPython Notebook tutorial). Frontiers in Microbiology, 2015, 6, 678.	1.5	28

#	Article	IF	CITATIONS
37	Wham: Identifying Structural Variants of Biological Consequence. PLoS Computational Biology, 2015, 11, e1004572.	1.5	105
38	Combined Targeted DNA Sequencing in Non-Small Cell Lung Cancer (NSCLC) Using UNCseq and NGScopy, and RNA Sequencing Using UNCqeR for the Detection of Genetic Aberrations in NSCLC. PLoS ONE, 2015, 10, e0129280.	1.1	36
39	Exome Capture with Heterologous Enrichment in Pig (Sus scrofa). PLoS ONE, 2015, 10, e0139328.	1.1	1
40	Whole-Genome Sequencing and Comparative Genome Analysis of Bacillus subtilis Strains Isolated from Non-Salted Fermented Soybean Foods. PLoS ONE, 2015, 10, e0141369.	1.1	32
41	miRge - A Multiplexed Method of Processing Small RNA-Seq Data to Determine MicroRNA Entropy. PLoS ONE, 2015, 10, e0143066.	1.1	87
42	Reliably Detecting Clinically Important Variants Requires Both Combined Variant Calls and Optimized Filtering Strategies. PLoS ONE, 2015, 10, e0143199.	1.1	38
43	De novo transcriptome profiling of cold-stressed siliques during pod filling stages in Indian mustard (Brassica juncea L.). Frontiers in Plant Science, 2015, 6, 932.	1.7	33
44	Structural variation discovery in the cancer genome using next generation sequencing: Computational solutions and perspectives. Oncotarget, 2015, 6, 5477-5489.	0.8	33
45	IMSEQ—a fast and error aware approach to immunogenetic sequence analysis. Bioinformatics, 2015, 31, 2963-2971.	1.8	98
46	Designing Cell-Type-Specific Genome-wide Experiments. Molecular Cell, 2015, 58, 621-631.	4.5	45
47	Identification of major factors associated with failed clinical molecular oncology testing performed by next generation sequencing (NGS). Molecular Oncology, 2015, 9, 1737-1743.	2.1	59
48	Western Blotting. Methods in Molecular Biology, 2015, , .	0.4	16
49	Diagnosis and treatment of cancer using genomics. BMJ, The, 2015, 350, h1832-h1832.	3.0	24
50	Transfer of energy pathway genes in microbial enhanced biological phosphorus removal communities. BMC Genomics, 2015, 16, 526.	1.2	6
51	BayesPI-BAR: a new biophysical model for characterization of regulatory sequence variations. Nucleic Acids Research, 2015, 43, gkv733.	6.5	17
52	Exploration of Microbial Cells: The Storehouse of Bio-wealth Through Metagenomics and Metatranscriptomics. , 2015, , 7-27.		2
53	Transmission Disequilibrium Tests Based on Read Counts for Low-Coverage Next-Generation Sequence Data. Human Heredity, 2015, 80, 36-49.	0.4	4
54	Impact of three Illumina library construction methods on GC bias and HLA genotype calling. Human Immunology, 2015, 76, 166-175.	1.2	80

# 55	ARTICLE Next-generation sequencing is a robust strategy for the high-throughput detection of zygosity in transgenic maize. Transgenic Research, 2015, 24, 615-623.	IF 1.3	Citations 9
56	Somatic Diseases (Cancer). , 2015, , 343-360.		0
57	(Epi)Genomics approaches and their applications. Methods, 2015, 72, 1-2.	1.9	2
58	Ligand-Dependent Enhancer Activation Regulated by Topoisomerase-I Activity. Cell, 2015, 160, 367-380.	13.5	122
59	Insertions and Deletions (Indels). , 2015, , 129-150.		12
60	Potential of genotyping-by-sequencing for genomic selection in livestock populations. Genetics Selection Evolution, 2015, 47, 12.	1.2	107
61	The Cancer Genomics Resource List 2014. Archives of Pathology and Laboratory Medicine, 2015, 139, 989-1008.	1.2	18
62	Sequence and analysis of a whole genome from Kuwaiti population subgroup of Persian ancestry. BMC Genomics, 2015, 16, 92.	1.2	34
63	Design and bioinformatics analysis of genome-wide CLIP experiments. Nucleic Acids Research, 2015, 43, 5263-5274.	6.5	65
64	Natural variations in OsγTMT contribute to diversity of the α-tocopherol content in rice. Molecular Genetics and Genomics, 2015, 290, 2121-2135.	1.0	25
65	On the design and analysis of next-generation sequencing genotyping for a cohort with haplotype-informative reads. Methods, 2015, 79-80, 41-46.	1.9	3
66	Elucidation of the growth delimitation of Dunaliella tertiolecta under nitrogen stress by integrating transcriptome and peptidome analysis. Bioresource Technology, 2015, 194, 57-66.	4.8	51
67	Next-generation sequencing as a tool for the molecular characterisation and risk assessment of genetically modified plants: Added value or not?. Trends in Food Science and Technology, 2015, 45, 319-326.	7.8	55
68	Towards understanding the molecular basis of cockroach tergal gland morphogenesis. A transcriptomic approach. Insect Biochemistry and Molecular Biology, 2015, 63, 104-112.	1.2	8
69	Whole genome sequences in pulse crops: a global community resource to expedite translational genomics and knowledge-based crop improvement. Biotechnology Letters, 2015, 37, 1529-1539.	1.1	23
70	A reliable method for the detection of BRCA1 and BRCA2 mutations in fixed tumour tissue utilising multiplex PCR-based targeted next generation sequencing. BMC Clinical Pathology, 2015, 15, 5.	1.8	47
71	Inter-individual differences in the gene content of human gut bacterial species. Genome Biology, 2015, 16, 82.	3.8	184
72	Inter-laboratory evaluation of SNP-based forensic identification by massively parallel sequencing using the Ion PGMâ,,¢. Forensic Science International: Genetics, 2015, 17, 110-121.	1.6	105

#	Article	IF	CITATIONS
73	Beyond fruit-flies: population genomic advances in non-Drosophila arthropods. Briefings in Functional Genomics, 2015, 14, 424-431.	1.3	14
74	Development of genomeâ€wide insertion/deletion markers in rice based on graphic pipeline platform. Journal of Integrative Plant Biology, 2015, 57, 980-991.	4.1	41
75	Transcriptome-wide identification of adenosine-to-inosine editing using the ICE-seq method. Nature Protocols, 2015, 10, 715-732.	5.5	67
76	Contemporary molecular tools in microbial ecology and their application to advancing biotechnology. Biotechnology Advances, 2015, 33, 1755-1773.	6.0	31
77	Allelic Ratio of <i>KRAS</i> Mutations in Pancreatic Cancer. Oncologist, 2015, 20, e8-e9.	1.9	36
78	Qualimap 2: advanced multi-sample quality control for high-throughput sequencing data. Bioinformatics, 2016, 32, 292-294.	1.8	1,362
79	A Rapid, High-Quality, Cost-Effective, Comprehensive and Expandable Targeted Next-Generation Sequencing Assay for Inherited Heart Diseases. Circulation Research, 2015, 117, 603-611.	2.0	34
80	Basidioascus undulatus: genome, origins, and sexuality. IMA Fungus, 2015, 6, 215-231.	1.7	9
81	Mapping of histone modifications in episomal HBV cccDNA uncovers an unusual chromatin organization amenable to epigenetic manipulation. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, E5715-24.	3.3	191
82	Digital gene expression approach over multiple RNA-Seq data sets to detect neoblast transcriptional changes in Schmidtea mediterranea. BMC Genomics, 2015, 16, 361.	1.2	17
83	Genome scale engineering techniques for metabolic engineering. Metabolic Engineering, 2015, 32, 143-154.	3.6	48
84	Rare variant discovery by deep whole-genome sequencing of 1,070 Japanese individuals. Nature Communications, 2015, 6, 8018.	5.8	352
85	Genetic variance estimation with imputed variants finds negligible missing heritability for human height and body mass index. Nature Genetics, 2015, 47, 1114-1120.	9.4	709
86	Molecular Biology Basics in the "Omics―Era: Genes to Proteins. , 2015, , 3-65.		1
87	RIG: Recalibration and Interrelation of Genomic Sequence Data with the GATK. G3: Genes, Genomes, Genetics, 2015, 5, 655-665.	0.8	75
88	Genomics of Adaptation to Multiple Concurrent Stresses: Insights from Comparative Transcriptomics of a Cichlid Fish from One of Earth's Most Extreme Environments, the Hypersaline Soda Lake Magadi in Kenya, East Africa. Journal of Molecular Evolution, 2015, 81, 90-109.	0.8	42
89	Mutational bias of Turnip Yellow Mosaic Virus in the context of host anti-viral gene silencing. Virology, 2015, 486, 2-6.	1.1	2
90	Differentiation of G:C <i>vs</i> A:T and G:C <i>vs</i> G:mC Base Pairs in the Latch Zone of α-Hemolysin. ACS Nano, 2015, 9, 11325-11332.	7.3	18

#	Article	IF	CITATIONS
91	Current strategies for mutation detection in phenotype-driven screens utilising next generation sequencing. Mammalian Genome, 2015, 26, 486-500.	1.0	28
92	Dual 3'Seq using deepSuperSAGE uncovers transcriptomes of interacting Salmonella enterica Typhimurium and human host cells. BMC Genomics, 2015, 16, 323.	1.2	12
93	Is the whole greater than the sum of its parts? De novo assembly strategies for bacterial genomes based on paired-end sequencing. BMC Genomics, 2015, 16, 648.	1.2	8
94	Demographic inferences using shortâ€read genomic data in an approximate Bayesian computation framework: in silico evaluation of power, biases and proof of concept in Atlantic walrus. Molecular Ecology, 2015, 24, 328-345.	2.0	54
95	Technology in MicroRNA Profiling: Circulating MicroRNAs as Noninvasive Cancer Biomarkers in Breast Cancer. Journal of the Association for Laboratory Automation, 2015, 20, 574-588.	2.8	42
96	Case-only exome sequencing and complex disease susceptibility gene discovery: study design considerations. Journal of Medical Genetics, 2015, 52, 10-16.	1.5	23
97	How do hosts react to endosymbionts? A new insight into the molecular mechanisms underlying the <i><scp>W</scp>olbachia</i> –host association. Insect Molecular Biology, 2015, 24, 1-12.	1.0	27
100	Biomechanisms of Comorbidity: Reviewing Integrative Analyses of Multi-omics Datasets and Electronic Health Records. Yearbook of Medical Informatics, 2016, 25, 194-206.	0.8	3
101	LOGIQA: a database dedicated to long-range genome interactions quality assessment. BMC Genomics, 2016, 17, 355.	1.2	3
102	Microbial Ecology: Where are we now?. Postdoc Journal, 2016, 4, 3-17.	0.4	23
103	Setting Up a Laboratory. , 2016, , 409-426.		1
104	Copy number variation contributes to cryptic genetic variation in outbreak lineages of Cryptococcus gattii from the North American Pacific Northwest. BMC Genomics, 2016, 17, 700.	1.2	36
105	Challenges of Identifying Clinically Actionable Genetic Variants for Precision Medicine. Journal of Healthcare Engineering, 2016, 2016, 1-14.	1.1	34
106	SRBreak: A Read-Depth and Split-Read Framework to Identify Breakpoints of Different Events Inside Simple Copy-Number Variable Regions. Frontiers in Genetics, 2016, 7, 160.	1.1	7
107			
	New Insights into the Genetic Diversity of Clostridium botulinum Group III through Extensive Genome Exploration. Frontiers in Microbiology, 2016, 7, 757.	1.5	18
108		1.5 1.5	18 8
	Exploration. Frontiers in Microbiology, 2016, 7, 757. Replicates, Read Numbers, and Other Important Experimental Design Considerations for Microbial		

#	Article	IF	Citations
111	Genome-wide Association Study Identifies Loci for the Polled Phenotype in Yak. PLoS ONE, 2016, 11, e0158642.	1.1	14
112	InFusion: Advancing Discovery of Fusion Genes and Chimeric Transcripts from Deep RNA-Sequencing Data. PLoS ONE, 2016, 11, e0167417.	1.1	62
113	Next-Generation Sequencing — An Overview of the History, Tools, and "Omic―Applications. , 0, , .		94
114	samExploreR: exploring reproducibility and robustness of RNA-seq results based on SAM files. Bioinformatics, 2016, 32, 3345-3347.	1.8	11
115	The Variable Regions of <i>Lactobacillus rhamnosus</i> Genomes Reveal the Dynamic Evolution of Metabolic and Host-Adaptation Repertoires. Genome Biology and Evolution, 2016, 8, 1889-1905.	1.1	53
116	Precision medicine in the age of big data: The present and future role of largeâ€scale unbiased sequencing in drug discovery and development. Clinical Pharmacology and Therapeutics, 2016, 99, 198-207.	2.3	42
117	Increasing Genome Sampling and Improving SNP Genotyping for Genotyping-by-Sequencing with New Combinations of Restriction Enzymes. G3: Genes, Genomes, Genetics, 2016, 6, 845-856.	0.8	51
118	Integrating next-generation sequencing into clinical oncology: strategies, promises and pitfalls. ESMO Open, 2016, 1, e000094.	2.0	126
119	Estimating theÂpopulation abundance of tissue-infiltrating immune and stromal cell populations using gene expression. Genome Biology, 2016, 17, 218.	3.8	1,980
120	DNA context represents transcription regulation of the gene in mouse embryonic stem cells. Scientific Reports, 2016, 6, 24343.	1.6	2
121	Transcriptomics. , 2016, , 160-165.		15
122	CloudControl. , 2016, , .		4
123	Diagnosing tuberculosis in the 21st century – Dawn of a genomics revolution?. International Journal of Mycobacteriology, 2016, 5, 384-391.	0.3	22
124	Exploiting the great potential of Sequence Capture data by a new tool, SUPER-CAP. DNA Research, 2016, 24, dsw050.	1.5	8
125	Genomic variation and DNA repair associated with soybean transgenesis: a comparison to cultivars and mutagenized plants. BMC Biotechnology, 2016, 16, 41.	1.7	54
126	Analysis of Base-Position Error Rate of Next-Generation Sequencing to Detect Tumor Mutations in Circulating DNA. Clinical Chemistry, 2016, 62, 1492-1503.	1.5	68
127	Undiscovered Physiology of Transcript and Protein Networks. , 2016, 6, 1851-1872.		0
128	Amplicon-based semiconductor sequencing of human exomes: performance evaluation and optimization strategies. Human Genetics, 2016, 135, 499-511.	1.8	50

		CITATION REPORT		
#	Article		IF	CITATIONS
129	Targeted capture in evolutionary and ecological genomics. Molecular Ecology, 2016, 2	5, 185-202.	2.0	295
130	The power and promise of <scp>RNA</scp> â€seq in ecology andÂevolution. Molecular 1224-1241.	Ecology, 2016, 25,	2.0	219
131	Transcriptomic Signature of the <i>SHATTERPROOF2</i> Expression Domain Reveals t Nature of Arabidopsis Gynoecial Medial Domain. Plant Physiology, 2016, 171, 42-61.	he Meristematic	2.3	32
132	Sequencing and comparative analyses of the genomes of zoysiagrasses. DNA Research	n, 2016, 23, 171-180.	1.5	68
133	Current tools for predicting cancer-specific T cell immunity. Oncolmmunology, 2016, 5	5, el177691.	2.1	45
134	The omic approach to parasitic trematode research—a review of techniques and deve the past 5Ayears. Parasitology Research, 2016, 115, 2523-2543.	elopments within	0.6	10
135	A novel three-round multiplex PCR for SNP genotyping with next generation sequencir and Bioanalytical Chemistry, 2016, 408, 4371-4377.	ıg. Analytical	1.9	80
136	Clinical Actionability of Comprehensive Genomic Profiling for Management of Rare or F Cancers. Oncologist, 2016, 21, 1315-1325.	Refractory	1.9	64
137	A Primer on Infectious Disease Bacterial Genomics. Clinical Microbiology Reviews, 201	6, 29, 881-913.	5.7	42
138	Discovery of new variable number tandem repeat loci in multiple Cryptosporidium part for the surveillance and investigation of outbreaks of cryptosporidiosis. Experimental F 2016, 169, 119-128.		0.5	20
139	MuffinInfo: HTML5-Based Statistics Extractor from Next-Generation Sequencing Data. Computational Biology, 2016, 23, 750-755.	Journal of	0.8	2
140	Identifying Centromeric RNAs Involved in Histone Dynamics In Vivo. Methods in Enzym 445-466.	iology, 2016, 573,	0.4	3
141	Exploring the Dynamic Relationship Between Cellular Metabolism and Chromatin Struc SILAC-Mass Spec and ChIP-Sequencing. Methods in Enzymology, 2016, 574, 311-329.		0.4	3
142	Dealing with paralogy in <scp>RAD</scp> seq data: in silico detection and single nucle polymorphism validation in <i>Robinia pseudoacacia</i> L. Ecology and Evolution, 202	otide 16, 6, 7323-7333.	0.8	32
144	Exome and genome sequencing for inborn errors of immunity. Journal of Allergy and C Immunology, 2016, 138, 957-969.	inical	1.5	187
145	Lessons for livestock genomics from genome and transcriptome sequencing in cattle a mammals. Genetics Selection Evolution, 2016, 48, 59.	nd other	1.2	25
146	Je, a versatile suite to handle multiplexed NGS libraries with unique molecular identifier Bioinformatics, 2016, 17, 419.	s. BMC	1.2	121
147	Exon Junction Complexes Show a Distributional Bias toward Alternatively Spliced mRN mRNAs Coding for Ribosomal Proteins. Cell Reports, 2016, 16, 1588-1603.	As and against	2.9	65

		CITATION RE	PORT	
#	Article		IF	CITATIONS
148	Representing genetic variation with synthetic DNA standards. Nature Methods, 2016,	13, 784-791.	9.0	37
149	A Sorghum Mutant Resource as an Efficient Platform for Gene Discovery in Grasses. Pla 28, tpc.00373.2016.	ant Cell, 2016,	3.1	113
150	Systems Biology Approaches to Improve Drought Stress Tolerance in Plants: State of t Future Challenges. , 2016, , 433-471.	he Art and		1
151	Exploiting the potential of next-generation sequencing in genomic medicine. Expert Re Molecular Diagnostics, 2016, 16, 1037-1047.	view of	1.5	5
152	Critical re-evaluation of neuroglobin expression reveals conserved patterns among mai Neuroscience, 2016, 337, 339-354.	mmals.	1.1	38
153	Cardiometabolic risk loci share downstream cis- and trans-gene regulation across tissu diseases. Science, 2016, 353, 827-830.	es and	6.0	241
154	Hepatocellular carcinoma cell lines retain the genomic and transcriptomic landscapes of human cancers. Scientific Reports, 2016, 6, 27411.	of primary	1.6	49
155	Clinical Versus Research Sequencing. Cold Spring Harbor Perspectives in Medicine, 202	16, 6, a025809.	2.9	24
156	Developmental Transcriptomics of the Hawaiian Anchialine ShrimpHalocaridina rubraH (Crustacea: Atyidae). Integrative and Comparative Biology, 2016, 56, 1170-1182.	olthuis, 1963	0.9	10
157	Here We Are, But Where Do We Go? A Systematic Review of Crustacean Transcriptom 2014–2015. Integrative and Comparative Biology, 2016, 56, 1055-1066.	ic Studies from	0.9	21
158	<scp>RAD</scp> cap: sequence capture of dualâ€digest <scp>RAD</scp> seq libraries duplicates and reduced missing data. Molecular Ecology Resources, 2016, 16, 1264-12	with identifiable 278.	2.2	117
159	Cellular identity at the single-cell level. Molecular BioSystems, 2016, 12, 2965-2979.		2.9	17
160	The present and future of <i>de novo</i> whole-genome assembly. Briefings in Bioinford bbw096.	matics, 2018, 19,	3.2	139
161	Guidelines for the selection of functional assays to evaluate the hallmarks of cancer. Bi Biophysica Acta: Reviews on Cancer, 2016, 1866, 300-319.	iochimica Et	3.3	89
162	Pan-cancer transcriptomic analysis associates long non-coding RNAs with key mutation events. Nature Communications, 2016, 7, 13197.	nal driver	5.8	54
163	Hybridization-Based Enrichment and Next Generation Sequencing to Explore Genetic E Plants. , 2016, , 117-136.	Diversity in		2
164	Computational identification of putative lincRNAs in mouse embryonic stem cell. Scier 2016, 6, 34892.	itific Reports,	1.6	3
165	RNA Sequencing Applied to Livestock Production. , 2016, , 63-94.			0

ARTICLE IF CITATIONS Dynamics of Mathematical Models in Biology., 2016,,. 1 166 Next-generation sequencing of human opioid receptor genes based on a custom AmpliSeqâ,,¢ library and ion torrent personal genome machine. Clinica Chimica Acta, 2016, 463, 32-38. 168 Systems Biology in Animal Production and Health, Vol. 1., 2016, , . 0 A Multilayered Screening Method for the Identification of Regulatory Genes in Rice by Agronomic 169 Traits. Evolutionary Bioinformatics, 2016, 12, EBO.S40622. The Rise and Rise of Exome Sequencing. Public Health Genomics, 2016, 19, 315-324. 170 0.6 15 Critical evaluation of the expression of gastrin-releasing peptide in dorsal root ganglia and spinal cord. Molecular Pain, 2016, 12, 174480691664372. 171 1.0 172 Whole-Genome Sequencing Recommendations., 2016, , 13-41. 2 Targeted DNA Region Re-sequencing., 2016, , 43-68. 9 174 Transcriptome Profiling Strategies., 2016, , 69-104. 0 An ultra-high-density bin map facilitates high-throughput QTL mapping of horticultural traits in 1.5 pepper (<i>Capsicum annuum</i>). DNA Research, 2016, 23, 81-91. Next-generation sequencing of amplicons is a rapid and reliable method for the detection of 176 4 1.0 polymorphisms relevant for barley breeding. Molecular Breeding, 2016, 36, 1. A comparison of tools for the simulation of genomic next-generation sequencing data. Nature Reviews Genetics, 2016, 17, 459-469. Salinity-induced changes in gene expression from anterior and posterior gills of Callinectes sapidus 178 (Crustacea: Portunidae) with implications for crustacean ecological genomics. Comparative 0.4 22 Biochemistry and Physiology Part D: Genomics and Proteomics, 2016, 19, 34-44. Inter-laboratory evaluation of the EUROFORGEN Global ancestry-informative SNP panel by massively 179 1.6 65 parallel sequencing using the Ion PGMâ,, ¢. Forensic Science International: Genetics, 2016, 23, 178-189. Systematic evaluation of the impact of ChIP-seq read designs on genome coverage, peak identification, 180 1.2 6 and allele-specific binding detection. BMC Bioinformatics, 2016, 17, 96. Rapid gene identification in sugar beet using deep sequencing of DNA from phenotypic pools selected 1.2 from breeding panels. BMC Genomics, 2016, 17, 236. Evaluation of the methods to identify patients who may benefit from PARP inhibitor use. 182 1.6 28 Endocrine-Related Cancer, 2016, 23, R267-R285. Enhanced diagnostic yield in Meckel-Gruber and Joubert syndrome through exome sequencing 2.1 supplemented with split-read mapping. BMC Medical Genetics, 2016, 17, 1.

ARTICLE IF CITATIONS Conservation genomics of natural and managed populations: building a conceptual and practical 2.0 141 184 framework. Molecular Ecology, 2016, 25, 2967-2977. Measuring the biodiversity of microbial communities by flow cytometry. Methods in Ecology and 2.2 Evolution, 2016, 7, 1376-1385. Deep resequencing of 131 Crohn's disease associated genes in pooled DNA confirmed three reported 186 6.1 62 variants and identified eight novel variants. Gut, 2016, 65, 788-796. Treatment Algorithms Based on Tumor Molecular Profiling: The Essence of Precision Medicine Trials. Journal of the National Cancer Institute, 2016, 108, djv362. Limited resources of genome sequencing in developing countries: Challenges and solutions. Applied & 188 2.1 91 Translational Genomics, 2016, 9, 15-19. RNA-seq reveals a diminished acclimation response to the combined effects of ocean acidification and 0.4 elevated seawater temperature in Pagothenia borchgrevinki. Marine Genomics, 2016, 28, 87-97. Recent advances in ChIP-seq analysis: from quality management to whole-genome annotation. 190 3.2 107 Briefings in Bioinformatics, 2017, 18, bbw023. PutativeBRAFactivating fusion in a medullary thyroid cancer. Journal of Physical Education and 14 Sports Management, 2016, 2, a000729. Budding off: bringing functional genomics toCandida albicans. Briefings in Functional Genomics, 2016, 192 1.3 9 15, 85-94. Study Design for Sequencing Studies. Methods in Molecular Biology, 2016, 1418, 39-66. 0.4 Optimization of nextâ€generation sequencing transcriptome annotation for species lacking sequenced 194 2.2 23 genomes. Molecular Ecology Resources, 2016, 16, 446-458. Pyrosequencing on a glass surface. Lab on A Chip, 2016, 16, 1063-1071. 3.1 An empirical Bayes change-point model for identifying 3â€² and 5â€² alternative splicing by next-generation 196 1.8 13 RNA sequencing. Bioinformatics, 2016, 32, 1823-1831. Epigenetic regulation of mitochondrial function in neurodegenerative disease: New insights from 1.0 34 advances in genomic technologies. Neuroscience Letters, 2016, 625, 47-55. 198 Ultra-Deep Sequencing of Bisulfite-Modified DNA., 2016, , 47-72. 0 Next-Generation Sequencing for the Analysis of Cancer Specimens., 2016, , 911-931. 199 200 A survey of best practices for RNA-seq data analysis. Genome Biology, 2016, 17, 13. 3.8 1,898 Genomic tools for new insights to variation, adaptation, and evolution in the salmonid fishes: a 201 34 perspective for charr. Hydrobiologia, 2016, 783, 191-208.

#	Article	IF	CITATIONS
202	Estimating genomic heritabilities at the level of family-pool samples of perennial ryegrass using genotyping-by-sequencing. Theoretical and Applied Genetics, 2016, 129, 45-52.	1.8	51
203	Single-Cell Sequencing for Precise Cancer Research: Progress and Prospects. Cancer Research, 2016, 76, 1305-1312.	0.4	111
204	Molecular testing for familial hypercholesterolaemia-associated mutations in a UK-based cohort: development of an NGS-based method and comparison with multiplex polymerase chain reaction and oligonucleotide arrays. Annals of Clinical Biochemistry, 2016, 53, 654-662.	0.8	9
205	Analysis of the microbiome: Advantages of whole genome shotgun versus 16S amplicon sequencing. Biochemical and Biophysical Research Communications, 2016, 469, 967-977.	1.0	637
206	Displaying Variation in Large Datasets: Plotting a Visual Summary of Effect Sizes. Journal of Computational and Graphical Statistics, 2016, 25, 971-979.	0.9	87
207	Superinfection exclusion and the long-term survival of honey bees in Varroa-infested colonies. ISME Journal, 2016, 10, 1182-1191.	4.4	88
208	Discovery and functional analysis of IncRNAs: Methodologies to investigate an uncharacterized transcriptome. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 3-15.	0.9	178
209	Next Generation Sequencing in Alzheimer's Disease. Methods in Molecular Biology, 2016, 1303, 281-297.	0.4	18
210	Prenatal Diagnosis Innovation: Genome Sequencing of Maternal Plasma. Annual Review of Medicine, 2016, 67, 419-432.	5.0	97
211	The specificity of long noncoding RNA expression. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2016, 1859, 16-22.	0.9	167
212	Statistical framework for detection of genetically modified organisms based on Next Generation Sequencing. Food Chemistry, 2016, 192, 788-798.	4.2	47
213	The nephrologist of tomorrow: towards a kidney-omic future. Pediatric Nephrology, 2017, 32, 393-404.	0.9	19
214	Chromosomal polymorphism in mammals: an evolutionary perspective. Biological Reviews, 2017, 92, 1-21.	4.7	63
215	Copy Number Variations Detection: Unravelling the Problem in Tangible Aspects. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 1237-1250.	1.9	6
216	UMI-tools: modeling sequencing errors in Unique Molecular Identifiers to improve quantification accuracy. Genome Research, 2017, 27, 491-499.	2.4	1,316
217	Genomic insights in gynecologic cancer. Current Problems in Cancer, 2017, 41, 8-36.	1.0	13
218	Degradation in forensic trace DNA samples explored by massively parallel sequencing. Forensic Science International: Genetics, 2017, 27, 160-166.	1.6	16
219	Performance of the ForenSeq TM DNA Signature Prep kit on highly degraded samples. Electrophoresis, 2017, 38, 1163-1174.	1.3	59

#	Article	IF	CITATIONS
220	Retrieving Chromatin Patterns from Deep Sequencing Data Using Correlation Functions. Biophysical Journal, 2017, 112, 473-490.	0.2	18
221	Exploring the transcriptome of non-model oleaginous microalga Dunaliella tertiolecta through high-throughput sequencing and high performance computing. BMC Bioinformatics, 2017, 18, 122.	1.2	17
222	Defining the diverse spectrum of inversions, complex structural variation, and chromothripsis in the morbid humanÂgenome. Genome Biology, 2017, 18, 36.	3.8	159
223	The role of genomics in common variable immunodeficiency disorders. Clinical and Experimental Immunology, 2017, 188, 326-332.	1.1	75
224	Landscape of genomic diversity and host adaptation in Fusarium graminearum. BMC Genomics, 2017, 18, 203.	1.2	28
225	Advances in the application of high-throughput sequencing in invertebrate virology. Journal of Invertebrate Pathology, 2017, 147, 145-156.	1.5	12
226	Cognitive Functions: Human vs. Animal–Â4:1 Advantage -FAM72–SRGAP2- . Journal of Molecular Neuroscience, 2017, 61, 603-606.	1.1	9
227	Regulatory functions and chromatin loading dynamics of linker histone H1 during endoreplication in <i>Drosophila</i> . Genes and Development, 2017, 31, 603-616.	2.7	30
228	Protein-Carbohydrate Interactions. Methods in Molecular Biology, 2017, , .	0.4	4
229	Metagenomics and CAZyme Discovery. Methods in Molecular Biology, 2017, 1588, 255-277.	0.4	19
230	Frequency of Frequencies Distributions and Size-Dependent Exchangeable Random Partitions. Journal of the American Statistical Association, 2017, 112, 1623-1635.	1.8	8
231	RNA sequencing reveals pronounced changes in the noncoding transcriptome of aging synaptosomes. Neurobiology of Aging, 2017, 56, 67-77.	1.5	17
232	Asymmetrical barcode adapter-assisted recovery of duplicate reads and error correction strategy to detect rare mutations in circulating tumor DNA. Scientific Reports, 2017, 7, 46678.	1.6	6
233	GeneImp: Fast Imputation to Large Reference Panels Using Genotype Likelihoods from Ultralow Coverage Sequencing. Genetics, 2017, 206, 91-104.	1.2	38
234	The specific problems of the experimental design in the high-throughput sequencing studies of transcriptome. Russian Journal of Genetics: Applied Research, 2017, 7, 258-265.	0.4	0
235	Developing the Evidence to Support Clinical Use of Genomics. , 2017, , 175-188.		0
236	Sequencing on the SOLiD 5500xl System – in-depth characterization of the GC bias. Nucleus, 2017, 8, 370-380.	0.6	4
237	Pitfalls and Opportunities for Epigenomic Analyses Focused on Disease Diagnosis, Prognosis, and Therapy. Trends in Pharmacological Sciences, 2017, 38, 765-770.	4.0	11

#	Article	IF	CITATIONS
238	Evaluation of whole exome sequencing by targeted gene sequencing and Sanger sequencing. Clinica Chimica Acta, 2017, 471, 222-232.	0.5	10
239	Reference standards for next-generation sequencing. Nature Reviews Genetics, 2017, 18, 473-484.	7.7	194
240	Temporal dynamics of gene expression and histone marks at the Arabidopsis shoot meristem during flowering. Nature Communications, 2017, 8, 15120.	5.8	96
241	Diagnosis of Tuberculosis in <scp>HIV</scp> Coâ€infected Individuals: Current Status, Challenges and Opportunities for the Future. Scandinavian Journal of Immunology, 2017, 86, 76-82.	1.3	37
242	RNAseq based transcriptomics study of SMCs from carotid atherosclerotic plaque: BMP2 and IDs proteins are crucial regulators of plaque stability. Scientific Reports, 2017, 7, 3470.	1.6	21
243	Inspecting Targeted Deep Sequencing of Whole Genome Amplified DNA Versus Fresh DNA for Somatic Mutation Detection: A Genetic Study in Myelodysplastic Syndrome Patients. Biopreservation and Biobanking, 2017, 15, 360-365.	0.5	0
244	Ribosome RNA Profiling to Quantify Ovarian Development and Identify Sex in Fish. Scientific Reports, 2017, 7, 4196.	1.6	8
245	Precision oncology based on omics data: The NCT Heidelberg experience. International Journal of Cancer, 2017, 141, 877-886.	2.3	133
246	De novo transcriptome assembly and annotation for the desert rainbowfish (Melanotaenia splendida) Tj ETQq0 () 0 rgBT /C	verlock 10 T
247	PhredEM: a phred-score-informed genotype-calling approach for next-generation sequencing studies. Genetic Epidemiology, 2017, 41, 375-387.	0.6	21
248	Bisulfite-independent analysis of CpG island methylation enables genome-scale stratification of single cells. Nucleic Acids Research, 2017, 45, gkx026.	6.5	31
249	Resequencing Helminth Genomes for Population and Genetic Studies. Trends in Parasitology, 2017, 33, 388-399.	1.5	31
251	Simultaneous human platelet antigen genotyping and detection of novel single nucleotide polymorphisms by targeted nextâ \in generation sequencing. Transfusion, 2017, 57, 1497-1504.	0.8	10
252	Analysis of High-Throughput RNA Bisulfite Sequencing Data. Methods in Molecular Biology, 2017, 1562, 143-154.	0.4	2
253	Application of cDNA-AFLP to biomarker exploration in a non-model species Grandidierella japonica. Ecotoxicology and Environmental Safety, 2017, 140, 206-213.	2.9	5
254	Single-Cell Transcriptional Analysis. Annual Review of Analytical Chemistry, 2017, 10, 439-462.	2.8	93
255	Extensive Copy Number Variation in Fermentation-Related Genes Among <i>Saccharomyces cerevisiae</i> Wine Strains. G3: Genes, Genomes, Genetics, 2017, 7, 1475-1485.	0.8	77

256	Animal tracking meets migration genomics: transcriptomic analysis of a partially migratory bird species. Molecular Ecology, 2017, 26, 3204-3216.	2.0	48
-----	--	-----	----

#	Article	IF	CITATIONS
257	Guidelines for Validation of Next-Generation Sequencing–Based Oncology Panels. Journal of Molecular Diagnostics, 2017, 19, 341-365.	1.2	524
258	Indelâ€seq: a fastâ€forward genetics approach for identification of traitâ€associated putative candidate genomic regions and its application in pigeonpea (<i>Cajanus cajan</i>). Plant Biotechnology Journal, 2017, 15, 906-914.	4.1	67
259	<scp>QTL</scp> â€seq approach identified genomic regions and diagnostic markers for rust and late leaf spot resistance in groundnut (<i><scp>A</scp>rachis hypogaea </i> <scp>L</scp> .). Plant Biotechnology Journal, 2017, 15, 927-941.	4.1	198
260	The importance of dynamic re-analysis in diagnostic whole exome sequencing. Journal of Medical Genetics, 2017, 54, 155-156.	1.5	38
261	HapCUT2: robust and accurate haplotype assembly for diverse sequencing technologies. Genome Research, 2017, 27, 801-812.	2.4	285
262	Crossâ€ s pecies analysis of the canine and human bladder cancer transcriptome and exome. Genes Chromosomes and Cancer, 2017, 56, 328-343.	1.5	34
263	Genomic translational research: Paving the way to individualized cardiac functional analyses and personalized cardiology. International Journal of Cardiology, 2017, 230, 384-401.	0.8	21
264	Structural Variation and the Soybean Genome. Compendium of Plant Genomes, 2017, , 57-72.	0.3	Ο
265	Integrated Analysis of Whole-Genome ChIP-Seq and RNA-Seq Data of Primary Head and Neck Tumor Samples Associates HPV Integration Sites with Open Chromatin Marks. Cancer Research, 2017, 77, 6538-6550.	0.4	50
266	Comparative transcriptome analysis provides clues to molecular mechanisms underlying blue-green eggshell color in the Jinding duck (Anas platyrhynchos). BMC Genomics, 2017, 18, 725.	1.2	24
267	Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life. Nature Microbiology, 2017, 2, 1533-1542.	5.9	1,465
268	Inferring Microbial Interactions from Metagenomic Time-series Using Prior Biological Knowledge. , 2017, , .		8
269	Synthetic Circulating Cell-free DNA as Quality Control Materials for Somatic Mutation Detection in Liquid Biopsy for Cancer. Clinical Chemistry, 2017, 63, 1465-1475.	1.5	34
270	Targeted next-generation sequencing supports epidermoid metaplasia of the esophagus as a precursor to esophageal squamous neoplasia. Modern Pathology, 2017, 30, 1613-1621.	2.9	43
271	Transcriptome landscape of human primary monocytes at different sequencing depth. Genomics, 2017, 109, 463-470.	1.3	9
272	<scp>RNA</scp> sequencing in postâ€mortem human brains of neuropsychiatric disorders. Psychiatry and Clinical Neurosciences, 2017, 71, 663-672.	1.0	14
273	Wholeâ€genome sequencing approaches for conservation biology: Advantages, limitations and practical recommendations. Molecular Ecology, 2017, 26, 5369-5406.	2.0	249
274	Novel metrics to measure coverage in whole exome sequencing datasets reveal local and global non-uniformity. Scientific Reports, 2017, 7, 885.	1.6	43

# 275	ARTICLE High resolution temporal transcriptomics of mouse embryoid body development reveals complex expression dynamics of coding and noncoding loci. Scientific Reports, 2017, 7, 6731.	IF 1.6	CITATIONS
276	Metagenomic Analysis of Silage. Journal of Visualized Experiments, 2017, , .	0.2	7
277	A bioinformatics approach for identifying transgene insertion sites using whole genome sequencing data. BMC Biotechnology, 2017, 17, 67.	1.7	42
278	De novo Assembly of a Genome. , 2017, , 107-125.		0
279	An Efficient Pipeline to Generate Data for Studies in Plastid Population Genomics and Phylogeography. Applications in Plant Sciences, 2017, 5, 1700053.	0.8	6
280	Next generation sequencing: clinicalÂapplications in solid tumours. Memo - Magazine of European Medical Oncology, 2017, 10, 244-247.	0.3	24
281	Fingerprints of Modified RNA Bases from Deep Sequencing Profiles. Journal of the American Chemical Society, 2017, 139, 17074-17081.	6.6	35
282	The effect of genetic variation on promoter usage and enhancer activity. Nature Communications, 2017, 8, 1358.	5.8	50
283	Genome-wide discovery of long intergenic noncoding RNAs and their epigenetic signatures in the rat. Scientific Reports, 2017, 7, 14817.	1.6	3
284	Microarray-Based Gene Expression Analysis for Veterinary Pathologists: A Review. Veterinary Pathology, 2017, 54, 734-755.	0.8	13
285	Unraveling long non-coding RNAs through analysis of high-throughput RNA-sequencing data. Non-coding RNA Research, 2017, 2, 111-118.	2.4	22
286	Quasispecies evolution of the prototypical genotype 1 porcine reproductive and respiratory syndrome virus early during in vivo infection is rapid and tissue specific. Archives of Virology, 2017, 162, 2203-2210.	0.9	5
287	An evaluation of copy number variation detection tools for cancer using whole exome sequencing data. BMC Bioinformatics, 2017, 18, 286.	1.2	132
288	RNA sequencing and transcriptome arrays analyses show opposing results for alternative splicing in patient derived samples. BMC Genomics, 2017, 18, 443.	1.2	74
289	A pipeline combining multiple strategies for prioritizing heterozygous variants for the identification of candidate genes in exome datasets. Human Genomics, 2017, 11, 11.	1.4	20
290	Bioinformatic processing of RADâ€seq data dramatically impacts downstream population genetic inference. Methods in Ecology and Evolution, 2017, 8, 907-917.	2.2	253
291	Low-, high-coverage, and two-stage DNA sequencing in the design of the genetic association study. Genetic Epidemiology, 2017, 41, 187-197.	0.6	20
292	Human <i>RECQ</i> Helicase Pathogenic Variants, Population Variation and "Missing―Diseases. Human Mutation, 2017, 38, 193-203.	1.1	24

ARTICLE IF CITATIONS # Acute Lung Injury and Repair. Respiratory Medicine, 2017, , . 293 0.1 1 Spatiotemporal regulation of enhancers during cardiogenesis. Cellular and Molecular Life Sciences, 294 2.4 <u>2017, 74, 257-265.</u> Practical lowâ€coverage genomewide sequencing of hundreds of individually barcoded samples for population and evolutionary genomics in nonmodel species. Molecular Ecology Resources, 2017, 17, 295 2.2 104 194-208. Genetic analysis of uterine aspirates improves the diagnostic value and captures the intra-tumor heterogeneity of endometrial cancers. Modern Pathology, 2017, 30, 134-145. Exploration of de Bruijn Graph Filtering for de novo Assembly Using GraphLab., 2017, , . 297 0 Reconstruction of high read-depth signals from low-depth whole genome sequencing data using deep 298 learning., 2017,,. Whole exome sequencing identified sixty-five coding mutations in four neuroblastoma tumors. 299 1.6 8 Scientific Reports, 2017, 7, 17787. Transcriptomic analysis of gene signatures associated with sickle pain. Scientific Data, 2017, 4, 170051. 2.4 300 302 Salvia Biotechnology., 2017,,. 7 High-resolution analysis of selection sweeps identified between fine-wool Merino and coarse-wool 1.2 Churra sheep breeds. Genetics Selection Evolution, 2017, 49, 81. Four study design principles for genetic investigations using next generation sequencing. BMJ: British 304 4 2.4 Medical Journal, 2017, 359, j4069. CloudEC: A MapReduce-based algorithm for correcting errors in next-generation sequencing big data. Determination of Nucleopolyhedrovirus' Taxonomic Position., 2017,,. 306 1 De novo assembly of Phlomis purpurea after challenging with Phytophthora cinnamomi. BMC Genomics, 2017, 18, 700. 1.2 308 RNAâ€seq: Applications and Best Practices. , 0, , . 17 REVIEW-ARTICLE Bioinformatics: an overview and its applications. Genetics and Molecular Research, 309 2017, 16, . Big Data Analytics for Genomic Medicine. International Journal of Molecular Sciences, 2017, 18, 412. 310 1.8 121Rapid Identification of Pathogenic Variants in Two Cases of Charcot-Marie-Tooth Disease by Gene-Panel 1.8 Sequencing. International Journal of Molecular Sciences, 2017, 18, 770.

#	Article	IF	CITATIONS
312	Burn Injury Leads to Increase in Relative Abundance of Opportunistic Pathogens in the Rat Gastrointestinal Microbiome. Frontiers in Microbiology, 2017, 8, 1237.	1.5	36
313	A PCR-Based Assay Targeting the Major Capsid Protein Gene of a Dinorna-Like ssRNA Virus That Infects Coral Photosymbionts. Frontiers in Microbiology, 2017, 8, 1665.	1.5	17
314	Defining the location of promoter-associated R-loops at near-nucleotide resolution using bisDRIP-seq. ELife, 2017, 6, .	2.8	97
315	Comparative Genome Sequencing Reveals Within-Host Genetic Changes in Neisseria meningitidis during Invasive Disease. PLoS ONE, 2017, 12, e0169892.	1.1	26
316	Antimicrobial resistance of Klebsiella pneumoniae stool isolates circulating in Kenya. PLoS ONE, 2017, 12, e0178880.	1.1	40
317	DNA isolation protocol effects on nuclear DNA analysis by microarrays, droplet digital PCR, and whole genome sequencing, and on mitochondrial DNA copy number estimation. PLoS ONE, 2017, 12, e0180467.	1.1	27
318	Resolving host–pathogen interactions by dual RNA-seq. PLoS Pathogens, 2017, 13, e1006033.	2.1	245
319	A pilot systematic genomic comparison of recurrence risks of hepatitis B virus-associated hepatocellular carcinoma with low- and high-degree liver fibrosis. BMC Medicine, 2017, 15, 214.	2.3	64
320	Intergenic disease-associated regions are abundant in novel transcripts. Genome Biology, 2017, 18, 241.	3.8	45
322	Computational Errors and Biases in Short Read Next Generation Sequencing. Journal of Proteomics and Bioinformatics, 2017, 10, .	0.4	26
323	Genetic Mosaicism and Cancer: Cause and Effect. Cancer Research, 2018, 78, 1375-1378.	0.4	19
324	Computational Methods for Assessing Chromatin Hierarchy. Computational and Structural Biotechnology Journal, 2018, 16, 43-53.	1.9	22
325	ShRangeSim: Simulation of Single Nucleotide Polymorphism Clusters in Next-Generation Sequencing Data. Journal of Computational Biology, 2018, 25, 613-622.	0.8	2
326	Impact of sequencing depth on the characterization of the microbiome and resistome. Scientific Reports, 2018, 8, 5890.	1.6	174
327	Batch effects in a multiyear sequencing study: False biological trends due to changes in read lengths. Molecular Ecology Resources, 2018, 18, 778-788.	2.2	36
328	Cyber–Physical Digital-Microfluidic Biochips: Bridging the Gap Between Microfluidics and Microbiology. Proceedings of the IEEE, 2018, 106, 1717-1743.	16.4	14
329	Illumina Library Preparation for Sequencing the GC-Rich Fraction of Heterogeneous Genomic DNA. Genome Biology and Evolution, 2018, 10, 616-622.	1.1	32
330	A robust targeted sequencing approach for low input and variable quality DNA from clinical samples. Npj Genomic Medicine, 2018, 3, 2.	1.7	20

#	Article	IF	CITATIONS
331	Data integration and predictive modeling methods for multi-omics datasets. Molecular Omics, 2018, 14, 8-25.	1.4	73
332	Performance of the Early Access AmpliSeqâ,,¢ Mitochondrial Panel with degraded DNA samples using the Ion Torrentâ,,¢ platform. Electrophoresis, 2018, 39, 2776-2784.	1.3	13
333	Interactive or static reports to guide clinical interpretation of cancer genomics. Journal of the American Medical Informatics Association: JAMIA, 2018, 25, 458-464.	2.2	14
334	Cost-effective and accurate method of measuring fetal fraction using SNP imputation. Bioinformatics, 2018, 34, 1086-1091.	1.8	7
335	Detecting Somatic Mutations in Normal Cells. Trends in Genetics, 2018, 34, 545-557.	2.9	92
336	Diversity within diversity: Parasite species richness in poison frogs assessed by transcriptomics. Molecular Phylogenetics and Evolution, 2018, 125, 40-50.	1.2	12
337	Recent computational developments on CLIP-seq data analysis and microRNA targeting implications. Briefings in Bioinformatics, 2018, 19, 1290-1301.	3.2	25
338	Dietary Analysis of Marine Fish Species: Enhancing the Detection of Prey-Specific DNA Sequences via High-Throughput Sequencing Using Blocking Primers. Estuaries and Coasts, 2018, 41, 560-571.	1.0	20
339	The molecular complexity of primary ovarian insufficiency aetiology and the use of massively parallel sequencing. Molecular and Cellular Endocrinology, 2018, 460, 170-180.	1.6	27
340	<scp>ABA</scp> signalling manipulation suppresses senescence of a leafy vegetable stored at room temperature. Plant Biotechnology Journal, 2018, 16, 530-544.	4.1	23
341	Genomic Approaches to Analyze Alternative Splicing, A Key Regulator of Transcriptome and Proteome Diversity in Brachypodium distachyon. Methods in Molecular Biology, 2018, 1667, 73-85.	0.4	4
342	Clinical efficacy of a nextâ€generation sequencing gene panel for primary immunodeficiency diagnostics. Clinical Genetics, 2018, 93, 647-655.	1.0	63
343	Whole Transcriptome Profiling: An RNA‣eq Primer and Implications for Pharmacogenomics Research. Clinical and Translational Science, 2018, 11, 153-161.	1.5	10
344	A Workflow Guide to RNA-seq Analysis of Chaperone Function and Beyond. Methods in Molecular Biology, 2018, 1709, 233-252.	0.4	3
345	Postâ€genomic behavioral genetics: From revolution to routine. Genes, Brain and Behavior, 2018, 17, e12441.	1.1	17
346	Identifying cell populations with scRNASeq. Molecular Aspects of Medicine, 2018, 59, 114-122.	2.7	205
347	A Pilot Study to Non-Invasively Track PIK3CA Mutation in Head and Neck Cancer. Diagnostics, 2018, 8, 79.	1.3	19
348	Exploiting advances in transcriptomics to improve on human-relevant toxicology. Current Opinion in Toxicology, 2018, 11-12, 43-50.	2.6	3

#	Article	IF	CITATIONS
350	Negative Binomial Optimization for Biomedical Structural Variant Signal Reconstruction. , 2018, , .		6
351	A Comparison of PAR-CLIP Peak Calling Approaches on Noisy Data. , 2018, , .		1
352	Structural Variant Prediction in Extended Pedigrees Through Sparse Negative Binomial Genome Signal Recovery. , 2018, 2018, 1311-1314.		0
353	Insights into the seasonal adaptive mechanisms of Chinese alligators (Alligator sinensis) from transcriptomic analyses. Australian Journal of Zoology, 2018, 66, 93.	0.6	9
354	Chromium sequencing: the doors open for genomics of obligate plant pathogens. BioTechniques, 2018, 65, 253-257.	0.8	11
355	Characterisation of the British honey bee metagenome. Nature Communications, 2018, 9, 4995.	5.8	51
356	CODEX2: full-spectrum copy number variation detection by high-throughput DNA sequencing. Genome Biology, 2018, 19, 202.	3.8	62
357	Technical Note on the quality of DNA sequencing for the molecular characterisation of genetically modified plants. EFSA Journal, 2018, 16, e05345.	0.9	23
358	Human Leukocyte Antigen Typing by Next-Generation Sequencing. Clinics in Laboratory Medicine, 2018, 38, 565-578.	0.7	25
359	Challenges in the introduction of next-generation sequencing (NGS) for diagnostics of myeloid malignancies into clinical routine use. Blood Cancer Journal, 2018, 8, 113.	2.8	90
360	Reliability of Whole-Exome Sequencing for Assessing Intratumor Genetic Heterogeneity. Cell Reports, 2018, 25, 1446-1457.	2.9	76
361	Dissecting the Mutational Landscape of Cutaneous Melanoma: An Omic Analysis Based on Patients from Greece. Cancers, 2018, 10, 96.	1.7	18
362	Different types of viral‑host junction found in HBV integration breakpoints in HBV‑infected patients. Molecular Medicine Reports, 2018, 19, 1410-1416.	1.1	12
363	SVEngine: an efficient and versatile simulator of genome structural variations with features of cancer clonal evolution. GigaScience, 2018, 7, .	3.3	15
364	Whole Genome Resequencing from Bulked Populations as a Rapid QTL and Gene Identification Method in Rice. International Journal of Molecular Sciences, 2018, 19, 4000.	1.8	23
365	Inter- and Intra-Host Nucleotide Variations in Hepatitis A Virus in Culture and Clinical Samples Detected by Next-Generation Sequencing. Viruses, 2018, 10, 619.	1.5	10
366	Cell Type-Selective Expression of Circular RNAs in Human Pancreatic Islets. Non-coding RNA, 2018, 4, 38.	1.3	26
367	Molecular Regulation of Catalpol and Acteoside Accumulation in Radial Striation and non-Radial Striation of Rehmannia glutinosa Tuberous Root. International Journal of Molecular Sciences, 2018, 19, 3751.	1.8	21

#	Article	IF	CITATIONS
368	Transcriptomics. Learning Materials in Biosciences, 2018, , 177-188.	0.2	0
369	Microbial Community Composition and Predicted Functional Attributes of Antarctic Lithobionts Using Targeted Next-Generation Sequencing and Bioinformatics Tools. Methods in Microbiology, 2018, , 243-290.	0.4	3
370	Analysis of porcine body size variation using re-sequencing data of miniature and large pigs. BMC Genomics, 2018, 19, 687.	1.2	12
371	First draft genome sequencing of fennel (Foeniculum vulgare Mill.): identification of simple sequence repeats and their application in marker-assisted breeding. Molecular Breeding, 2018, 38, 1.	1.0	24
372	Binning enables efficient host genome reconstruction in cnidarian holobionts. GigaScience, 2018, 7, .	3.3	16
373	Revisiting signatures of neutral tumor evolution in the light of complexity of cancer genomic data. Nature Genetics, 2018, 50, 1626-1628.	9.4	18
374	Sequana Coverage: Detection and Characterization of Genomic Variations using Running Median and Mixture Models. GigaScience, 2018, 7, .	3.3	11
375	Targeted next‑generation sequencing of cancer‑related genes in thyroid carcinoma: A single institution's experience. Oncology Letters, 2018, 16, 7278-7286.	0.8	17
376	DeviCNV: detection and visualization of exon-level copy number variants in targeted next-generation sequencing data. BMC Bioinformatics, 2018, 19, 381.	1.2	11
377	Impact of Variable RNA-Sequencing Depth on Gene Expression Signatures and Target Compound Robustness: Case Study Examining Brain Tumor (Glioma) Disease Progression. JCO Precision Oncology, 2018, 2, 1-17.	1.5	3
378	Plasmid-normalized quantification of relative mitochondrial DNA copy number. Scientific Reports, 2018, 8, 15347.	1.6	61
379	Molecular Pathways in Melanomagenesis: What We Learned from Next-Generation Sequencing Approaches. Current Oncology Reports, 2018, 20, 86.	1.8	61
380	Genome-wide characterization of genetic variants and putative regions under selection in meat and egg-type chicken lines. BMC Genomics, 2018, 19, 83.	1.2	39
381	A Computational Protocol to Analyze Metatranscriptomic Data Capturing Fungal–Host Interactions. Methods in Molecular Biology, 2018, 1848, 207-233.	0.4	1
382	OBSOLETE: Bioinformatics Principles for Deciphering Cardiovascular Diseases. , 2018, , .		1
383	Plant Pathogenic Fungi and Oomycetes. Methods in Molecular Biology, 2018, , .	0.4	4
384	Genomic Prediction in Tetraploid Ryegrass Using Allele Frequencies Based on Genotyping by Sequencing. Frontiers in Plant Science, 2018, 9, 1165.	1.7	40
385	RNAseqâ€based transcriptome assembly of <i>Clostridium acetobutylicum</i> for functional genome annotation and discovery. AICHE lournal, 2018, 64, 4271-4280.	1.8	6

#	Article	IF	CITATIONS
386	Sub-femtomolar detection of DNA and discrimination of mutant strands using microwell-array assisted digital enzyme-linked oligonucleotide assay. Analytica Chimica Acta, 2018, 1041, 122-130.	2.6	9
387	Genome-Guided Transcriptomics, DNA-Protein Interactions, and Variant Calling. , 2018, , .		0
388	Identifying Transcription Factor Olig2 Genomic Binding Sites in Acutely Purified PDGFRα+ Cells by Low-cell Chromatin Immunoprecipitation Sequencing Analysis. Journal of Visualized Experiments, 2018, , .	0.2	2
389	RNA-Seq and Expression Arrays: Selection Guidelines for Genome-Wide Expression Profiling. Methods in Molecular Biology, 2018, 1783, 7-33.	0.4	8
390	Gene Expression Analysis. Methods in Molecular Biology, 2018, , .	0.4	3
391	Asn391Thr Mutation of Î ² -Myosin Heavy Chain in a Hypertrophic Cardiomyopathy Family. International Heart Journal, 2018, 59, 596-600.	0.5	5
392	High Throughput Sequencing-Based Approaches for Gene Expression Analysis. Methods in Molecular Biology, 2018, 1783, 299-323.	0.4	8
393	TriPoly: haplotype estimation for polyploids using sequencing data of related individuals. Bioinformatics, 2018, 34, 3864-3872.	1.8	28
394	Bioinformatics Principles for Deciphering Cardiovascular Diseases. , 2018, , 273-292.		3
395	Validation of CZECANCA (CZEch CAncer paNel for Clinical Application) for targeted NGS-based analysis of hereditary cancer syndromes. PLoS ONE, 2018, 13, e0195761.	1.1	31
396	High-resolution melting analysis coupled with next-generation sequencing as a simple tool for the identification of a novel somatic BRCA2 variant: a case report. Human Genome Variation, 2018, 5, 10.	0.4	4
397	Wild tomato endosperm transcriptomes reveal common roles of genomic imprinting in both nuclear and cellular endosperm. Plant Journal, 2018, 95, 1084-1101.	2.8	38
398	RNA sequencing, <i>de novo</i> assembly and differential analysis of the gill transcriptome of freshwater climbing perch <i>Anabas testudineus</i> after 6 days of seawater exposure. Journal of Fish Biology, 2018, 93, 215-228.	0.7	10
399	Copy Number Variants. Methods in Molecular Biology, 2018, , .	0.4	0
400	Design and evaluation of a sequence capture system for genome-wide SNP genotyping in highly heterozygous plant genomes: a case study with a keystone Neotropical hardwood tree genome. DNA Research, 2018, 25, 535-545.	1.5	12
401	Plant Cell Culture Protocols. Methods in Molecular Biology, 2018, , .	0.4	14
402	WB1, a Regulator of Endosperm Development in Rice, Is Identified by a Modified MutMap Method. International Journal of Molecular Sciences, 2018, 19, 2159.	1.8	27
403	Next Generation Sequencing Methods for Diagnosis of Epilepsy Syndromes. Frontiers in Genetics, 2018, 9, 20.	1.1	102

		CITATION REP	PORT	
#	Article		IF	CITATIONS
404	Single Cell RNA Sequencing of Rare Immune Cell Populations. Frontiers in Immunology, 2018, 9	, 1553.	2.2	94
405	Customized biomedical informatics. Big Data Analytics, 2018, 3, .		2.2	4
406	Elaboration of Transcriptome During the Induction of Somatic Embryogenesis. Methods in Mole Biology, 2018, 1815, 411-427.	ecular	0.4	2
407	Lung Innate Immunity and Inflammation. Methods in Molecular Biology, 2018, , .		0.4	2
408	Perennial Grain Legume Domestication Phase I: Criteria for Candidate Species Selection. Sustain 2018, 10, 730.	1ability,	1.6	35
409	Improved molecular karyotyping in glioblastoma. Mutation Research - Fundamental and Molecu Mechanisms of Mutagenesis, 2018, 811, 16-26.	lar	0.4	5
410	Computational Analysis of RNA-Seq Data from Airway Epithelial Cells for Studying Lung Disease Methods in Molecular Biology, 2018, 1809, 203-235.		0.4	0
411	P_RNA_scaffolder: a fast and accurate genome scaffolder using paired-end RNA-sequencing rea BMC Genomics, 2018, 19, 175.	ds.	1.2	49
412	Species classifier choice is a key consideration when analysing low-complexity food microbiome Microbiome, 2018, 6, 50.	data.	4.9	65
413	Beyond genomics: understanding exposotypes through metabolomics. Human Genomics, 2018	5, 12, 4.	1.4	73
414	Strategies for identification of somatic variants using the Ion Torrent deep targeted sequencing platform. BMC Bioinformatics, 2018, 19, 5.	ŗ	1.2	24
415	An Introduction to Tools, Databases, and Practical Guidelines for NGS Data Analysis. , 2018, , 62	1-89.		0
416	Biotinylated amplicon sequencing: A method for preserving DNA samples of limited quantity. Pr Laboratory Medicine, 2018, 12, e00108.	actical	0.6	3
417	High-throughput evaluation of T7 promoter variants using biased randomization and DNA barco PLoS ONE, 2018, 13, e0196905.	oding.	1.1	25
418	MERIT reveals the impact of genomic context on sequencing error rate in ultra-deep application Bioinformatics, 2018, 19, 219.	s. BMC	1.2	4
419	Enrichment of low-density symbiont DNA from minute insects. Journal of Microbiological Metho 2018, 151, 16-19.	øds,	0.7	7
420	Assessment of a Targeted Gene Panel for Identification of Genes Associated With Movement Di JAMA Neurology, 2018, 75, 1234.	isorders.	4.5	64
421	A comprehensive iterative approach is highly effective in diagnosing individuals who are exome negative. Genetics in Medicine, 2019, 21, 161-172.		1.1	60

#	Article	IF	CITATIONS
422	Highâ€depth transcriptomic profiling reveals the temporal gene signature of human mesenchymal stem cells during chondrogenesis. FASEB Journal, 2019, 33, 358-372.	0.2	43
423	Transcriptome Analysis. , 2019, , 792-805.		8
424	Frequent Antiviral Treatment Failures in Patients Infected With Hepatitis C Virus Genotype 4, Subtype 4r. Hepatology, 2019, 69, 513-523.	3.6	79
425	Metagenomics analysis of cocoa bean fermentation microbiome identifying species diversity and putative functional capabilities. Heliyon, 2019, 5, e02170.	1.4	56
426	Paired-end mappability of transposable elements in the human genome. Mobile DNA, 2019, 10, 29.	1.3	26
427	Analysis of the 4q35 chromatin organization reveals distinct long-range interactions in patients affected with Facio-Scapulo-Humeral Dystrophy. Scientific Reports, 2019, 9, 10327.	1.6	12
428	Paleomicrobiology: Diagnosis and Evolution of Ancient Pathogens. Annual Review of Microbiology, 2019, 73, 639-666.	2.9	36
429	Systematic evaluation of RNA-Seq preparation protocol performance. BMC Genomics, 2019, 20, 571.	1.2	38
430	Networks of mRNA Processing and Alternative Splicing Regulation in Health and Disease. Advances in Experimental Medicine and Biology, 2019, 1157, 1-27.	0.8	9
431	Methods for the analysis of transcriptome dynamics. Toxicology Research, 2019, 8, 597-612.	0.9	6
432	Systematic comparison of germline variant calling pipelines cross multiple next-generation sequencers. Scientific Reports, 2019, 9, 9345.	1.6	77
433	Essentials of Bioinformatics, Volume II. , 2019, , .		1
434	Phylogenetic analysis provides insights into the evolution of Asian fireflies and adult bioluminescence. Molecular Phylogenetics and Evolution, 2019, 140, 106600.	1.2	24
435	Hippocampal Subregions Express Distinct Dendritic Transcriptomes that Reveal Differences in Mitochondrial Function in CA2. Cell Reports, 2019, 29, 522-539.e6.	2.9	61
436	Longshot enables accurate variant calling in diploid genomes from single-molecule long read sequencing. Nature Communications, 2019, 10, 4660.	5.8	156
437	Characterization of genome-wide variations induced by gamma-ray radiation in barley using RNA-Seq. BMC Genomics, 2019, 20, 783.	1.2	9
438	Discovery of Functional SNPs via Genome-Wide Exploration of Malaysian Pigmented Rice Varieties. International Journal of Genomics, 2019, 2019, 1-12.	0.8	4
439	RNA Fragmentation and Sequencing (RFâ€Seq): Costâ€Effective, Timeâ€Efficient, and Highâ€Throughput 3′ m Sequencing Library Construction in a Single Tube. Current Protocols in Molecular Biology, 2019, 129, e109.	1RNA 2.9	4

#	Article	IF	CITATIONS
440	Detection of Point Mutations and Chromosomal Translocations Based on Massive Parallel Sequencing of Enriched 3C Libraries. Russian Journal of Genetics, 2019, 55, 1273-1281.	0.2	7
441	Genomic Mutation Identification in Mice Using Illumina Sequencing and Linuxâ€Based Computational Methods. Current Protocols in Mouse Biology, 2019, 9, e64.	1.2	0
442	Screening human cell lines for viral infections applying RNA-Seq data analysis. PLoS ONE, 2019, 14, e0210404.	1.1	13
443	Methylation alteration of <i>SHANK1</i> as a predictive, diagnostic and prognostic biomarker for chronic lymphocytic leukemia. Oncotarget, 2019, 10, 4987-5002.	0.8	18
444	In silico genomic mining reveals unexplored bioactive potential of rare actinobacteria isolated from Egyptian soil. Bulletin of the National Research Centre, 2019, 43, .	0.7	12
445	The clinical and genetic characteristics of permanent neonatal diabetes (PNDM) in the state of Qatar. Molecular Genetics & Genomic Medicine, 2019, 7, e00753.	0.6	21
446	Emerging Use of CRISPR Technology — Chasing the Elusive HIV Cure. New England Journal of Medicine, 2019, 381, 1281-1283.	13.9	8
447	Weighted Gene Co-Expression Analyses Point to Long Non-Coding RNA Hub Genes at Different Schistosoma mansoni Life-Cycle Stages. Frontiers in Genetics, 2019, 10, 823.	1.1	22
448	Integrated Proteogenomic Characterization of HBV-Related Hepatocellular Carcinoma. Cell, 2019, 179, 561-577.e22.	13.5	629
449	Realizing the potential of full-length transcriptome sequencing. Philosophical Transactions of the Royal Society B: Biological Sciences, 2019, 374, 20190097.	1.8	92
450	Brazilian forensic casework analysis through MPS applications: Statistical weight-of-evidence and biological nature of criminal samples as an influence factor in quality metrics. Forensic Science International, 2019, 303, 109938.	1.3	6
451	Next-generation forward genetic screens: using simulated data to improve the design of mapping-by-sequencing experiments in Arabidopsis. Nucleic Acids Research, 2019, 47, e140-e140.	6.5	10
452	Effects of missing data and data type on phylotranscriptomic analysis of stony corals (Cnidaria:) Tj ETQq0 0 0 rgE	BT /Overloo 1.2	ck 10 Tf 50 2 14
453	Microfluidic MeDIP-seq for low-input methylomic analysis of mammary tumorigenesis in mice. Analyst, The, 2019, 144, 1904-1915.	1.7	8
454	Experimental validation of in silico predicted RAD locus frequencies using genomic resources and short read data from a model marine mammal. BMC Genomics, 2019, 20, 72.	1.2	4
455	Implementing TMB measurement in clinical practice: considerations on assay requirements. ESMO Open, 2019, 4, e000442.	2.0	257
456	New insight into the biogeochemical cycling of methane, S and Fe above the Sulfate-Methane Transition Zone in methane hydrate-bearing sediments: A case study in the Dongsha area, South China Sea. Deep-Sea Research Part I: Oceanographic Research Papers, 2019, 145, 97-108.	0.6	17
457	Targeted expression profiling by RNA-Seq improves detection of cellular dynamics during pregnancy and identifies a role for T cells in term parturition. Scientific Reports, 2019, 9, 848.	1.6	46

#	Article	IF	CITATIONS
458	Hydrogen production efficiency and microbial community of ethanol-type fermentation. Journal of Renewable and Sustainable Energy, 2019, 11, 013105.	0.8	3
459	Genetic Diversity and Gene Family Expansions in Members of the Genus <i>Entamoeba</i> . Genome Biology and Evolution, 2019, 11, 688-705.	1.1	22
460	Phloem Companion Cell-Specific Transcriptomic and Epigenomic Analyses Identify MRF1, a Regulator of Flowering. Plant Cell, 2019, 31, 325-345.	3.1	30
461	Genomic Selection in Aquaculture: Application, Limitations and Opportunities With Special Reference to Marine Shrimp and Pearl Oysters. Frontiers in Genetics, 2018, 9, 693.	1.1	149
462	The ReproGenomics Viewer: a multi-omics and cross-species resource compatible with single-cell studies for the reproductive science community. Bioinformatics, 2019, 35, 3133-3139.	1.8	49
463	Taking Advantage of the Genomics Revolution for Monitoring and Conservation of Chondrichthyan Populations. Diversity, 2019, 11, 49.	0.7	18
464	Singleâ€cell technologies in reproductive immunology. American Journal of Reproductive Immunology, 2019, 82, e13157.	1.2	9
465	Use of synthetic DNA spike-in controls (sequins) for human genome sequencing. Nature Protocols, 2019, 14, 2119-2151.	5.5	22
466	Non-invasive prenatal testing to detect chromosome aneuploidies in 57,204 pregnancies. Molecular Cytogenetics, 2019, 12, 29.	0.4	30
467	Genomic analysis reveals variant association with high altitude adaptation in native chickens. Scientific Reports, 2019, 9, 9224.	1.6	11
468	De novo transcriptome assembly of a facultative parasitic nematode Pelodera (syn. Rhabditis) strongyloides. Gene, 2019, 710, 30-38.	1.0	3
469	Current challenges and solutions of <i>de novo</i> assembly. Quantitative Biology, 2019, 7, 90-109.	0.3	46
470	Comparative genomic analysis of monosporidial and monoteliosporic cultures for unraveling the complexity of molecular pathogenesis of Tilletia indica pathogen of wheat. Scientific Reports, 2019, 9, 8185.	1.6	16
472	Sequencing XMET genes to promote genotype-guided risk assessment and precision medicine. Science China Life Sciences, 2019, 62, 895-904.	2.3	5
473	Accurate sequence variant genotyping in cattle using variation-aware genome graphs. Genetics Selection Evolution, 2019, 51, 21.	1.2	26
474	Next Generation Sequencing for the Detection of Foodborne Microbial Pathogens. , 2019, , 311-337.		0
475	RADâ€sequencing for estimating genomic relatedness matrixâ€based heritability in the wild: A case study in roe deer. Molecular Ecology Resources, 2019, 19, 1205-1217.	2.2	18
476	GenHap: a novel computational method based on genetic algorithms for haplotype assembly. BMC Bioinformatics, 2019, 20, 172.	1.2	26

#	Article	IF	CITATIONS
477	A comparative analysis of methods for de novo assembly of hymenopteran genomes using either haploid or diploid samples. Scientific Reports, 2019, 9, 6480.	1.6	19
478	Targeted capture-based NCS is superior to multiplex PCR-based NGS for hereditary BRCA1 and BRCA2 gene analysis in FFPE tumor samples. BMC Cancer, 2019, 19, 396.	1.1	30
479	Defense Against Biological Attacks. , 2019, , .		2
480	Highly efficient hypothesis testing methods for regression-type tests with correlated observations and heterogeneous variance structure. BMC Bioinformatics, 2019, 20, 185.	1.2	3
481	Draft genome of Santalum album L. provides genomic resources for accelerated trait improvement. Tree Genetics and Genomes, 2019, 15, 1.	0.6	15
482	Applying Genome-Resolved Metagenomics to Deconvolute the Halophilic Microbiome. Genes, 2019, 10, 220.	1.0	32
483	Molecular Heterogeneity in Large-Scale Biological Data: Techniques and Applications. Annual Review of Biomedical Data Science, 2019, 2, 39-67.	2.8	3
484	Genetic Variants Contributing to Early Recurrent Pregnancy Loss Etiology Identified by Sequencing Approaches. Reproductive Sciences, 2019, , 193371911983176.	1.1	12
485	Solid-state nanopore hydrodynamics and transport. Biomicrofluidics, 2019, 13, 011301.	1.2	32
486	Mapping the dsRNA World. Cold Spring Harbor Perspectives in Biology, 2019, 11, a035352.	2.3	39
487	RNA-sequencing in ophthalmology research: considerations for experimental design and analysis. Therapeutic Advances in Ophthalmology, 2019, 11, 251584141983546.	0.8	6
488	Application of next-generation sequencing technology to precision medicine in cancer: joint consensus of the Tumor Biomarker Committee of the Chinese Society of Clinical Oncology. Cancer Biology and Medicine, 2019, 16, 189.	1.4	16
489	Deciphering Within-Host Microevolution of <i>Mycobacterium tuberculosis</i> through Whole-Genome Sequencing: the Phenotypic Impact and Way Forward. Microbiology and Molecular Biology Reviews, 2019, 83, .	2.9	43
490	Beyond Biodiversity: Can Environmental DNA (eDNA) Cut It as a Population Genetics Tool?. Genes, 2019, 10, 192.	1.0	160
491	MitoZ: a toolkit for animal mitochondrial genome assembly, annotation and visualization. Nucleic Acids Research, 2019, 47, e63-e63.	6.5	593
492	Performance evaluation of commercial library construction kits for PCR-based targeted sequencing using a unique molecular identifier. BMC Genomics, 2019, 20, 216.	1.2	11
493	Transcriptomic Responses to Thermal Stress and Varied Phosphorus Conditions in Fugacium kawagutii. Microorganisms, 2019, 7, 96.	1.6	30
494	Science in Focus: Bioinformatics Part 1 – Lost in Translation. Clinical Oncology, 2019, 31, 337-340.	0.6	1

#	Article	IF	CITATIONS
495	Next-generation sequencing of HIV-1 single genome amplicons. Biomolecular Detection and Quantification, 2019, 17, 100080.	7.0	7
496	Chiral DNA sequences as commutable controls for clinical genomics. Nature Communications, 2019, 10, 1342.	5.8	11
497	Liver Cancer Gene Discovery Using Gene Targeting, Sleeping Beauty, and CRISPR/Cas9. Seminars in Liver Disease, 2019, 39, 261-274.	1.8	21
498	Generally applicable transcriptome-wide analysis of translation using anota2seq. Nucleic Acids Research, 2019, 47, e70-e70.	6.5	70
499	Systematic Evaluation of Statistical Methods for Identifying Looping Interactions in 5C Data. Cell Systems, 2019, 8, 197-211.e13.	2.9	15
500	De Novo Transcriptome Assembly of Agave H11648 by Illumina Sequencing and Identification of Cellulose Synthase Genes in Agave Species. Genes, 2019, 10, 103.	1.0	22
501	Unravelling Intratumoral Heterogeneity through High-Sensitivity Single-Cell Mutational Analysis and Parallel RNA Sequencing. Molecular Cell, 2019, 73, 1292-1305.e8.	4.5	218
502	Testing of library preparation methods for transcriptome sequencing of real life glioblastoma and brain tissue specimens: A comparative study with special focus on long non-coding RNAs. PLoS ONE, 2019, 14, e0211978.	1.1	7
503	Free-access copy-number variant detection tools for targeted next-generation sequencing data. Mutation Research - Reviews in Mutation Research, 2019, 779, 114-125.	2.4	46
504	Integrated analysis of population genomics, transcriptomics and virulence provides novel insights into Streptococcus pyogenes pathogenesis. Nature Genetics, 2019, 51, 548-559.	9.4	58
505	Data Analysis of ChIP-Seq Experiments. , 2019, , 67-77.		0
506	Alternative Splicing in Apicomplexan Parasites. MBio, 2019, 10, .	1.8	19
507	Tackling the Challenges of FASTQ Referential Compression. Bioinformatics and Biology Insights, 2019, 13, 117793221882137.	1.0	3
508	High Performance Computing for Haplotyping: Models and Platforms. Lecture Notes in Computer Science, 2019, , 650-661.	1.0	1
509	Nucleotide composition bias in high throughput gene expression measurement methods. , 2019, , .		1
510	6. Practical overview of bioinformatics data mining in environmental genomics. , 2019, , 127-150.		0
511	Utilizing field collected insects for next generation sequencing: Effects of sampling, storage, and DNA extraction methods. Ecology and Evolution, 2019, 9, 13690-13705.	0.8	18
512	The difference of detection rate of avian influenza virus in the wild bird surveillance using various methods. Journal of Veterinary Science, 2019, 20, e56.	0.5	10

ARTICLE IF CITATIONS # Optimal sequencing depth design for whole genome re-sequencing in pigs. BMC Bioinformatics, 2019, 513 1.2 28 20, 556. Potential utility of metagenomic sequencing for improving etiologic diagnosis of infective endocarditis. Future Cardiology, 2019, 15, 411-424. 514 Bayesian hierarchical negative binomial models for multivariable analyses with applications to human 515 1.1 5 microbiome count data. PLoS ONE, 2019, 14, e0220961. Relationships between Iraqi Rice Varieties at the Nuclear and Plastid Genome Levels. Plants, 2019, 8, 481. 516 Gencore: an efficient tool to generate consensus reads for error suppressing and duplicate removing 517 1.2 43 of NGS data. BMC Bioinformatics, 2019, 20, 606. Association of CMV genomic mutations with symptomatic infection and hearing loss in congenital CMV infection. BMC Infectious Diseases, 2019, 19, 1046. 1.3 519 1. Genomic Technology/ Next-Generation Sequencing., 2019, , 1-35. 0 A Hidden Markov Model for Identifying Differentially Methylated Sites in Bisulfite Sequencing Data. 520 0.8 9 Biometrics, 2019, 75, 210-221. Decoding systems biology of plant stress for sustainable agriculture development and optimized food 521 1.4 15 production. Progress in Biophysics and Molecular Biology, 2019, 145, 19-39. Mitochondrial dysfunction in type 2 diabetes mellitus: an organ-based analysis. American Journal of 1.8 222 Physiology - Endocrinology and Metabolism, 2019, 316, E268-E285. Exploring the effect of library preparation on RNA sequencing experiments. Genomics, 2019, 111, 523 1.3 3 1752-1759. Y Chromosome Sequences Reveal a Short Beringian Standstill, Rapid Expansion, and early Population 524 1.8 94 structure of Native American Founders. Current Biology, 2019, 29, 149-157.e3. An Objective Method for Evaluating Next-Generation Sequencing Panels. Journal of Child Neurology, 525 0.7 3 2019, 34, 139-143. Next Generation-Targeted Amplicon Sequencing (NG-TAS): an optimised protocol and computational pipeline for cost-effective profiling of circulating tumour DNA. Genome Medicine, 2019, 11, 1. 3.6 84 Differential gene expression during placentation in pregnancies conceived with different fertility 527 0.5 12 treatments compared with spontaneous pregnancies. Fertility and Sterility, 2019, 111, 535-546. Faecal phageome of healthy individuals: presence of antibiotic resistance genes and variations caused 24 by ciprofloxacin treatment. Journal of Antimicrobial Chemotherapy, 2019, 74, 854-864. A roadmap for highâ€throughput sequencing studies of wild animal populations using noninvasive 530 2.224 samples and hybridization capture. Molecular Ecology Resources, 2019, 19, 609-622. Established and emerging strategies to crack the genetic code of obesity. Obesity Reviews, 2019, 20, 3.1 212-240.

# 532	ARTICLE Bioinformatics tools to assess metagenomic data for applied microbiology. Applied Microbiology and Biotechnology, 2019, 103, 69-82.	IF 1.7	CITATIONS
533	Microbial Community Structures' Response to Seasonal Variation in a Full-Scale Municipal Wastewater Treatment Plant. Environmental Engineering Science, 2019, 36, 172-179.	0.8	19
534	Transcriptome Sequencing (RNA-Seq). , 2019, , 33-49.		1
535	Nanopore sequencing: An enrichmentâ€free alternative to mitochondrial DNA sequencing. Electrophoresis, 2019, 40, 272-280.	1.3	34
536	Genome-wide probing RNA structure with the modified DMS-MaPseq in Arabidopsis. Methods, 2019, 155, 30-40.	1.9	17
537	New Breeding Techniques: Detection and Identification of the Techniques andÂDerived Products. , 2019, , 320-336.		3
538	Nonequivalent lethal equivalents: Models and inbreeding metrics for unbiased estimation of inbreeding load. Evolutionary Applications, 2019, 12, 266-279.	1.5	43
539	MicroRNA profile analysis for discrimination of monozygotic twins using massively parallel sequencing and real-time PCR. Forensic Science International: Genetics, 2019, 38, 23-31.	1.6	15
540	Symposium review: Omics in dairy and animal science—Promise, potential, and pitfalls. Journal of Dairy Science, 2019, 102, 4741-4754.	1.4	9
541	Diagnostic targETEd seQuencing adjudicaTion (DETEQT). Journal of Molecular Diagnostics, 2019, 21, 99-110.	1.2	5
542	Single-Cell Genomics and Metagenomics for Microbial Diversity Analysis. SpringerBriefs in Environmental Science, 2020, , 33-49.	0.3	0
544	Identifying functions and prognostic biomarkers of network motifs marked by diverse chromatin states in human cell lines. Oncogene, 2020, 39, 677-689.	2.6	11
545	Diagnostic interpretation of genetic studies in patients with primary immunodeficiency diseases: AÂworking group report of the Primary Immunodeficiency Diseases Committee of the American Academy of Allergy, Asthma & Immunology. Journal of Allergy and Clinical Immunology, 2020, 145, 46-69.	1.5	54
547	PattRec: An easy-to-use CNV detection tool optimized for targeted NGS assays with diagnostic purposes. Genomics, 2020, 112, 1245-1256.	1.3	10
548	Predicting the Number of Bases to Attain Sufficient Coverage in High-Throughput Sequencing Experiments. Journal of Computational Biology, 2020, 27, 1130-1143.	0.8	2
549	An RNA-seq primer for pulmonologists. European Respiratory Journal, 2020, 55, 1801625.	3.1	2
550	Evaluating the performance of targeted sequence capture, RNA‣eq, and degenerateâ€primer PCR cloning for sequencing the largest mammalian multigene family. Molecular Ecology Resources, 2020, 20, 140-153.	2.2	15
551	Clinical application of genomic high-throughput data: Infrastructural, ethical, legal and psychosocial aspects. European Neuropsychopharmacology, 2020, 31, 1-15.	0.3	4

#	Article	IF	CITATIONS
552	Saliva as a comparable-quality source of DNA for Whole Exome Sequencing on Ion platforms. Genomics, 2020, 112, 1437-1443.	1.3	4
553	Key Questions for Next-Generation Biomonitoring. Frontiers in Environmental Science, 2020, 7, .	1.5	68
554	Nextâ€generation sequencing for measurable residual disease detection in acute myeloid leukaemia. British Journal of Haematology, 2020, 188, 77-85.	1.2	34
555	Managing batch effects in microbiome data. Briefings in Bioinformatics, 2020, 21, 1954-1970.	3.2	71
556	Targeted insertional mutagenesis libraries for deep domain insertion profiling. Nucleic Acids Research, 2020, 48, e11-e11.	6.5	23
557	An Overview of Bioinformatics Tools for DNA Meta-Barcoding Analysis of Microbial Communities of Bioaerosols: Digest for Microbiologists. Life, 2020, 10, 185.	1.1	4
558	Diagnosis of hepatic glycogen storage disease patients with overlapping clinical symptoms by massively parallel sequencing: a systematic review of literature. Orphanet Journal of Rare Diseases, 2020, 15, 286.	1.2	16
559	seekCRIT: Detecting and characterizing differentially expressed circular RNAs using high-throughput sequencing data. PLoS Computational Biology, 2020, 16, e1008338.	1.5	14
560	IsoXpressor: A Tool to Assess Transcriptional Activity within Isochores. Genome Biology and Evolution, 2020, 12, 1573-1578.	1.1	3
561	Forensic evaluation of the Asia Pacific ancestry-informative MAPlex assay. Forensic Science International: Genetics, 2020, 48, 102344.	1.6	17
562	HRT Atlas v1.0 database: redefining human and mouse housekeeping genes and candidate reference transcripts by mining massive RNA-seq datasets. Nucleic Acids Research, 2021, 49, D947-D955.	6.5	145
563	Genomic, Transcriptomic and Epigenomic Tools to Study the Domestication of Plants and Animals: A Field Guide for Beginners. Frontiers in Genetics, 2020, 11, 742.	1.1	21
564	Monitoring genome-wide chromatin accessibility by formaldehyde-assisted isolation of regulatory elements sequencing (FAIRE-seq). , 2020, , 353-369.		1
565	Genome Size Versus Genome Assemblies: Are the Genomes Truly Expanded in Polyploid Fungal Symbionts?. Genome Biology and Evolution, 2020, 12, 2384-2390.	1.1	6
566	A High Quality Asian Genome Assembly Identifies Features of Common Missing Regions. Genes, 2020, 11, 1350.	1.0	0
567	Finding a suitable library size to call variants in RNA-Seq. BMC Bioinformatics, 2020, 21, 553.	1.2	3
568	Circular RNA CircFAM188B Encodes a Protein That Regulates Proliferation and Differentiation of Chicken Skeletal Muscle Satellite Cells. Frontiers in Cell and Developmental Biology, 2020, 8, 522588.	1.8	31
569	STROBE-metagenomics: a STROBE extension statement to guide the reporting of metagenomics studies. Lancet Infectious Diseases, The, 2020, 20, e251-e260.	4.6	40

#	Article	IF	CITATIONS
570	SHAMAN: a user-friendly website for metataxonomic analysis from raw reads to statistical analysis. BMC Bioinformatics, 2020, 21, 345.	1.2	41
571	Intestinal Stem Cells. Methods in Molecular Biology, 2020, , .	0.4	1
572	Shotgun-Metagenomics on Positive Blood Culture Bottles Inoculated With Prosthetic Joint Tissue: A Proof of Concept Study. Frontiers in Microbiology, 2020, 11, 1687.	1.5	10
573	A Meta-Analysis of <i>Wolbachia</i> Transcriptomics Reveals a Stage-Specific <i>Wolbachia</i> Transcriptional Response Shared Across Different Hosts. G3: Genes, Genomes, Genetics, 2020, 10, 3243-3260.	0.8	3
574	Patterns of DNA variation between the autosomes, the X chromosome and the Y chromosome in Bos taurus genome. Scientific Reports, 2020, 10, 13641.	1.6	4
575	Novel Compound Heterozygous Mutations in CRTAP Cause Rare Autosomal Recessive Osteogenesis Imperfecta. Frontiers in Genetics, 2020, 11, 897.	1.1	4
576	Methods of analysis of chloroplast genomes of C3, Kranz type C4 and Single Cell C4 photosynthetic members of Chenopodiaceae. Plant Methods, 2020, 16, 119.	1.9	7
577	ScanITD: Detecting internal tandem duplication with robust variant allele frequency estimation. GigaScience, 2020, 9, .	3.3	9
578	The Biological Significance of Multi-copy Regions and Their Impact on Variant Discovery. Genomics, Proteomics and Bioinformatics, 2020, 18, 516-524.	3.0	1
579	Retrospective evaluation of whole exome and genome mutation calls in 746 cancer samples. Nature Communications, 2020, 11, 4748.	5.8	27
580	Feasibility and Comparison Study of Fecal Sample Collection Methods in Healthy Volunteers and Solid Organ Transplant Recipients Using 16S rRNA and Metagenomics Approaches. Biopreservation and Biobanking, 2020, 18, 425-440.	0.5	10
581	Secuenciación de nueva generación (NGS) de ADN: presente y futuro en la práctica clÃnica. Revista Universitas Medica, 2020, 61, .	0.0	7
582	International consensus recommendations on the diagnostic work-up for malformations of cortical development. Nature Reviews Neurology, 2020, 16, 618-635.	4.9	53
583	The Malignant Role of Exosomes as Nanocarriers of Rare RNA Species. International Journal of Molecular Sciences, 2020, 21, 5866.	1.8	16
584	Using whole-genome sequencing data to derive the homologous recombination deficiency scores. Npj Breast Cancer, 2020, 6, 33.	2.3	19
585	Sanger Validation of High-Throughput Sequencing in Genetic Diagnosis: Still the Best Practice?. Frontiers in Genetics, 2020, 11, 592588.	1.1	20
586	Eukaryotic and Prokaryotic Microbiota Interactions. Microorganisms, 2020, 8, 2018.	1.6	11
587	Selective Sweeps Lead to Evolutionary Success in an Amazonian Hyperdominant Palm. Frontiers in Genetics, 2020, 11, 596662.	1.1	4

#	ARTICLE	IF	CITATIONS
588	Deep sampling and pooled amplicon sequencing reveals hidden genic variation in heterogeneous rye accessions. BMC Genomics, 2020, 21, 845.	1.2	11
589	Genetic Improvement of Cereals and Grain Legumes. Genes, 2020, 11, 1255.	1.0	11
590	Wildlife Population Genomics: Applications and Approaches. Population Genomics, 2020, , 3-59.	0.2	7
591	Cenetic Variants Contributing to Early Recurrent Pregnancy Loss Etiology Identified by Sequencing Approaches. Reproductive Sciences, 2020, 27, 1541-1552.	1.1	16
592	Bayesian modeling reveals host genetics associated with rumen microbiota jointly influence methane emission in dairy cows. ISME Journal, 2020, 14, 2019-2033.	4.4	48
593	Liquid biopsy-based tumor profiling for metastatic colorectal cancer patients with ultra-deep targeted sequencing. PLoS ONE, 2020, 15, e0232754.	1.1	19
594	Challenges in the diagnosis and discovery of rare genetic disorders using contemporary sequencing technologies. Briefings in Functional Genomics, 2020, 19, 243-258.	1.3	27
595	Design, challenges, and the potential of transcriptomics to understand social behavior. Environmental Epigenetics, 2020, 66, 321-330.	0.9	6
596	The wound microbiome. , 2020, , 237-258.		3
597	Genetics of premature ovarian insufficiency. , 2020, , 173-199.		1
597 598	Genetics of premature ovarian insufficiency. , 2020, , 173-199. Seq-ing answers: Current data integration approaches to uncover mechanisms of transcriptional regulation. Computational and Structural Biotechnology Journal, 2020, 18, 1330-1341.	1.9	1
	Seq-ing answers: Current data integration approaches to uncover mechanisms of transcriptional	1.9	
598	Seq-ing answers: Current data integration approaches to uncover mechanisms of transcriptional regulation. Computational and Structural Biotechnology Journal, 2020, 18, 1330-1341.		16
598 599	Seq-ing answers: Current data integration approaches to uncover mechanisms of transcriptional regulation. Computational and Structural Biotechnology Journal, 2020, 18, 1330-1341. PACVr: plastome assembly coverage visualization in R. BMC Bioinformatics, 2020, 21, 207. Medium-coverage DNA sequencing in the design of the genetic association study. European Journal of	1.2	16 227
598 599 600	Seq-ing answers: Current data integration approaches to uncover mechanisms of transcriptional regulation. Computational and Structural Biotechnology Journal, 2020, 18, 1330-1341. PACVr: plastome assembly coverage visualization in R. BMC Bioinformatics, 2020, 21, 207. Medium-coverage DNA sequencing in the design of the genetic association study. European Journal of Human Genetics, 2020, 28, 1459-1466.	1.2 1.4	16 227 2
598 599 600 601	Seq-ing answers: Current data integration approaches to uncover mechanisms of transcriptional regulation. Computational and Structural Biotechnology Journal, 2020, 18, 1330-1341. PACVr: plastome assembly coverage visualization in R. BMC Bioinformatics, 2020, 21, 207. Medium-coverage DNA sequencing in the design of the genetic association study. European Journal of Human Genetics, 2020, 28, 1459-1466. The microbiome of the infertile male. Current Opinion in Urology, 2020, 30, 355-362. Gill Transcriptome Sequencing and De Novo Annotation of Acanthogobius ommaturus in Response to	1.2 1.4 0.9	16 227 2 27
598 599 600 601 602	Seq-ing answers: Current data integration approaches to uncover mechanisms of transcriptional regulation. Computational and Structural Biotechnology Journal, 2020, 18, 1330-1341. PACVr: plastome assembly coverage visualization in R. BMC Bioinformatics, 2020, 21, 207. Medium-coverage DNA sequencing in the design of the genetic association study. European Journal of Human Genetics, 2020, 28, 1459-1466. The microbiome of the infertile male. Current Opinion in Urology, 2020, 30, 355-362. Gill Transcriptome Sequencing and De Novo Annotation of Acanthogobius ommaturus in Response to Salinity Stress. Genes, 2020, 11, 631. Development of Cellular Models to Study Efficiency and Safety of Gene Edition by Homologous	1.2 1.4 0.9 1.0	16 227 2 27 16

#	Article	IF	CITATIONS
606	Integrated analysis of a compendium of RNA-Seq datasets for splicing factors. Scientific Data, 2020, 7, 178.	2.4	2
607	From Genetics to Genomics: Facing the Liability Implications in Clinical Care. Journal of Law, Medicine and Ethics, 2020, 48, 11-43.	0.4	37
608	Exploring the Molecular Aetiology of Preeclampsia by Massive Parallel Sequencing of DNA. Current Hypertension Reports, 2020, 22, 31.	1.5	6
609	Identification and characterization of alternative <i>STK39</i> transcripts within human and mouse kidneys reveals speciesâ€specific regulation of blood pressure. Physiological Reports, 2020, 8, e14379.	0.7	4
610	Colorectal Cancer Early Detection in Stool Samples Tracing CpG Islands Methylation Alterations Affecting Gene Expression. International Journal of Molecular Sciences, 2020, 21, 4494.	1.8	24
611	Shedding light on dark genes: enhanced targeted resequencing by optimizing the combination of enrichment technology and DNA fragment length. Scientific Reports, 2020, 10, 9424.	1.6	5
612	Targeted RNA sequencing enhances gene expression profiling of ultra-low input samples. RNA Biology, 2020, 17, 1741-1753.	1.5	10
613	Methodologies for Transcript Profiling Using Long-Read Technologies. Frontiers in Genetics, 2020, 11, 606.	1.1	70
614	Minimal Residual Disease Detection in Acute Lymphoblastic Leukemia. International Journal of Molecular Sciences, 2020, 21, 1054.	1.8	61
615	Gut microbiota of <i>Spodoptera frugiperda</i> (J.E. Smith) larvae as revealed by metatranscriptomic analysis. Journal of Applied Entomology, 2020, 144, 351-363.	0.8	21
616	Helping decision making for reliable and costâ€effective 2bâ€RAD sequencing and genotyping analyses in nonâ€model species. Molecular Ecology Resources, 2020, 20, 795-806.	2.2	12
617	Comparison of sequencing methods and data processing pipelines for whole genome sequencing and minority single nucleotide variant (mSNV) analysis during an influenza A/H5N8 outbreak. PLoS ONE, 2020, 15, e0229326.	1.1	1
618	Incorporation of Second-Tier Biomarker Testing Improves the Specificity of Newborn Screening for Mucopolysaccharidosis Type I. International Journal of Neonatal Screening, 2020, 6, 10.	1.2	32
619	Robust Linear Trend Test for Low-Coverage Next-Generation Sequence Data Controlling for Covariates. Mathematics, 2020, 8, 217.	1.1	0
620	Microbial resolution of whole genome shotgun and 16S amplicon metagenomic sequencing using publicly available NEON data. PLoS ONE, 2020, 15, e0228899.	1.1	107
621	How "simple―methodological decisions affect interpretation of population structure based on reduced representation library DNA sequencing: A case study using the lake whitefish. PLoS ONE, 2020, 15, e0226608.	1.1	20
622	Emerging next-generation sequencing-based discoveries for targeted osteosarcoma therapy. Cancer Letters, 2020, 474, 158-167.	3.2	54
623	Comparative transcriptome analysis of wild and lab populations of <i>Astyanax mexicanus</i> uncovers differential effects of environment and morphotype on gene expression. Journal of Experimental Zoology Part B: Molecular and Developmental Evolution, 2020, 334, 530-539.	0.6	33

#	ARTICLE	IF	CITATIONS
624	Comparison of multiple algorithms to reliably detect structural variants in pears. BMC Genomics, 2020, 21, 61.	1.2	15
625	A Preliminary Study to Investigate the Genetic Background of Longevity Based on Whole-Genome Sequence Data of Two Methuselah Dogs. Frontiers in Genetics, 2020, 11, 315.	1.1	4
626	Comparison of Transcriptome Profiles of the Fungus Botrytis cinerea and Insect Pest Bradysia odoriphaga in Response to Benzothiazole. Frontiers in Microbiology, 2020, 11, 1043.	1.5	9
627	Exploring the Brazilian diversity of Aspergillus sp. strains for lovastatin and itaconic acid production. Fungal Genetics and Biology, 2020, 138, 103367.	0.9	1
628	Applying next-generation sequencing to unravel the mutational landscape in viral quasispecies. Virus Research, 2020, 283, 197963.	1.1	35
629	Genetic innovations and our understanding of stillbirth. Human Genetics, 2020, 139, 1161-1172.	1.8	18
630	Comparison of Illumina MiSeq and the Ion Torrent PGM and S5 platforms for whole-genome sequencing of picornaviruses and caliciviruses. Journal of Virological Methods, 2020, 280, 113865.	1.0	20
631	Advanced Resistance Studies Identify Two Discrete Mechanisms in Staphylococcus aureus to Overcome Antibacterial Compounds that Target Biotin Protein Ligase. Antibiotics, 2020, 9, 165.	1.5	3
632	Sequence repetitiveness quantification and <i>de novo</i> repeat detection by weighted k-mer coverage. Briefings in Bioinformatics, 2021, 22, .	3.2	4
633	Variant Calling in Next Generation Sequencing Data. , 2021, , 129-140.		0
634	Cell Surface Protein mRNAs Show Differential Transcription in Pyramidal and Fast-Spiking Cells as Revealed by Single-Cell Sequencing. Cerebral Cortex, 2021, 31, 731-745.	1.6	5
635	Mini-metagenome analysis of psychrophilic electroactive biofilms based on single cell sorting. Science of the Total Environment, 2021, 762, 144328.	3.9	9
636	Study of indiscriminate distribution of restrained antimicrobial resistome of different environmental niches. Environmental Science and Pollution Research, 2021, 28, 10780-10790.	2.7	11
637	Cytometric fingerprints of gut microbiota predict Crohn's disease state. ISME Journal, 2021, 15, 354-358.	4.4	19
638	Distinct peripheral blood monocyte and neutrophil transcriptional programs following intracerebral hemorrhage and different etiologies of ischemic stroke. Journal of Cerebral Blood Flow and Metabolism, 2021, 41, 1398-1416.	2.4	27
639	De Novo Profiling of Long Non-Coding RNAs Involved in MC-LR-Induced Liver Injury in Whitefish: Discovery and Perspectives. International Journal of Molecular Sciences, 2021, 22, 941.	1.8	2
640	A benchmark and an algorithm for detecting germline transposon insertions and measuring <i>de novo</i> transposon insertion frequencies. Nucleic Acids Research, 2021, 49, e44-e44.	6.5	26
641	Next-generation sequencing for identification of actionable gene mutations in intestinal-type sinonasal adenocarcinoma. Scientific Reports, 2021, 11, 2247.	1.6	21

#	Article	IF	CITATIONS
642	Robustness of differential gene expression analysis of RNA-seq. Computational and Structural Biotechnology Journal, 2021, 19, 3470-3481.	1.9	39
643	Comparative Transcriptomic Analysis of Gene Expression Inheritance Patterns Associated with Cabbage Head Heterosis. Plants, 2021, 10, 275.	1.6	7
644	Genetic Epidemiology of Complex Phenotypes. Methods in Molecular Biology, 2021, 2249, 335-367.	0.4	3
645	Experimental and Computational Workflow for RNA in Mycobacterium tuberculosis: From Total RNA to Differentially Expressed Genes. Methods in Molecular Biology, 2021, 2314, 481-512.	0.4	1
646	Biological Perspectives of RNA-Sequencing Experimental Design. Methods in Molecular Biology, 2021, 2243, 327-337.	0.4	0
647	Genome and Transcriptome of Amaranth Species. Compendium of Plant Genomes, 2021, , 1-15.	0.3	3
648	Bladder Cancer Genomics: Indications for Sequencing and Diagnostic Implications. , 2021, , 193-205.		0
650	Prenatal Exome Sequencing: Background, Current Practice and Future Perspectives—A Systematic Review. Diagnostics, 2021, 11, 224.	1.3	16
651	Metataxonomic profiling of bacterial communities and their predictive functional profiles in traditionally preserved meat products of Sikkim state in India. Food Research International, 2021, 140, 110002.	2.9	15
653	Accelerating the base-level alignment step of DNA assembling in Minimap2 Algorithm using FPGA. , 2021, , .		3
654	The equine graying with age mutation of the <i>STX17</i> gene: A copy number study using droplet digital PCR reveals a new pattern. Animal Genetics, 2021, 52, 223-227.	0.6	5
655	Bioinformatic strategies for the analysis of genomic aberrations detected by targeted NGS panels with clinical application. PeerJ, 2021, 9, e10897.	0.9	4
656	Near-infrared spectroscopy outperforms genomics for predicting sugarcane feedstock quality traits. PLoS ONE, 2021, 16, e0236853.	1.1	11
657	Validation strategy of a bioinformatics whole genome sequencing workflow for Shiga toxin-producing Escherichia coli using a reference collection extensively characterized with conventional methods. Microbial Genomics, 2021, 7, .	1.0	20
658	Marine health of the Arabian Gulf: Drivers of pollution and assessment approaches focusing on desalination activities. Marine Pollution Bulletin, 2021, 164, 112085.	2.3	26
659	Robustness in quantifying the abundance of antimicrobial resistance genes in pooled faeces samples from batches of slaughter pigs using metagenomics analysis. Journal of Global Antimicrobial Resistance, 2021, 24, 398-402.	0.9	7
660	Tuberculosis Diagnosis by Metagenomic Next-generation Sequencing on Bronchoalveolar Lavage Fluid: a cross-sectional analysis. International Journal of Infectious Diseases, 2021, 104, 50-57.	1.5	26
661	Next-generation sequencing technologies: An overview. Human Immunology, 2021, 82, 801-811.	1.2	274

#	Article	IF	CITATIONS
662	Cross-oncopanel study reveals high sensitivity and accuracy with overall analytical performance depending on genomic regions. Genome Biology, 2021, 22, 109.	3.8	20
663	Next-generation sequencing for constitutional variants in the clinical laboratory, 2021 revision: a technical standard of the American College of Medical Genetics and Genomics (ACMG). Genetics in Medicine, 2021, 23, 1399-1415.	1.1	64
664	Challenges in the application of NGS in the clinical laboratory. Human Immunology, 2021, 82, 812-819.	1.2	16
665	Human OMICs and Computational Biology Research in Africa: Current Challenges and Prospects. OMICS A Journal of Integrative Biology, 2021, 25, 213-233.	1.0	13
666	A genomic dataset of singleâ€nucleotide polymorphisms generated by ddRAD tag sequencing in Q. petraea (Matt.) Liebl. populations from Central-Eastern Europe and Balkan Peninsula. Annals of Forest Science, 2021, 78, 1.	0.8	2
667	DNA assembly method for a non-model organism using a more distantly-related reference sequence. , 2021, , .		0
668	Sampling cores and sequencing depths affected the measurement of microbial diversity in soil quadrats. Science of the Total Environment, 2021, 767, 144966.	3.9	14
669	KRAS G12C–Mutant Non–Small Cell Lung Cancer. Journal of Molecular Diagnostics, 2021, 23, 507-520.	1.2	40
671	Differentiation and activation of fibroblastic reticular cells. Immunological Reviews, 2021, 302, 32-46.	2.8	25
672	Single-cell sequencing of the small and AT-skewed genome of malaria parasites. Genome Medicine, 2021, 13, 75.	3.6	5
673	Discovering Cellular Mitochondrial Heteroplasmy Heterogeneity with Single Cell RNA and ATAC Sequencing. Biology, 2021, 10, 503.	1.3	6
674	Rapid identification of mutations caused by fast neutron bombardment in Medicago truncatula. Plant Methods, 2021, 17, 62.	1.9	4
675	A multi-task CNN learning model for taxonomic assignment of human viruses. BMC Bioinformatics, 2021, 22, 194.	1.2	3
676	RNA-Seq Data for Reliable SNP Detection and Genotype Calling: Interest for Coding Variant Characterization and Cis-Regulation Analysis by Allele-Specific Expression in Livestock Species. Frontiers in Genetics, 2021, 12, 655707.	1.1	30
677	Targeted next-generation sequencing supports serrated epithelial change as an early precursor to inflammatory bowel disease–associated colorectal neoplasia. Human Pathology, 2021, 112, 9-19.	1.1	8
678	Evaluation of Oxford Nanopore MinION RNA-Seq Performance for Human Primary Cells. International Journal of Molecular Sciences, 2021, 22, 6317.	1.8	8
680	Empirical evaluation of methods for <i>de novo</i> genome assembly. PeerJ Computer Science, 2021, 7, e636.	2.7	15
681	Phylogenetic relationships in the <i>Sorghum</i> genus based on sequencing of the chloroplast and nuclear genes. Plant Genome, 2021, 14, e20123.	1.6	13

#	Article	IF	CITATIONS
683	Long non oding RNAs: Emerging roles in periodontitis. Journal of Periodontal Research, 2021, 56, 848-862.	1.4	9
685	Genomic selection in salmonids: new discoveries and future perspectives. Aquaculture International, 2021, 29, 2259-2289.	1.1	13
686	Calculation of Fetal Fraction for Non-Invasive Prenatal Testing. BioTech, 2021, 10, 17.	1.3	2
687	Non-Coding Variants in Cancer: Mechanistic Insights and Clinical Potential for Personalized Medicine. Non-coding RNA, 2021, 7, 47.	1.3	6
688	New insights from Whole Genome Sequencing: BCLAF1 deletion as a structural variant that predisposes cells towards cellular transformation. Oncology Reports, 2021, 46, .	1.2	1
689	Genomic Sequence Analysis of Methicillin- and Carbapenem-Resistant Bacteria Isolated from Raw Sewage. Microbiology Spectrum, 2021, 9, e0012821.	1.2	1
690	Biallelic Mutations in ACACA Cause a Disruption in Lipid Homeostasis That Is Associated With Global Developmental Delay, Microcephaly, and Dysmorphic Facial Features. Frontiers in Cell and Developmental Biology, 2021, 9, 618492.	1.8	6
691	Expanding the conservation genomics toolbox: Incorporating structural variants to enhance genomic studies for species of conservation concern. Molecular Ecology, 2021, 30, 5949-5965.	2.0	26
692	Study on the concordance between different SNPâ€genotyping platforms in sheep. Animal Genetics, 2021, 52, 868-880.	0.6	3
693	Application of whole-genome sequencing for norovirus outbreak tracking and surveillance efforts in Orange County, CA. Food Microbiology, 2021, 98, 103796.	2.1	9
694	Molecular Mechanism of EGFR-TKI Resistance in EGFR-Mutated Non-Small Cell Lung Cancer: Application to Biological Diagnostic and Monitoring. Cancers, 2021, 13, 4926.	1.7	52
695	Chromosomal sex determination system in brachyurans and its potential application in aquaculture. Aquaculture, 2021, 543, 736990.	1.7	4
696	Western Blot Analysis of Protein-DNA Complexes Formed during Gel Shift Experiments. Techniques in Life Science and Biomedicine for the Non-expert, 2021, , 311-330.	0.1	0
697	A De Novo Transcriptomics Approach Reveals Genes Involved in Thrips Tabaci Resistance to Spinosad. Insects, 2021, 12, 67.	1.0	7
698	Understanding Exome Sequencing: Tips for the Pediatrician. Indian Pediatrics, 2021, 58, 771-774.	0.2	1
699	Population Genomics of Fungal Plant Pathogens and the Analyses of Rapidly Evolving Genome Compartments. Methods in Molecular Biology, 2020, 2090, 337-355.	0.4	16
700	Single-Cell Transcriptional Profiling of the Intestinal Epithelium. Methods in Molecular Biology, 2020, 2171, 129-153.	0.4	7
701	Shift-Western Blotting: Separate Analysis of Protein and DNA from Protein–DNA Complexes. Methods in Molecular Biology, 2015, 1312, 355-373.	0.4	7

#	Article	IF	CITATIONS
702	Considerations on Experimental Design and Data Analysis of Chromatin Immunoprecipitation Experiments. Methods in Molecular Biology, 2018, 1689, 9-28.	0.4	5
703	Read Depth Analysis to Identify CNV in Bacteria Using CNOGpro. Methods in Molecular Biology, 2018, 1833, 73-81.	0.4	6
704	Measuring the microbiome: Best practices for developing and benchmarking microbiomics methods. Computational and Structural Biotechnology Journal, 2020, 18, 4048-4062.	1.9	37
705	Undibacterium piscinae sp. nov., isolated from Korean shiner intestine. International Journal of Systematic and Evolutionary Microbiology, 2019, 69, 3148-3154.	0.8	17
706	Jeotgalibaca ciconiae sp. nov., isolated from the faeces of an Oriental stork. International Journal of Systematic and Evolutionary Microbiology, 2020, 70, 3247-3254.	0.8	12
730	Whole exome HBV DNA integration is independent of the intrahepatic HBV reservoir in HBeAg-negative chronic hepatitis B. Gut, 2021, 70, 2337-2348.	6.1	36
731	Host immunology and rational immunotherapy for carbapenem-resistant Klebsiella pneumoniae infection. JCl Insight, 2020, 5, .	2.3	13
732	Simulating metagenomic stable isotope probing datasets with MetaSIPSim. BMC Bioinformatics, 2020, 21, 37.	1.2	15
733	Semiconductor Sequencing Analysis of Chromosomal Copy Number Variations in Spontaneous Miscarriage. Medical Science Monitor, 2017, 23, 5550-5557.	0.5	7
734	Next-generation sequencing of microbial cell-free DNA for rapid noninvasive diagnosis of infectious diseases in immunocompromised hosts. F1000Research, 2019, 8, 1194.	0.8	37
735	MPLasso: Inferring microbial association networks using prior microbial knowledge. PLoS Computational Biology, 2017, 13, e1005915.	1.5	28
736	Testing Rare-Variant Association without Calling Genotypes Allows for Systematic Differences in Sequencing between Cases and Controls. PLoS Genetics, 2016, 12, e1006040.	1.5	26
737	Successful Recovery of Nuclear Protein-Coding Genes from Small Insects in Museums Using Illumina Sequencing. PLoS ONE, 2015, 10, e0143929.	1.1	55
738	Molecular Characterization of Transgenic Events Using Next Generation Sequencing Approach. PLoS ONE, 2016, 11, e0149515.	1.1	57
739	A Cost-Effective Approach to Sequence Hundreds of Complete Mitochondrial Genomes. PLoS ONE, 2016, 11, e0160958.	1.1	9
740	Sensitive Detection and Simultaneous Discrimination of Influenza A and B Viruses in Nasopharyngeal Swabs in a Single Assay Using Next-Generation Sequencing-Based Diagnostics. PLoS ONE, 2016, 11, e0163175.	1.1	30
741	Use of Combined MSAP and NGS Techniques to Identify Differentially Methylated Regions in Somaclones: A Case Study of Two Stable Somatic Wheat Mutants. PLoS ONE, 2016, 11, e0165749.	1.1	15
742	Identification of vaccine-derived rotavirus strains in children with acute gastroenteritis in Japan, 2012-2015. PLoS ONE, 2017, 12, e0184067.	1.1	15

#	Article	IF	CITATIONS
743	In silico analysis of mismatches in RT-qPCR assays of 177 SARS-CoV-2 sequences from Brazil. Revista Da Sociedade Brasileira De Medicina Tropical, 2020, 53, e20200657.	0.4	4
744	Data- and knowledge-based modeling of gene regulatory networks: an update. EXCLI Journal, 2015, 14, 346-78.	0.5	35
745	Insights into study design and statistical analyses in translational microbiome studies. Annals of Translational Medicine, 2017, 5, 249-249.	0.7	21
746	covtobed: a simple and fast tool to extract coverage tracks from BAM files. Journal of Open Source Software, 2020, 5, 2119.	2.0	7
747	Dual RNA-Sequencing to Elucidate the Plant-Pathogen Duel. Current Issues in Molecular Biology, 2018, 27, 127-142.	1.0	46
748	Longitudinal effects of enrofloxacin or tulathromycin use in preweaned calves at high risk of bovine respiratory disease on the shedding of antimicrobial-resistant fecal Escherichia coli. Journal of Dairy Science, 2020, 103, 10547-10559.	1.4	14
749	The Progress of Multi-Omics Technologies: Determining Function in Lactic Acid Bacteria Using a Systems Level Approach. Frontiers in Microbiology, 2019, 10, 3084.	1.5	54
750	Next-Generation Sequencing Approaches in Cancer: Where Have They Brought Us and Where Will They Take Us?. Cancers, 2015, 7, 1925-1958.	1.7	51
751	Molecular-Assisted Distinctness and Uniformity Testing Using SLAF-Sequencing Approach in Soybean. Genes, 2020, 11, 175.	1.0	18
752	Multiplexed molecular profiling of lung cancer with malignant pleural effusion using next generation sequencing in Chinese patients. Oncology Letters, 2020, 19, 3495-3505.	0.8	9
753	Molecular genetic decoding of malformations of cortical development. Journal of Genetic Medicine, 2015, 12, 12-18.	0.1	2
754	Resolving rates of mutation in the brain using single-neuron genomics. ELife, 2016, 5, .	2.8	139
755	Getting the most out of RNA-seq data analysis. PeerJ, 2015, 3, e1360.	0.9	29
756	Assessing the utility of the Oxford Nanopore MinION for snake venom gland cDNA sequencing. PeerJ, 2015, 3, e1441.	0.9	34
757	GROM-RD: resolving genomic biases to improve read depth detection of copy number variants. PeerJ, 2015, 3, e836.	0.9	29
758	Comparative Analysis of 16S rRNA Gene and Metagenome Sequencing in Pediatric Gut Microbiomes. Frontiers in Microbiology, 2021, 12, 670336.	1.5	63
759	Application of second-generation sequencing (SGS) and third generation sequencing (TGS) in aquaculture breeding program. Aquaculture, 2022, 548, 737633.	1.7	12
761	Blood Group Genotyping. Advances in Molecular Pathology, 2021, 4, 127-143.	0.2	3

#	Article	IF	CITATIONS
762	Next-Generation Sequencing for Measurable Residual Disease Assessment in Acute Leukemia. Advances in Molecular Pathology, 2021, 4, 49-63.	0.2	2
767	Genetic and Genomic Approaches to Acute Lung Injury. Respiratory Medicine, 2017, , 133-159.	0.1	0
769	Genomic Analysis and In Vivo Functional Validation of Brain Somatic Mutations Leading to Focal Cortical Malformations. Neuromethods, 2017, , 299-327.	0.2	0
770	The Concepts of 'Species' and 'Population' in Considering Ancient DNA and Building Phylogenetic Trees of Hominid Evolution. SSRN Electronic Journal, 0, , .	0.4	0
771	Cancer as a result of genetic mosaicism. Uspehi Molekularnoj Onkologii, 2017, 4, 26-35.	0.1	0
773	Chapter 4. Tracing domestication and selection in animal genomes. , 2017, , 107-137.		0
779	Update in Clinical Genetics and Metabolics. , 2018, , 369-390.		0
780	Approaches to Understanding the Genetic Basis of Complex Diseases: Overview—What Is the Rationale for the Genome-Wide Approach to Understand Complex Diseases, Its Application and Limitations. Respiratory Disease Series, 2018, , 15-35.	0.1	0
781	Probability, Populations, Phylogenetics, and Hominin Speciation. Human Biology, 2018, 90, 129.	0.4	1
787	Genomic Revolution-Driven Cancer Research. , 2019, , 39-60.		0
788	Quality Control Metrics for Extraction-Free Targeted RNA-Seq Under a Compositional Framework. Springer Proceedings in Mathematics and Statistics, 2019, , 299-314.	0.1	0
789	BIOTHINGS: A Pipeline Creation Tool for PAR-CLIP Sequence Analsys. Lecture Notes in Computer Science, 2019, , 327-336.	1.0	0
792	Understanding the adaptive response of Streptomyces coelicolor to the glycopeptide antibiotic teicoplanin. Access Microbiology, 2019, 1, .	0.2	0
797	Tumor Sequencing: Enabling Personalized Targeted Treatments with Informatics. Computers in Health Care, 2020, , 161-174.	0.2	0
798	DNA Methylation and Transcriptomic Next-Generation Technologies in Cereal Genomics. Methods in Molecular Biology, 2020, 2072, 65-84.	0.4	0
800	RNA-Sequencing of Snake Venom Glands. Methods in Molecular Biology, 2020, 2068, 87-96.	0.4	0
803	QCKer. , 2019, , .		0
807	Recalibration of mapping quality scores in Illumina short-read alignments improves SNP detection results in low-coverage sequencing data. PeerJ, 2020, 8, e10501.	0.9	3

			_
#	ARTICLE	IF	CITATIONS
809	Diversity Assessment of an Endemic Carpinus oblongifolia (Betulaceae) Using Specific-Locus Amplified Fragment Sequencing and Implications for Conservation. Phyton, 2022, 91, 617-632.	0.4	0
812	New technologies for the diagnosis of drug-resistant tuberculosis. Vestnik Rossiiskoi Akademii Meditsinskikh Nauk, 2019, 74, 413-422.	0.2	1
814	Computational Metagenomics: State-of-the-Art, Facts and Artifacts. , 2020, , 199-227.		0
815	Generalized Additive Models for the Detection of Copy Number Variations (CNVs) Using Multi-gene Panel Sequencing Data. Studies in Classification, Data Analysis, and Knowledge Organization, 2020, , 199-213.	0.1	0
816	Genome Sequencing in Esophageal Squamous Cell Carcinoma. Methods in Molecular Biology, 2020, 2129, 217-240.	0.4	0
817	Development of SSR Markers Based on Transcriptome Sequences of the Wolf Spider Pardosa pseudoannulata (Araneae: Lycosidae)1. Entomological News, 2020, 129, 6.	0.1	2
818	Methodological differences can affect sequencing depth with a possible impact on the accuracy of genetic diagnosis. Genetics and Molecular Biology, 2020, 43, e20190270.	0.6	2
819	Analytical Challenges of Next-generation Sequencing in Precision Medicine. RSC Detection Science, 2020, , 153-168.	0.0	0
821	Evaluation of WGS performance for bacterial pathogen characterization with the Illumina technology optimized for time-critical situations. Microbial Genomics, 2021, 7, .	1.0	4
823	A glimpse of antimicrobial resistance gene diversity in kefir and yoghurt. Scientific Reports, 2020, 10, 22458.	1.6	27
824	Automation of molecular-based analyses: a primer on massively parallel sequencing. Clinical Biochemist Reviews, 2014, 35, 169-76.	3.3	6
825	Pitfalls and pointers: An accessible guide to marker gene amplicon sequencing in ecological applications. Methods in Ecology and Evolution, 2022, 13, 266-277.	2.2	6
827	Genomic Data and Big Data Analytics. Lecture Notes in Networks and Systems, 2022, , 187-201.	0.5	0
828	RiboReport - benchmarking tools for ribosome profiling-based identification of open reading frames in bacteria. Briefings in Bioinformatics, 2022, 23, .	3.2	15
829	Assessing reproducibility of inherited variants detected with short-read whole genome sequencing. Genome Biology, 2022, 23, 2.	3.8	18
830	Comment on â€~SARS-CoV-2 suppresses anticoagulant and fibrinolytic gene expression in the lung'. ELife, 2022, 11, .	2.8	5
831	Detecting novel genomic structural variants through negative binomial optimization. , 2020, , .		1
832	Revisiting hematopoiesis: applications of the bulk and single-cell transcriptomics dissecting transcriptional heterogeneity in hematopoietic stem cells. Briefings in Functional Genomics, 2022, 21, 159-176.	1.3	15

#	Article	IF	CITATIONS
834	Next Generation Sequencing of Human Platelet Antigens for Routine Clinical Investigations and Donor Screening. Transfusion Medicine Reviews, 2022, , .	0.9	0
835	Characterization of genomic variation on three Indonesian oil palm genotypes analyzed using next-generation sequencing HiSeq. AIP Conference Proceedings, 2022, , .	0.3	1
836	Genetic variation of olfactory receptor gene family in a Japanese population. Anthropological Science, 2022, 130, 93-106.	0.2	3
837	Tracing the source and route of uterine colonization by exploring the genetic relationship of Escherichia coli isolated from the reproductive and gastrointestinal tract of dairy cows. Veterinary Microbiology, 2022, 266, 109355.	0.8	4
838	Wild epigenetics: insights from epigenetic studies on natural populations. Proceedings of the Royal Society B: Biological Sciences, 2022, 289, 20211633.	1.2	18
839	Identification of Copy Number Alterations from Next-Generation Sequencing Data. Advances in Experimental Medicine and Biology, 2022, 1361, 55-74.	0.8	2
842	Assessing reproducibility of highâ€ŧhroughput experiments in the case of missing data. Statistics in Medicine, 2022, 41, 1884-1899.	0.8	1
843	Single-cell gene fusion detection by scFusion. Nature Communications, 2022, 13, 1084.	5.8	8
844	Using Omics to Study Leprosy, Tuberculosis, and Other Mycobacterial Diseases. Frontiers in Cellular and Infection Microbiology, 2022, 12, 792617.	1.8	7
845	Differential Selection on Caste-Associated Genes in a Subterranean Termite. Insects, 2022, 13, 224.	1.0	2
846	evSeq: Cost-Effective Amplicon Sequencing of Every Variant in a Protein Library. ACS Synthetic Biology, 2022, 11, 1313-1324.	1.9	19
848	Nyssorhynchus darlingi genome-wide studies related to microgeographic dispersion and blood-seeking behavior. Parasites and Vectors, 2022, 15, 106.	1.0	2
850	Antimicrobial resistance determinants in silage. Scientific Reports, 2022, 12, 5243.	1.6	2
851	Participation of Histones in DNA Damage and Repair within Nucleosome Core Particles: Mechanism and Applications. Accounts of Chemical Research, 2022, 55, 1059-1073.	7.6	5
852	Mitochondria as the Target of Hepatotoxicity and Drug-Induced Liver Injury: Molecular Mechanisms and Detection Methods. International Journal of Molecular Sciences, 2022, 23, 3315.	1.8	33
853	Powerful eQTL mapping through low-coverage RNA sequencing. Human Genetics and Genomics Advances, 2022, 3, 100103.	1.0	2
854	Next-generation sequencing: insights to advance clinical investigations of the microbiome. Journal of Clinical Investigation, 2022, 132, .	3.9	116
855	Transcriptomic profile dataset of embryonic stem cells (Wild-type and IPO13-Knock Out) with and without oxidative stress. Data in Brief, 2022, 42, 108099.	0.5	3

#	Article	IF	CITATIONS
856	Novel structural variant genome detection in extended pedigrees through negative binomial optimization. , 2021, , .		0
857	ModEst: Accurate estimation of genome size from next generation sequencing data. Molecular Ecology Resources, 2022, 22, 1454-1464.	2.2	17
860	Multipopulational transcriptome analysis of post-weaned beef cattle at arrival further validates candidate biomarkers for predicting clinical bovine respiratory disease. Scientific Reports, 2021, 11, 23877.	1.6	9
861	Cognitive Function Associated with Gut Microbial Abundance in Sucrose and S-Adenosyl-L-Methionine (SAMe) Metabolic Pathways. Journal of Alzheimer's Disease, 2022, 87, 1115-1130.	1.2	14
862	Development of colorectal cancer detection and prediction based on gut microbiome big-data. Medicine in Microecology, 2022, 12, 100053.	0.7	2
863	The Effects of Predictive Factors on Patient Prognosis in the Administration of Medical and Surgical Treatment in Patients with Acute Pancreatitis. The Journal of Tepecik Education and Research Hospital, 2022, 32, 107-114.	0.2	0
918	Genotyping, the Usefulness of Imputation to Increase SNP Density, and Imputation Methods and Tools. Methods in Molecular Biology, 2022, 2467, 113-138.	0.4	9
919	An ecologist's guide for studying DNA methylation variation in wild vertebrates. Molecular Ecology Resources, 2023, 23, 1488-1508.	2.2	13
920	Next generation genomics: toward decoding domestication history of crops. , 2022, , 209-220.		0
922	Evolutionary Ecology of Plant-Arthropod Interactions in Light of the "Omics―Sciences: A Broad Guide. Frontiers in Plant Science, 2022, 13, 808427.	1.7	1
923	A European-wide dataset to uncover adaptive traits of Listeria monocytogenes to diverse ecological niches. Scientific Data, 2022, 9, 190.	2.4	9
924	Validating Amino Acid Variants in Proteogenomics Using Sequence Coverage by Multiple Reads. Journal of Proteome Research, 2022, 21, 1438-1448.	1.8	6
925	Towards Strain-Level Complexity: Sequencing Depth Required for Comprehensive Single-Nucleotide Polymorphism Analysis of the Human Gut Microbiome. Frontiers in Microbiology, 2022, 13, .	1.5	0
926	Pulling needles out of a haystack: Subtractive Community Metatranscriptomics retrieves anaerobic o-xylene degradation pathway genes out of a mixed microbial culture. Journal of Microbiological Methods, 2022, 197, 106481.	0.7	1
928	Comparative Analysis and Data Provenance for 1,113 Bacterial Genome Assemblies. MSphere, 2022, 7, e0007722.	1.3	4
929	Prevalence of bacterial genes in the phage fraction of food viromes. Food Research International, 2022, 156, 111342.	2.9	2
930	Cytomegalovirus variation among newborns treated with valganciclovir. Antiviral Research, 2022, 203, 105326.	1.9	1
931	Transcriptomic Diversity of Solanum tuberosum Varieties: A Drive towards Future Analysis of Its Polyploidy Genome. , 2021, 11, .		Ο

ARTICLE IF CITATIONS # Innovative in Silico Approaches for Characterization of Genes and Proteins. Frontiers in Genetics, 932 1.1 6 2022, 13, . Eph and Ephrin Variants in Malaysian Neural Tube Defect Families. Genes, 2022, 13, 952. 1.0 RNA-Seq and 16S rRNA Analysis Revealed the Effect of Deltamethrin on Channel Catfish in the Early 935 2.2 4 Stage of Acute Exposure. Frontiers in Immunology, 2022, 13, . Bioinformatics Methods for ChIP-seq Histone Analysis. Methods in Molecular Biology, 2022, , 267-293. 937 Genetic testing in neurology: What every neurologist must know. Annals of Indian Academy of 938 0.2 5 Neurology, 2022, 25, 350. Survey on Carbapenem-Resistant Bacteria in Pigs at Slaughter and Comparison with Human Clinical 939 1.5 Isolates in Italy. Antibiotics, 2022, 11, 777. The Activation of Protamine 1 Using Epigenome Editing Decreases the Proliferation of Tumorigenic 940 2.7 2 Cells. Frontiers in Genome Editing, 0, 4, . Carotenoid Biosynthesis: Genome-Wide Profiling, Pathway Identification in Rhodotorula glutinis X-20, 1.6 and High-Level Production. Frontiers in Nutrition, 0, 9, . Moment estimators of relatedness from low-depth whole-genome sequencing data. BMC 942 1.2 1 Bioinformatics, 2022, 23, . Genome diploidization associates with cladogenesis, trait disparity, and plastid gene evolution. Plant 943 2.3 Physiology, 2022, 190, 403-420. CleanSeq: A Pipeline for Contamination Detection, Cleanup, and Mutation Verifications from 944 3 1.3 Microbial Genome Sequencing Data. Applied Sciences (Switzerland), 2022, 12, 6209. Comprehensive Validation of Diagnostic Next-Generation Sequencing Panels for Acute Myeloid 945 1.2 Leukemia Patients. Journal of Molecular Diagnostics, 2022, , . The Revolution of Omics Technology in Plant Science., 2022, , 23-56. 947 1 Seminal Microbiota of Idiopathic Infertile Patients and Its Relationship With Sperm DNA Integrity. 948 1.8 Frontiers in Cell and Developmental Biology, 0, 10, . Fecal Microbiota Transplantation as New Therapeutic Avenue for Human Diseases. Journal of Clinical 949 1.0 28 Medicine, 2022, 11, 4119. Evaluation of nine statistics to identify QTLs in bulk segregant analysis using next generation 1.2 sequencing approaches. BMC Genomics, 2022, 23, . Uncovering the Contribution of Moderate-Penetrance Susceptibility Genes to Breast Cancer by 951 Whole-Exome Sequencing and Targeted Enrichment Sequencing of Candidate Genes in Women of 1.7 2 European Ancestry. Cancers, 2022, 14, 3363. Software Choice and Sequencing Coverage Can Impact Plastid Genome Assembly–A Case Study in the Narrow Endemic Calligonum bakuense. Frontiers in Plant Science, 0, 13, .

#	Article	IF	CITATIONS
954	Variability among the Isolates of Broad Bean Mottle Virus and Encapsidation of Host RNAs. Pathogens, 2022, 11, 817.	1.2	1
956	Ribosomal RNA-Depletion Provides an Efficient Method for Successful Dual RNA-Seq Expression Profiling of a Marine Sponge Holobiont. Marine Biotechnology, 0, , .	1.1	0
958	Genomic differentiation of three picoâ€phytoplankton species in the Mediterranean Sea. Environmental Microbiology, 2022, 24, 6086-6099.	1.8	2
959	Transcriptional search to identify and assess reference genes for expression analysis in Solanum lycopersicum under stress and hormone treatment conditions. Journal of Integrative Agriculture, 2022, , .	1.7	0
960	Immunobiology of Testicular Cancer. , 2022, , .		3
961	Functional characterization of prokaryotic dark matter: the road so far and what lies ahead. Current Research in Microbial Sciences, 2022, 3, 100159.	1.4	2
962	Transcriptomics. , 2023, , 363-371.		1
963	Modelling the Effectiveness of Surveillance Based on Metagenomics in Detecting, Monitoring, and Forecasting Antimicrobial Resistance in Livestock Production Under Economic Constraints. SSRN Electronic Journal, 0, , .	0.4	0
965	Novel mutations in <scp> <i>HTRA1</i> </scp> â€related cerebral small vessel disease and comparison with <scp>CADASIL</scp> . Annals of Clinical and Translational Neurology, 2022, 9, 1586-1595.	1.7	3
967	DETexT: An SNV detection enhancement for low read depth by integrating mutational signatures into TextCNN. Frontiers in Genetics, 0, 13, .	1.1	1
968	Segmented Correspondence Curve Regression for Quantifying Covariate Effects on the Reproducibility of High-Throughput Experiments. Biometrics, 2023, 79, 2272-2285.	0.8	0
969	Prediction of transcript isoforms in 19 chicken tissues by Oxford Nanopore long-read sequencing. Frontiers in Genetics, 0, 13, .	1.1	8
970	Low STR variability in the threatened marsh deer, Blastocerus dichotomus, detected through amplicon sequencing in non-invasive samples. Genetics and Molecular Biology, 2022, 45, .	0.6	1
971	Recent insights into crosstalk between genetic parasites and their host genome. Briefings in Functional Genomics, 2024, 23, 15-23.	1.3	0
973	Developing an effective quality evaluation strategy of next-generation sequencing for accurate detecting non-small cell lung cancer samples with variable characteristics: a real-world clinical practice. Journal of Cancer Research and Clinical Oncology, 2023, 149, 4889-4897.	1.2	1
974	Integrated proteogenomic characterization across major histological types of pituitary neuroendocrine tumors. Cell Research, 2022, 32, 1047-1067.	5.7	18
976	Differential H3K9me2 heterochromatin levels and concordant mRNA expression in postmortem brain tissue of individuals with schizophrenia, bipolar, and controls. Frontiers in Psychiatry, 0, 13, .	1.3	1
977	Transcriptome Analysis of Duck and Chicken Brains Infected with Aquatic Bird Bornavirus-1 (ABBV-1). Viruses, 2022, 14, 2211.	1.5	5

#	Article	IF	CITATIONS
980	The association between the respiratory tract microbiome and clinical outcomes in patients with COPD. Microbiological Research, 2023, 266, 127244.	2.5	2
981	Identification of RP1 as the genetic cause of retinitis pigmentosa in a multi-generational pedigree using Extremely Low-Coverage Whole Genome Sequencing (XLC-WGS). Gene, 2023, 851, 146956.	1.0	0
982	Integrated proteogenomic characterization of medullary thyroid carcinoma. Cell Discovery, 2022, 8, .	3.1	18
983	Capturing SARS-CoV-2 from patient samples with low viral abundance: a comparative analysis. Scientific Reports, 2022, 12, .	1.6	1
984	Targeting intraâ€ŧumoral heterogeneity of human brain tumors with in vivo imaging: A roadmap for imaging genomics from multiparametric MR signals. Medical Physics, 2023, 50, 2590-2606.	1.6	0
985	Blood Group Genotyping. Clinics in Laboratory Medicine, 2022, 42, 645-668.	0.7	3
986	Statistical Challenges in Mutational Signature Analyses of Cancer Sequencing Data. Springer Proceedings in Mathematics and Statistics, 2022, , 241-258.	0.1	0
987	Biology and medicine in the landscape of quantum advantages. Journal of the Royal Society Interface, 2022, 19, .	1.5	24
988	Advances in experimental and computational methodologies for the study of microbial-surface interactions at different omics levels. Frontiers in Microbiology, 0, 13, .	1.5	2
989	Open-Access Worldwide Population STR Database Constructed Using High-Coverage Massively Parallel Sequencing Data Obtained from the 1000 Genomes Project. Genes, 2022, 13, 2205.	1.0	2
992	Performance evaluation of six popular short-read simulators. Heredity, 2023, 130, 55-63.	1.2	4
993	The impact of sequencing depth and relatedness of the reference genome in population genomic studies: A case study with two caddisfly species (Trichoptera, Rhyacophilidae, <i>Himalopsyche</i>). Ecology and Evolution, 2022, 12, .	0.8	3
994	DNA High-Throughput Sequencing for Arthropod Gut Content Analysis to Evaluate Effectiveness and Safety of Biological Control Agents. Neotropical Entomology, 2023, 52, 302-332.	0.5	3
995	Optimal microRNA Sequencing Depth to Predict Cancer Patient Survival with Random Forest and Cox Models. Genes, 2022, 13, 2275.	1.0	2
996	Comparison of structural variants detected by PacBio-CLR and ONT sequencing in pear. BMC Genomics, 2022, 23, .	1.2	2
997	A brief account on enzyme mining using metagenomic approach. Frontiers in Systems Biology, 0, 2, .	0.5	7
998	Short-circuiting biology: Digital phenotypes, digital biomarkers, and shifting gazes in psychiatry. Big Data and Society, 2023, 10, 205395172211456.	2.6	1
999	Navigating the pitfalls of mapping DNA and RNA modifications. Nature Reviews Genetics, 2023, 24, 363-381.	7.7	8

#	Article	IF	CITATIONS
1000	In-depth analysis of large-scale screening of WRKY members based on genome-wide identification. Frontiers in Genetics, 0, 13, .	1.1	2
1001	Quality assessment and refinement of chromatin accessibility data using a sequence-based predictive model. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	4
1002	Transcriptomic and Epigenomic Approaches for Epilepsy. , 2022, , 19-40.		0
1003	Genetic fineâ€mapping reveals single nucleotide polymorphism mutations in the <scp>MC1R</scp> regulatory region associated with duck melanism. Molecular Ecology, 2023, 32, 3076-3088.	2.0	2
1005	Runs of homozygosity reveal past bottlenecks and contemporary inbreeding across diverging populations of an islandâ€colonizing bird. Molecular Ecology, 2023, 32, 1972-1989.	2.0	6
1006	Genome Sequencing. , 2021, , 298-317.		0
1007	Rapid Pathogen Detection in Infectious Uveitis Using Nanopore Metagenomic Next-Generation Sequencing: A Preliminary Study. Ocular Immunology and Inflammation, 0, , 1-7.	1.0	1
1008	Epigenetic and chromosomal features drive transposon insertion in <i>Drosophila melanogaster</i> . Nucleic Acids Research, 2023, 51, 2066-2086.	6.5	6
1010	Koala Genome Survey: An Open Data Resource to Improve Conservation Planning. Genes, 2023, 14, 546.	1.0	5
1011	Robust Performance of SARS-CoV-2 Whole-Genome Sequencing from Wastewater with a Nonselective Virus Concentration Method. ACS ES&T Water, 2023, 3, 954-962.	2.3	3
1012	Depth of Sequencing Plays a Determining Role in the Characterization of Phage Display Peptide Libraries by NGS. International Journal of Molecular Sciences, 2023, 24, 5396.	1.8	0
1013	Genome-wide profiling of rice Double-stranded RNA-Binding Protein 1–associated RNAs by targeted RNA editing. Plant Physiology, 2023, 192, 805-820.	2.3	5
1014	Whole-genome Study of Carbapenem-resistant <i>Acinetobacter baumannii</i> Virulence and Resistance. Iranian Journal of Medical Microbiology, 2023, 17, 90-102.	0.1	0
1015	Verification of prognostic expression biomarkers is improved by examining enriched leukemic blasts rather than mononuclear cells from acute myeloid leukemia patients. Biomarker Research, 2023, 11, .	2.8	0
1016	Microbiota Mediate Enhanced Exercise Capacity Induced by Exercise Training. Medicine and Science in Sports and Exercise, 0, Publish Ahead of Print, .	0.2	0
1018	Identifying prognostic gene panels in acute myeloid leukemia. Expert Review of Hematology, 2023, 16, 277-287.	1.0	1
1019	Highly accurate long reads are crucial for realizing the potential of biodiversity genomics. BMC Genomics, 2023, 24, .	1.2	7
1020	Circulating and urinary tumour DNA in urothelial carcinoma— upper tract, lower tract and metastatic disease. Nature Reviews Urology, 2023, 20, 406-419.	1.9	6

#	Article	IF	CITATIONS
1021	Validation and depth evaluation of low-pass genome sequencing in prenatal diagnosis using 387 amniotic fluid samples. Journal of Medical Genetics, 2023, 60, 933-938.	1.5	1
1023	Improved eukaryotic detection compatible with large-scale automated analysis of metagenomes. Microbiome, 2023, 11, .	4.9	0
1024	Comparing genomic variant identification protocols for Candida auris. Microbial Genomics, 2023, 9, .	1.0	2
1025	On the causes, consequences, and avoidance of <scp>PCR</scp> duplicates: Towards a theory of library complexity. Molecular Ecology Resources, 2023, 23, 1299-1318.	2.2	5
1030	Long-Read Metagenomics and CAZyme Discovery. Methods in Molecular Biology, 2023, , 253-284.	0.4	0
1041	Understanding the Molecular Mechanisms of Orchid Mycorrhizal Symbiosis from Genetic Information. , 2023, , 1-25.		0
1044	Transkriptomik. , 2023, , 201-214.		0
1047	Optimizing Variant Calling forÂHuman Genome Analysis: A Comprehensive Pipeline Approach. Lecture Notes in Computer Science, 2023, , 72-85.	1.0	0
1054	A Workflow Guide to RNA-Seq Analysis of Chaperone Function and Beyond. Methods in Molecular Biology, 2023, , 39-60.	0.4	0
1062	Denoising sparse microbial signals from single-cell sequencing of mammalian host tissues. Nature Computational Science, 2023, 3, 741-747.	3.8	0
1081	Bioprospecting of unexplored halophilic actinobacteria against human infectious pathogens. 3 Biotech, 2023, 13, .	1.1	1
1090	Transcriptomics. Learning Materials in Biosciences, 2023, , 201-213.	0.2	0
1098	Guidelines and important considerations for $\hat{a} \in \tilde{a}$ omics-level studies. , 2024, , 189-209.		0
1105	Genetic Diagnosis and Counseling in Muscular Dystrophies. Current Clinical Neurology, 2023, , 221-231.	0.1	0
1114	New biotechnological tools for grapevine improvement. Advances in Botanical Research, 2024, , .	0.5	0