Performance comparison of benchtop high-throughput

Nature Biotechnology 30, 434-439

DOI: 10.1038/nbt.2198

Citation Report

#	Article	IF	CITATIONS
1	Malignant external otitis. Journal of Laryngology and Otology, 1987, 101, 205-210.	0.4	62
2	Routine Use of Microbial Whole Genome Sequencing in Diagnostic and Public Health Microbiology. PLoS Pathogens, 2012, 8, e1002824.	2.1	450
3	Next-generation sequencing in breast cancer. Current Opinion in Oncology, 2012, 24, 597-604.	1.1	76
4	Rapid Development of Microsatellite Markers for the Endangered Fish Schizothorax biddulphi (GA½nther) Using Next Generation Sequencing and Cross-Species Amplification. International Journal of Molecular Sciences, 2012, 13, 14946-14955.	1.8	41
5	Diagnostic applications of next generation sequencing: working towards quality standards/Diagnostische Anwendung von Next Generation Sequencing: Auf dem Weg zu QualitÃ u standards. Laboratoriums Medizin, 2012, 36, .	0.1	4
6	Challenges and opportunities in estimating viral genetic diversity from next-generation sequencing data. Frontiers in Microbiology, 2012, 3, 329.	1.5	204
7	The battle for sequencing supremacy. Nature Biotechnology, 2012, 30, 1023-1026.	9.4	20
8	Online Tools for Bioinformatics Analyses in Nutrition Sciences. Advances in Nutrition, 2012, 3, 654-665.	2.9	13
9	The expanding scope of DNA sequencing. Nature Biotechnology, 2012, 30, 1084-1094.	9.4	280
10	Wrestling with the repertoire: The promise and perils of next generation sequencing for antigen receptors. European Journal of Immunology, 2012, 42, 2834-2839.	1.6	52
11	Next-Generation Sequencing of Microbial Communities in the Athabasca River and Its Tributaries in Relation to Oil Sands Mining Activities. Applied and Environmental Microbiology, 2012, 78, 7626-7637.	1.4	193
12	SNVerGUI: a desktop tool for variant analysis of next-generation sequencing data. Journal of Medical Genetics, 2012, 49, 753-755.	1.5	15
13	Application of next-generation sequencing technologies in virology. Journal of General Virology, 2012, 93, 1853-1868.	1.3	241
14	Transforming clinical microbiology with bacterial genome sequencing. Nature Reviews Genetics, 2012, 13, 601-612.	7.7	684
15	Complete genome sequence of an astrovirus identified in a domestic rabbit (Oryctolagus cuniculus) with gastroenteritis. Virology Journal, 2012, 9, 216.	1.4	21
16	DNA and RNA analyses in detection of genetic predisposition to cancer. Hereditary Cancer in Clinical Practice, 2012, 10, 17.	0.6	6
17	Bacterial Community Shift in Treated Periodontitis Patients Revealed by Ion Torrent 16S rRNA Gene Amplicon Sequencing. PLoS ONE, 2012, 7, e41606.	1.1	116
18	High-throughput bacterial genome sequencing: an embarrassment of choice, a world of opportunity. Nature Reviews Microbiology, 2012, 10, 599-606.	13.6	367

#	Article	IF	Citations
19	Current mutation discovery approaches in Retinitis Pigmentosa. Vision Research, 2012, 75, 117-129.	0.7	57
20	Clinical Integration of Next-Generation Sequencing Technology. Clinics in Laboratory Medicine, 2012, 32, 585-599.	0.7	57
21	Long-range Transcriptome Sequencing Reveals Cancer Cell Growth Regulatory Chimeric mRNA. Neoplasia, 2012, 14, 1087-49.	2.3	19
23	Mutational spectrum of WTX, WT1, CTNNB1, APC and PLCG2 genes in Wilms tumor defined by massive parallel resequencing. BMC Proceedings, 2012, 6, .	1.8	1
24	Characterization of European Sea Bass Transcripts by RNA SEQ After Oral Vaccine Against V. anguillarum. Marine Biotechnology, 2012, 14, 634-642.	1.1	52
25	Improving Indel Detection Specificity of the Ion Torrent PGM Benchtop Sequencer. PLoS ONE, 2012, 7, e45798.	1.1	48
26	Use of Four Next-Generation Sequencing Platforms to Determine HIV-1 Coreceptor Tropism. PLoS ONE, 2012, 7, e49602.	1.1	78
27	Conveniently Pre-Tagged and Pre-Packaged: Extended Molecular Identification and Metagenomics Using Complete Metazoan Mitochondrial Genomes. PLoS ONE, 2012, 7, e51263.	1.1	14
28	Next-generation genome sequencers compared. Nature, 2012, , .	13.7	1
30	The uncertain road towards genomic medicine. Trends in Genetics, 2012, 28, 303-305.	2.9	8
31	Characterizing and measuring bias in sequence data. Genome Biology, 2013, 14, R51.	13.9	695
32	Tumor-associated copy number changes in the circulation of patients with prostate cancer identified through whole-genome sequencing. Genome Medicine, 2013, 5, 30.	3.6	306
33	Biological Aging. Methods in Molecular Biology, 2013, , .	0.4	1
34	Clinical Validation of a Next-Generation Sequencing Screen for Mutational Hotspots in 46 Cancer-Related Genes. Journal of Molecular Diagnostics, 2013, 15, 607-622.	1.2	314
35	Survival in hostile territory: the microbiota of the stomach. FEMS Microbiology Reviews, 2013, 37, 736-761.	3.9	126
36	Read and assembly metrics inconsequential for clinical utility of whole-genome sequencing in mapping outbreaks. Nature Biotechnology, 2013, 31, 592-594.	9.4	26
37	Routine performance and errors of 454 HLA exon sequencing in diagnostics. BMC Bioinformatics, 2013, 14, 176.	1.2	20
38	Sequencing platform and library preparation choices impact viral metagenomes. BMC Genomics, 2013, 14, 320.	1.2	90

#	Article	IF	CITATIONS
39	Genome sequencing of bacteria: sequencing, de novo assembly and rapid analysis using open source tools. BMC Genomics, 2013, 14, 211.	1.2	43
40	Deep sequencing for de novo construction of a marine fish (Sparus aurata)transcriptome database with a large coverage of protein-coding transcripts. BMC Genomics, 2013, 14, 178.	1.2	90
41	Evolutionary change driven by metal exposure as revealed by coding SNP genome scan in wild yellow perch (Perca flavescens). Ecotoxicology, 2013, 22, 938-957.	1.1	38
42	Advanced Techniques for Detection and Identification of Microbial Agents of Gastroenteritis. Clinics in Laboratory Medicine, 2013, 33, 527-552.	0.7	22
43	Environmental effects on biofilm bacterial communities: a comparison of natural and anthropogenic factors in <scp>N</scp> ew <scp>Z</scp> ealand streams. Freshwater Biology, 2013, 58, 2277-2286.	1.2	9
44	The Evolution of High-Throughput Sequencing Technologies: From Sanger to Single-Molecule Sequencing. , 2013, , 1-30.		0
46	New Advances in the Precision Medicine of Lung Cancer. Current Pathobiology Reports, 2013, 1, 1-8.	1.6	4
47	Microbial phylogenetic profiling with the Pacific Biosciences sequencing platform. Microbiome, 2013, 1, 10.	4.9	121
48	The Genomics of Emerging Pathogens. Annual Review of Genomics and Human Genetics, 2013, 14, 281-300.	2.5	50
49	Single-Cell Semiconductor Sequencing. Methods in Molecular Biology, 2013, 1048, 247-284.	0.4	16
50	Evaluation of general 16S ribosomal RNA gene PCR primers for classical and next-generation sequencing-based diversity studies. Nucleic Acids Research, 2013, 41, e1-e1.	6.5	6,268
51	A Clinically Validated Diagnostic Second-Generation Sequencing Assay for Detection of Hereditary BRCA1 and BRCA2 Mutations. Journal of Molecular Diagnostics, 2013, 15, 796-809.	1.2	29
52	Culture-Independent Molecular Tools for Soil and Rhizosphere Microbiology. Diversity, 2013, 5, 581-612.	0.7	88
53	Vancomycin-Modified Mesoporous Silica Nanoparticles for Selective Recognition and Killing of Pathogenic Gram-Positive Bacteria Over Macrophage-Like Cells. ACS Applied Materials & Samp; Interfaces, 2013, 5, 10874-10881.	4.0	165
54	Genome engineering using the CRISPR-Cas9 system. Nature Protocols, 2013, 8, 2281-2308.	5.5	9,114
55	Selection on haemagglutinin imposes a bottleneck during mammalian transmission of reassortant H5N1 influenza viruses. Nature Communications, 2013, 4, 2636.	5.8	80
56	High-Throughput Sequencing and Metagenomics: Moving Forward in the Culture-Independent Analysis of Food Microbial Ecology. Applied and Environmental Microbiology, 2013, 79, 3148-3155.	1.4	412
57	Molecular detection of CF lung pathogens: Current status and future potential. Journal of Cystic Fibrosis, 2013, 12, 194-205.	0.3	25

#	Article	IF	Citations
58	Genomics and metagenomics in medical microbiology. Journal of Microbiological Methods, 2013, 95, 415-424.	0.7	69
59	Genetic high throughput screening in Retinitis Pigmentosa based on high resolution melting (HRM) analysis. Experimental Eye Research, 2013, 116, 386-394.	1.2	14
60	Molecular-based diagnostics, including future trends. Medicine, 2013, 41, 663-666.	0.2	1
61	Intratumoral genetic heterogeneity in metastatic melanoma is accompanied by variation in malignant behaviors. BMC Medical Genomics, 2013, 6, 40.	0.7	28
62	Assessing De Novo transcriptome assembly metrics for consistency and utility. BMC Genomics, 2013, 14, 465.	1.2	105
63	Sequencing-based variant detection in the polyploid crop oilseed rape. BMC Plant Biology, 2013, 13, 111.	1.6	11
64	Significant variance in genetic diversity among populations of Schistosoma haematobium detected using microsatellite DNA loci from a genome-wide database. Parasites and Vectors, 2013, 6, 300.	1.0	26
65	High throughput sequencing methods and analysis for microbiome research. Journal of Microbiological Methods, 2013, 95, 401-414.	0.7	210
66	Future-Generation Sequencing and Clinical Microbiology. Clinics in Laboratory Medicine, 2013, 33, 685-704.	0.7	3
67	Targeted capture and sequencing for detection of mutations causing early onset epileptic encephalopathy. Epilepsia, 2013, 54, 1262-1269.	2.6	76
68	Lung Cancer Biomarkers: Present Status and Future Developments. Archives of Pathology and Laboratory Medicine, 2013, 137, 1191-1198.	1,2	105
69	PREMIER Turbo: Probabilistic error-correction using Markov inference in errored reads using the turbo principle. , 2013, , .		6
70	Genomics and outbreak investigation: from sequence to consequence. Genome Medicine, 2013, 5, 36.	3.6	64
71	BAC Library Development and Clone Characterization for Dormancy-Responsive DREB4A, DAM, and FT from Leafy Spurge (Euphorbia esula) Identifies Differential Splicing and Conserved Promoter Motifs. Weed Science, 2013, 61, 303-309.	0.8	11
72	Next-generation sequencing meets genetic diagnostics: development of a comprehensive workflow for the analysis of BRCA1 and BRCA2 genes. European Journal of Human Genetics, 2013, 21, 864-870.	1.4	94
7 3	The changing face of pathogen discovery and surveillance. Nature Reviews Microbiology, 2013, 11, 133-141.	13.6	145
74	Nextâ€generation sequencing – feasibility and practicality in haematology. British Journal of Haematology, 2013, 160, 736-753.	1,2	54
75	Nonoptical Massive Parallel DNA Sequencing of <i>BRCA1</i> and <i>BRCA2</i> Genes in a Diagnostic Setting. Human Mutation, 2013, 34, 629-635.	1.1	37

#	Article	IF	CITATIONS
76	Next-generation sequencing in the clinic: Promises and challenges. Cancer Letters, 2013, 340, 284-295.	3.2	272
77	Impacts of massively parallel sequencing for genetic diagnosis of neuromuscular disorders. Acta Neuropathologica, 2013, 125, 173-185.	3.9	37
78	Sequence assembly demystified. Nature Reviews Genetics, 2013, 14, 157-167.	7.7	396
79	Chemical fragmentation for massively parallel sequencing library preparation. Journal of Biotechnology, 2013, 168, 95-100.	1.9	2
80	Diagnostic Applications of Next Generation Sequencing in Immunogenetics and Molecular Oncology. Transfusion Medicine and Hemotherapy, 2013, 40, 196-206.	0.7	21
81	Performance and microbial community analysis of the anaerobic reactor with coke oven gas biomethanation and in situ biogas upgrading. Bioresource Technology, 2013, 146, 234-239.	4.8	138
82	Detection of variations and identifying genomic breakpoints for large deletions in the LDLR by Ion Torrent semiconductor sequencing. Atherosclerosis, 2013, 230, 249-255.	0.4	19
83	Recent transcriptomics advances and emerging applications in food science. TrAC - Trends in Analytical Chemistry, 2013, 52, 142-154.	5 . 8	54
84	In the Spotlight: Bioinformatics. IEEE Reviews in Biomedical Engineering, 2013, 6, 3-8.	13.1	2
85	Integrating nextâ€generation sequencing into the diagnostic testing of inherited cancer predisposition. Clinical Genetics, 2013, 83, 2-6.	1.0	23
86	Highâ€throughput sequencing of the melanoma genome. Experimental Dermatology, 2013, 22, 10-17.	1.4	33
87	Genes, behavior and nextâ€generation <scp>RNA</scp> sequencing. Genes, Brain and Behavior, 2013, 12, 1-12.	1.1	74
88	Rapid deep sequencing of patient-derived HIV with ion semiconductor technology. Journal of Virological Methods, 2013, 189, 232-234.	1.0	21
89	Investigation of antibiotic resistance in the genomic era of multidrug-resistant Gram-negative bacilli, especiallyEnterobacteriaceae,PseudomonasandAcinetobacter. Expert Review of Anti-Infective Therapy, 2013, 11, 277-296.	2.0	24
90	Evaluation of targeted next-generation sequencing–based preimplantation genetic diagnosis ofÂmonogenic disease. Fertility and Sterility, 2013, 99, 1377-1384.e6.	0.5	159
91	The impact of next-generation sequencing technology on preimplantation genetic diagnosis and screening. Fertility and Sterility, 2013, 99, 1054-1061.e3.	0.5	71
92	Beyond Gel Electrophoresis: Microfluidic Separations, Fluorescence Burst Analysis, and DNA Stretching. Chemical Reviews, 2013, 113, 2584-2667.	23.0	162
93	Combining Highly Multiplexed PCR with Semiconductor-Based Sequencing for Rapid Cancer Genotyping. Journal of Molecular Diagnostics, 2013, 15, 171-176.	1.2	140

#	Article	IF	CITATIONS
94	Existing and Emerging Technologies for Tumor Genomic Profiling. Journal of Clinical Oncology, 2013, 31, 1815-1824.	0.8	129
95	The role of high-throughput technologies in clinical cancer genomics. Expert Review of Molecular Diagnostics, 2013, 13, 167-181.	1.5	26
96	Targeted, High-Depth, Next-Generation Sequencing of Cancer Genes in Formalin-Fixed, Paraffin-Embedded and Fine-Needle Aspiration Tumor Specimens. Journal of Molecular Diagnostics, 2013, 15, 234-247.	1.2	192
97	Human Genome Variation Discovery via Exome and Whole-Genome Sequencing., 2013,, 94-101.		0
98	A magneto-DNA nanoparticle system for rapid detection and phenotyping of bacteria. Nature Nanotechnology, 2013, 8, 369-375.	15.6	307
99	Comprehensive DNA methylation and extensive mutation analyses reveal an association between the CpG island methylator phenotype and oncogenic mutations in gastric cancers. Cancer Letters, 2013, 330, 33-40.	3.2	57
100	The new sequencer on the block: comparison of Life Technology's Proton sequencer to an Illumina HiSeq for whole-exome sequencing. Human Genetics, 2013, 132, 1153-1163.	1.8	75
101	Viral surveillance and discovery. Current Opinion in Virology, 2013, 3, 199-204.	2.6	57
102	KRAS, BRAF, and TP53 Deep Sequencing for Colorectal Carcinoma Patient Diagnostics. Journal of Molecular Diagnostics, 2013, 15, 299-311.	1.2	27
103	Genetic Analysis in Neurology. JAMA Neurology, 2013, 70, 696.	4.5	13
104	High efficiency application of a mate-paired library from next-generation sequencing to postlight sequencing: Corynebacterium pseudotuberculosis as a case study for microbial de novo genome assembly. Journal of Microbiological Methods, 2013, 95, 441-447.	0.7	6
105	Next-generation sequencing in clinical microbiology. Expert Review of Molecular Diagnostics, 2013, 13, 225-227.	1.5	14
106	Updating benchtop sequencing performance comparison. Nature Biotechnology, 2013, 31, 294-296.	9.4	423
107	Anaerobic Digestion for Simultaneous Sewage Sludge Treatment and CO Biomethanation: Process Performance and Microbial Ecology. Environmental Science & Echnology, 2013, 47, 130904143045005.	4.6	61
108	High-Throughput Gene Expression and Mutation Profiling: Current Methods and Future Perspectives. Breast Care, 2013, 8, 401-406.	0.8	14
109	New strategy for virus discovery: viruses identified in human feces in the last decade. Science China Life Sciences, 2013, 56, 688-696.	2.3	15
110	123 of Metagenomics. , 2013, , 1-11.		1
111	Bacterial genomes in epidemiology—present and future. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20120202.	1.8	51

#	Article	IF	CITATIONS
112	Reply to Updating benchtop sequencing performance comparison. Nature Biotechnology, 2013, 31, 296-296.	9.4	7
113	The use of next-generation sequencing in clinical diagnosis of familial hypercholesterolemia. Genetics in Medicine, 2013, 15, 948-957.	1.1	69
114	The Effect of Preprocessing by Sequence-Independent, Single-Primer Amplification (SISPA) on Metagenomic Detection of Viruses. Biosecurity and Bioterrorism, 2013, 11, S227-S234.	1.2	43
116	Draft Genome Sequence for <i>Ralstonia</i> sp. Strain OR214, a Bacterium with Potential for Bioremediation. Genome Announcements, 2013, 1 , .	0.8	12
117	Draft Genome Sequence for <i>Caulobacter</i> sp. Strain OR37, a Bacterium Tolerant to Heavy Metals. Genome Announcements, 2013, 1, .	0.8	11
118	Haplessly Hoping: Macaque Major Histocompatibility Complex Made Easy. ILAR Journal, 2013, 54, 196-210.	1.8	98
119	The Proposed New Classification of Pulmonary Adenocarcinoma and the Conservation of Small Tissue Samples for Testing. Archives of Pathology and Laboratory Medicine, 2013, 137, 453-454.	1.2	3
120	IROme, a New High-Throughput Molecular Tool for the Diagnosis of Inherited Retinal Dystrophies. BioMed Research International, 2013, 2013, 1-9.	0.9	22
121	Novel cases of D-2-hydroxyglutaric aciduria with <i>IDH1 </i> i>or <i>IDH2 </i> mosaic mutations identified by amplicon deep sequencing. Journal of Medical Genetics, 2013, 50, 754-759.	1.5	19
122	Deep Sequencing Reveals Mutagenic Effects of Ribavirin during Monotherapy of Hepatitis C Virus Genotype 1-Infected Patients. Journal of Virology, 2013, 87, 6172-6181.	1.5	88
123	Shining a Light on Dark Sequencing: Characterising Errors in Ion Torrent PGM Data. PLoS Computational Biology, 2013, 9, e1003031.	1.5	265
124	Applications and data analysis of next-generation sequencing. Laboratoriums Medizin, 2013, 37, .	0.1	3
125	Next-Generation Sequence Assembly: Four Stages of Data Processing and Computational Challenges. PLoS Computational Biology, 2013, 9, e1003345.	1.5	120
126	Scrapheap Challenge: A novel bulk-bone metabarcoding method to investigate ancient DNA in faunal assemblages. Scientific Reports, 2013, 3, 3371.	1.6	72
127	Research and clinical applications of cancer genome sequencing. Current Opinion in Obstetrics and Gynecology, 2013, 25, 3-10.	0.9	14
128	Harnessing the genome: development of a hierarchical typing scheme for meticillin-resistant Staphylococcus aureus. Journal of Medical Microbiology, 2013, 62, 36-45.	0.7	4
129	The detection of microRNA associated with Alzheimer's disease in biological fluids using next-generation sequencing technologies. Frontiers in Genetics, 2013, 4, 150.	1.1	103
130	Filtering duplicate reads from 454 pyrosequencing data. Bioinformatics, 2013, 29, 830-836.	1.8	18

#	Article	IF	CITATIONS
131	Microbial Diversity in the Era of Omic Technologies. BioMed Research International, 2013, 2013, 1-15.	0.9	54
132	Reducing assembly complexity of microbial genomes with single-molecule sequencing. Genome Biology, 2013, 14, R101.	13.9	378
133	Rapid 16S rRNA Next-Generation Sequencing of Polymicrobial Clinical Samples for Diagnosis of Complex Bacterial Infections. PLoS ONE, 2013, 8, e65226.	1.1	186
134	FunGene: the functional gene pipeline and repository. Frontiers in Microbiology, 2013, 4, 291.	1.5	518
135	Non-Invasive Screening Tools for Down's Syndrome: A Review. Diagnostics, 2013, 3, 291-314.	1.3	10
136	The History of DNA Sequencing / ISTORIJAT SEKVENCIRANJA DNK. Journal of Medical Biochemistry, 2013, 32, 301-312.	0.7	21
137	Advances in the Molecular Diagnosis of Hepatitis B Infection: Providing Insight into the Next Generation of Disease. Seminars in Liver Disease, 2013, 33, 113-121.	1.8	10
138	Metagenomic Detection Methods in Biopreparedness Outbreak Scenarios. Biosecurity and Bioterrorism, 2013, 11, S146-S157.	1.2	15
139	Bacterial and archaeal community structure in the surface microlayer of high mountain lakes examined under two atmospheric aerosol loading scenarios. FEMS Microbiology Ecology, 2013, 84, 387-397.	1.3	36
140	Computational Toxicology Experience and Applications for Risk Assessment in the Pharmaceutical Industry., 2013,, 171-193.		0
141	Oligotyping: differentiating between closely related microbial taxa using 16S <scp>rRNA</scp> gene data. Methods in Ecology and Evolution, 2013, 4, 1111-1119.	2.2	652
142	High-throughput DNA sequencing errors are reduced by orders of magnitude using circle sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 19872-19877.	3.3	241
143	Big data challenges and opportunities in high-throughput sequencing. Systems Biomedicine (Austin,) Tj ETQq0 0	0 rgBT /O	verlock 10 Tf
144	Integrating next-generation sequencing into clinical cancer diagnostics. Expert Review of Molecular Diagnostics, 2013, 13, 647-650.	1.5	6
145	Targeted-capture massively-parallel sequencing enables robust detection of clinically informative mutations from formalin-fixed tumours. Scientific Reports, 2013, 3, 3494.	1.6	44
146	Multigene Assays in Metastatic Colorectal Cancer. Journal of the National Comprehensive Cancer Network: JNCCN, 2013, 11, S-9-S-17.	2.3	11
147	Error analysis of idealized nanopore sequencing. Electrophoresis, 2013, 34, 2137-2144.	1.3	30
148	Fragmentation of Genomic DNA using Microwave Irradiation. Journal of Biomolecular Techniques, 2013, 24, jbt.13-2402-005.	0.8	9

#	Article	IF	Citations
149	Culture-Independence for Surveillance and Epidemiology. Pathogens, 2013, 2, 556-570.	1.2	4
150	Rapid Clinical Bacteriology and Its Future Impact. Annals of Laboratory Medicine, 2013, 33, 14-27.	1.2	102
151	Enhanced De Novo Assembly of High Throughput Pyrosequencing Data Using Whole Genome Mapping. PLoS ONE, 2013, 8, e61762.	1.1	33
152	RESTseq – Efficient Benchtop Population Genomics with RESTriction Fragment SEQuencing. PLoS ONE, 2013, 8, e63960.	1.1	38
153	Simplified Large-Scale Sanger Genome Sequencing for Influenza A/H3N2 Virus. PLoS ONE, 2013, 8, e64785.	1.1	24
154	Towards Clinical Molecular Diagnosis of Inherited Cardiac Conditions: A Comparison of Bench-Top Genome DNA Sequencers. PLoS ONE, 2013, 8, e67744.	1.1	51
155	A Microfluidic DNA Library Preparation Platform for Next-Generation Sequencing. PLoS ONE, 2013, 8, e68988.	1.1	63
156	Validation of Next Generation Sequencing Technologies in Comparison to Current Diagnostic Gold Standards for BRAF, EGFR and KRAS Mutational Analysis. PLoS ONE, 2013, 8, e69604.	1.1	94
157	Performance Comparison of Bench-Top Next Generation Sequencers Using Microdroplet PCR-Based Enrichment for Targeted Sequencing in Patients with Autism Spectrum Disorder. PLoS ONE, 2013, 8, e74167.	1.1	31
158	Characterizing Immunoglobulin Repertoire from Whole Blood by a Personal Genome Sequencer. PLoS ONE, 2013, 8, e75294.	1.1	6
159	Application of Genotyping-by-Sequencing on Semiconductor Sequencing Platforms: A Comparison of Genetic and Reference-Based Marker Ordering in Barley. PLoS ONE, 2013, 8, e76925.	1.1	186
160	Simultaneous digital quantification and fluorescence-based size characterization of massively parallel sequencing libraries. BioTechniques, 2013, 55, 61-7.	0.8	26
161	From phenotyping to the study of clonal relationship of microbial isolates. Microbiologia Medica, 2013, 28, .	0.3	0
162	Forensic DNA profiling: state of the art. Research and Reports in Forensic Medical Science, 0, , 25.	0.0	4
163	Random Whole Metagenomic Sequencing for Forensic Discrimination of Soils. PLoS ONE, 2014, 9, e104996.	1.1	40
164	GABenchToB: A Genome Assembly Benchmark Tuned on Bacteria and Benchtop Sequencers. PLoS ONE, 2014, 9, e107014.	1.1	29
165	Direct Chloroplast Sequencing: Comparison of Sequencing Platforms and Analysis Tools for Whole Chloroplast Barcoding. PLoS ONE, 2014, 9, e110387.	1.1	22
166	High-Throughput Sequencing, a VersatileWeapon to Support Genome-Based Diagnosis in Infectious Diseases: Applications to Clinical Bacteriology. Pathogens, 2014, 3, 258-279.	1.2	22

#	Article	IF	CITATIONS
167	In Phase HLA Genotyping by Next Generation Sequencing â€" A Comparison Between Two Massively Parallel Sequencing Bench-Top Systems, the Roche GS Junior and Ion Torrent PGM. , 2014, , .		3
168	Mini Review Identifying human disease genes: advances in molecular genetics and computational approaches. Genetics and Molecular Research, 2014, 13, 5073-5087.	0.3	9
170	Microbial Profile of the Stomach: Comparison between Normal Mucosa and Cancer Tissue in the Same Patient. Journal of Bacteriology and Virology, 2014, 44, 162.	0.0	18
171	Performance Comparison of Benchtop Next-generation Sequencing Systems. Journal of Bacteriology and Virology, 2014, 44, 208.	0.0	2
172	Validation of Next Generation Sequencing Cancer Panels for Clinical Somatic Mutation Profiling-Identification of Source of Variations and Artifacts using FFPE Tissues. Journal of Next Generation Sequencing & Applications, 2014, 01, .	0.3	3
173	A workflow to increase verification rate of chromosomal structural rearrangements using high-throughput next-generation sequencing. BioTechniques, 2014, 57, 31-38.	0.8	O
174	Semiconductor Sequencing Reveals the Diversity of Bacterial Communities in an Amazonian Reservoir. Aquatic Science and Technology, 2014, 3, 18.	0.1	6
176	7. Human immunodeficiency virus. , 2014, , 97-112.		O
177	Metagenomics and novel gene discovery. Virulence, 2014, 5, 399-412.	1.8	103
179	Metagenomic analyses of bacteria on human hairs: a qualitative assessment for applications in forensic science. Investigative Genetics, 2014 , 5 , 16 .	3.3	69
180	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
181	Efficient DNA Fingerprinting Based on the Targeted Sequencing of Active Retrotransposon Insertion Sites Using a Bench-Top High-Throughput Sequencing Platform. DNA Research, 2014, 21, 491-498.	1.5	20
182	Application of high-throughput sequencing for studying genomic variations in congenital heart disease. Briefings in Functional Genomics, 2014, 13, 51-65.	1.3	16
183	Cross-clade simultaneous HIV drug resistance genotyping for reverse transcriptase, protease, and integrase inhibitor mutations by Illumina MiSeq. Retrovirology, 2014, 11, 122.	0.9	32
184	Diverse cell stresses induce unique patterns of tRNA up- and down-regulation: tRNA-seq for quantifying changes in tRNA copy number. Nucleic Acids Research, 2014, 42, e170-e170.	6.5	114
185	Genetic testing for nephrotic syndrome and FSGS in the era of next-generation sequencing. Kidney International, 2014, 85, 1030-1038.	2.6	61
186	Measuring the activity of protein variants on a large scale using deep mutational scanning. Nature Protocols, 2014, 9, 2267-2284.	5.5	147
187	Making the genomic leap in HCT: application of second-generation sequencing to clinical advances in hematopoietic cell transplantation. European Journal of Human Genetics, 2014, 22, 715-723.	1.4	5

#	Article	IF	CITATIONS
188	Full genome sequence analysis of a novel adenovirus of rhesus macaque origin indicates a new simian adenovirus type and species. Virology Reports, 2014, 3-4, 18-29.	0.4	11
189	The Antibody Genetics of Multiple Sclerosis: Comparing Next-Generation Sequencing to Sanger Sequencing. Frontiers in Neurology, 2014, 5, 166.	1.1	10
190	Historical Perspective, Development and Applications of Next-Generation Sequencing in Plant Virology. Viruses, 2014, 6, 106-136.	1.5	225
191	Applications of Next-Generation Sequencing Technologies to the Study of the Human Microbiome. Comprehensive Analytical Chemistry, 2014, , 75-106.	0.7	0
192	The antibody mining toolbox. MAbs, 2014, 6, 160-172.	2.6	41
193	Emerging Rapid Resistance Testing Methods for Clinical Microbiology Laboratories and Their Potential Impact on Patient Management. BioMed Research International, 2014, 2014, 1-19.	0.9	56
194	Characterization of in vitro haploid and doubled haploid Chrysanthemum morifolium plants via unfertilized ovule culture for phenotypical traits and DNA methylation pattern. Frontiers in Plant Science, 2014, 5, 738.	1.7	31
195	Neurofibromatosis Type 1 Gene Mutation Analysis Using Sequence Capture and High-throughput Sequencing. Acta Dermato-Venereologica, 2014, 94, 663-666.	0.6	8
196	The Impact of "Omic―and Imaging Technologies on Assessing the Host Immune Response to Biodefence Agents. Journal of Immunology Research, 2014, 2014, 1-17.	0.9	6
197	Seeking the source of <i>Pseudomonas aeruginosa </i> infections in a recently opened hospital: an observational study using whole-genome sequencing. BMJ Open, 2014, 4, e006278.	0.8	104
198	Next-Generation Sequencing (NGS) in Anatomic Pathology Discovery and Practice. Methods in Pharmacology and Toxicology, 2014, , 219-257.	0.1	1
199	Somatic Mutations in Cerebral Cortical Malformations. New England Journal of Medicine, 2014, 371, 2037-2038.	13.9	18
200	Next-generation sequencing-based multigene mutational screening for acute myeloid leukemia using MiSeq: applicability for diagnostics and disease monitoring. Haematologica, 2014, 99, 465-473.	1.7	165
201	"New turns from old STaRs― Enhancing the capabilities of forensic short tandem repeat analysis. Electrophoresis, 2014, 35, 3173-3187.	1.3	31
202	Whole-Genome Analyses. Methods in Microbiology, 2014, 41, 103-122.	0.4	59
203	Challenges using diagnostic next-generation sequencing in the clinical environment for inherited retinal disorders. Personalized Medicine, 2014, 11, 99-111.	0.8	7
204	Evolution of HIV-1 quasispecies and coreceptor use in cell reservoirs of patients on suppressive antiretroviral therapy. Journal of Antimicrobial Chemotherapy, 2014, 69, 2527-2530.	1.3	18
205	TP53 Mutation Analysis in Clinical Practice: Lessons From Chronic Lymphocytic Leukemia. Human Mutation, 2014, 35, 663-671.	1.1	24

#	Article	IF	CITATIONS
206	Characterizing immune repertoires by high throughput sequencing: strategies and applications. Trends in Immunology, 2014, 35, 581-590.	2.9	162
207	Testing mitochondrial marker efficacy for DNA barcoding in spiders: a test case using the dwarf spider genus Oedothorax (Araneae: Linyphiidae: Erigoninae). Invertebrate Systematics, 2014, 28, 501.	0.5	12
209	The identification of mitochondrial DNA variants in glioblastoma multiforme. Acta Neuropathologica Communications, 2014, 2, 1.	2.4	143
210	Choice of transcripts and software has a large effect on variant annotation. Genome Medicine, 2014, 6, 26.	3.6	158
211	Genomes correction and assembling: present methods and tools. Proceedings of SPIE, 2014, , .	0.8	6
212	Analysis of plant microbe interactions in the era of next generation sequencing technologies. Frontiers in Plant Science, 2014, 5, 216.	1.7	194
213	Next-generation sequencing reveals how RNA catalysts evolve from random space. Nucleic Acids Research, 2014, 42, 1303-1310.	6.5	31
214	PLEK: a tool for predicting long non-coding RNAs and messenger RNAs based on an improved k-mer scheme. BMC Bioinformatics, 2014, 15, 311.	1.2	574
215	A high-throughput screening strategy for detecting CRISPR-Cas9 induced mutations using next-generation sequencing. BMC Genomics, 2014, 15, 1002.	1.2	89
216	Flexible and scalable genotyping-by-sequencing strategies for population studies. BMC Genomics, 2014, 15, 979.	1.2	45
217	The Harvest suite for rapid core-genome alignment and visualization of thousands of intraspecific microbial genomes. Genome Biology, 2014, 15, 524.	3.8	1,428
218	Characterizing the genetic basis of bacterial phenotypes using genome-wide association studies: a new direction for bacteriology. Genome Medicine, 2014, 6, 109.	3.6	105
219	Impact of tumor sequencing on the use of anticancer drugs. Current Opinion in Oncology, 2014, 26, 347-356.	1.1	19
220	The neonatal bowel microbiome in health and infection. Current Opinion in Infectious Diseases, 2014, 27, 236-243.	1.3	59
221	NECTAR: a database of codon-centric missense variant annotations. Nucleic Acids Research, 2014, 42, D1013-D1019.	6.5	3
222	Analysis, Optimization and Verification of Illumina-Generated 16S rRNA Gene Amplicon Surveys. PLoS ONE, 2014, 9, e94249.	1.1	287
223	Genetic Epidemiology and Nonsyndromic Structural Birth Defects. JAMA Pediatrics, 2014, 168, 371.	3.3	36
224	Navigating the Rapids: The Development of Regulated Next-Generation Sequencing-Based Clinical Trial Assays and Companion Diagnostics. Frontiers in Oncology, 2014, 4, 78.	1.3	71

#	Article	IF	CITATIONS
225	Bacterial whole genome sequencing: The future of clinical bacteriology. Annals of Nigerian Medicine, 2014, 8, 51.	0.0	1
226	Cyanobacteria in New Zealand indigenous grasslands. New Zealand Journal of Botany, 2014, 52, 100-115.	0.8	5
227	RAMICS: trainable, high-speed and biologically relevant alignment of high-throughput sequencing reads to coding DNA. Nucleic Acids Research, 2014, 42, e106-e106.	6.5	7
228	Identification of target-binding peptide motifs by high-throughput sequencing of phage-selected peptides. Nucleic Acids Research, 2014, 42, e169-e169.	6.5	55
229	Prevalence of R5 and X4 HIV variants in antiretroviral treatment experienced patients with virologic failure. Journal of Clinical Virology, 2014, 60, 290-294.	1.6	12
230	Les méthodes de séquençage de « nouvelle génération » (NGS) et le cancer broncho-pulmonaire: principales technologies, applications et limites actuelles en pathologie. Revue Francophone Des Laboratoires, 2014, 2014, 51-58.	0.0	0
231	Genomic and systems approaches to translational biomarker discovery in immunological diseases. Drug Discovery Today, 2014, 19, 133-139.	3.2	3
232	Metagenomics Using Next-Generation Sequencing. Methods in Molecular Biology, 2014, 1096, 183-201.	0.4	77
233	Clinical impact of small TP53 mutated subclones in chronic lymphocytic leukemia. Blood, 2014, 123, 2139-2147.	0.6	302
234	Bioremediation of petroleum hydrocarbons: catabolic genes, microbial communities, and applications. Applied Microbiology and Biotechnology, 2014, 98, 4781-4794.	1.7	264
235	Comparison of three next-generation sequencing platforms for metagenomic sequencing and identification of pathogens in blood. BMC Genomics, 2014, 15, 96.	1.2	143
236	Non Optical Semi-Conductor Next Generation Sequencing of the Main Cardiac QT-Interval Duration Genes in Pooled DNA Samples. Journal of Cardiovascular Translational Research, 2014, 7, 133-137.	1.1	17
237	Deep sequencing of evolving pathogen populations: applications, errors, and bioinformatic solutions. Microbial Informatics and Experimentation, 2014, 4, 1.	7.6	75
238	Second-Generation Sequencing for Cancer Genome Analysis. , 2014, , 13-30.		2
239	Enhanced microbial diversity in the saliva microbiome induced by short-term probiotic intake revealed by 16S rRNA sequencing on the IonTorrent PGM platform. Journal of Biotechnology, 2014, 190, 30-39.	1.9	34
240	Deep Sequencing of Viral Genomes Provides Insight into the Evolution and Pathogenesis of Varicella Zoster Virus and Its Vaccine in Humans. Molecular Biology and Evolution, 2014, 31, 397-409.	3.5	91
241	Reactor performance and microbial ecology of a nitritation membrane bioreactor. Journal of Membrane Science, 2014, 462, 139-146.	4.1	51
242	The effects of read length, quality and quantity on microsatellite discovery and primer development: from <scp>I</scp> llumina to <scp>P</scp> ac <scp>B</scp> io. Molecular Ecology Resources, 2014, 14, 953-965.	2.2	28

#	Article	IF	CITATIONS
243	A labor- and cost-effective non-optical semiconductor (Ion Torrent) next-generation sequencing of the SLC12A3 and CLCNKA/B genes in Gitelman's syndrome patients. Journal of Human Genetics, 2014, 59, 376-380.	1.1	15
244	The role of replicates for error mitigation in next-generation sequencing. Nature Reviews Genetics, 2014, 15, 56-62.	7.7	267
245	A review of genomic data warehousing systems. Briefings in Bioinformatics, 2014, 15, 471-483.	3.2	22
246	The promise and challenge of high-throughput sequencing of the antibody repertoire. Nature Biotechnology, 2014, 32, 158-168.	9.4	633
247	BLESS: Bloom filter-based error correction solution for high-throughput sequencing reads. Bioinformatics, 2014, 30, 1354-1362.	1.8	113
248	Inference with viral quasispecies diversity indices: clonal and NGS approaches. Bioinformatics, 2014, 30, 1104-1111.	1.8	56
249	Bacterial genome sequencing in the clinic: bioinformatic challenges and solutions. Nature Reviews Genetics, 2014, 15, 49-55.	7.7	141
250	Prevention, diagnosis and treatment of highâ€throughput sequencing data pathologies. Molecular Ecology, 2014, 23, 1679-1700.	2.0	24
251	Distinct responses of soil microbial communities to elevated CO2 and O3 in a soybean agro-ecosystem. ISME Journal, 2014, 8, 714-726.	4.4	80
252	Decoding neural transcriptomes and epigenomes via high-throughput sequencing. Nature Neuroscience, 2014, 17, 1463-1475.	7.1	49
253	Personalized Diagnosis and Management of Congenital Cataract by Next-Generation Sequencing. Ophthalmology, 2014, 121, 2124-2137.e2.	2.5	153
254	Quick, sensitive and specific detection and evaluation of quantification of minor variants by high-throughput sequencing. Molecular BioSystems, 2014, 10, 206-214.	2.9	6
255	Performance of amplicon-based next generation DNA sequencing for diagnostic gene mutation profiling in oncopathology. Cellular Oncology (Dordrecht), 2014, 37, 353-361.	2.1	43
256	Progress and Potential: Training in Genomic Pathology. Archives of Pathology and Laboratory Medicine, 2014, 138, 498-504.	1.2	11
257	Performance Comparison of Illumina and Ion Torrent Next-Generation Sequencing Platforms for 16S rRNA-Based Bacterial Community Profiling. Applied and Environmental Microbiology, 2014, 80, 7583-7591.	1.4	277
258	Nextâ€generation sequencing is a credible strategy for blood group genotyping. British Journal of Haematology, 2014, 167, 554-562.	1.2	57
259	Genetic correction using engineered nucleases for gene therapy applications. Development Growth and Differentiation, 2014, 56, 63-77.	0.6	37
260	Bacterial Whole-Genome Sequencing Revisited: Portable, Scalable, and Standardized Analysis for Typing and Detection of Virulence and Antibiotic Resistance Genes. Journal of Clinical Microbiology, 2014, 52, 2365-2370.	1.8	250

#	Article	IF	Citations
261	Research on Neonatal Microbiomes: What Neonatologists Need to Know. Neonatology, 2014, 105, 14-24.	0.9	12
262	Discovery of a novel methanogen prevalent in thawing permafrost. Nature Communications, 2014, 5, 3212.	5.8	170
263	Arthropods as a source of new RNA viruses. Microbial Pathogenesis, 2014, 77, 136-141.	1.3	21
264	Sensitive Deep-Sequencing-Based HIV-1 Genotyping Assay To Simultaneously Determine Susceptibility to Protease, Reverse Transcriptase, Integrase, and Maturation Inhibitors, as Well as HIV-1 Coreceptor Tropism. Antimicrobial Agents and Chemotherapy, 2014, 58, 2167-2185.	1.4	61
265	Detection of genomic variations and DNA polymorphisms and impact on analysis of meiotic recombination and genetic mapping. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 10007-10012.	3.3	55
266	False Positives in Multiplex PCR-Based Next-Generation Sequencing Have Unique Signatures. Journal of Molecular Diagnostics, 2014, 16, 541-549.	1.2	43
267	Whole-genome sequencing to control antimicrobial resistance. Trends in Genetics, 2014, 30, 401-407.	2.9	232
268	RNA-Sequencing: A tool to explore new frontiers in animal genetics. Livestock Science, 2014, 166, 206-216.	0.6	53
269	Ten years of next-generation sequencing technology. Trends in Genetics, 2014, 30, 418-426.	2.9	1,240
270	Intratumor heterogeneity in localized lung adenocarcinomas delineated by multiregion sequencing. Science, 2014, 346, 256-259.	6.0	834
271	Massive parallele Sequenzierung in der Diagnostik hereditÄ r er <i>BRCA1-/-2</i> -Mutationen. Medizinische Genetik, 2014, 26, 255-263.	0.1	0
272	The Rapidly Emerging Role for Whole Exome Sequencing in Clinical Genetics. Current Genetic Medicine Reports, 2014, 2, 103-112.	1.9	5
273	Evaluation and optimisation of indel detection workflows for ion torrent sequencing of the BRCA1 and BRCA2 genes. BMC Genomics, 2014, 15, 516.	1.2	36
274	Validation of multiple single nucleotide variation calls by additional exome analysis with a semiconductor sequencer to supplement data of whole-genome sequencing of a human population. BMC Genomics, 2014, 15, 673.	1.2	10
275	Performance comparison of second- and third-generation sequencers using a bacterial genome with two chromosomes. BMC Genomics, 2014, 15, 699.	1.2	93
276	Rapid molecular genetic diagnosis of hypertrophic cardiomyopathy by semiconductor sequencing. Journal of Translational Medicine, 2014, 12, 173.	1.8	21
277	Choice of bacterial DNA extraction method from fecal material influences community structure as evaluated by metagenomic analysis. Microbiome, 2014, 2, 19.	4.9	228
278	Capturing needles in haystacks: a comparison of B-cell receptor sequencing methods. BMC Immunology, 2014, 15, 29.	0.9	62

#	Article	IF	CITATIONS
279	Data analysis for 16S microbial profiling from different benchtop sequencing platforms. Journal of Microbiological Methods, 2014, 107, 30-37.	0.7	221
280	Multi-platform assessment of transcriptome profiling using RNA-seq in the ABRF next-generation sequencing study. Nature Biotechnology, 2014, 32, 915-925.	9.4	217
281	Detecting and correcting systematic variation in large-scale RNA sequencing data. Nature Biotechnology, 2014, 32, 888-895.	9.4	174
282	A first look at the Oxford Nanopore MinION sequencer. Molecular Ecology Resources, 2014, 14, 1097-1102.	2.2	362
283	Nanoparticle approaches against bacterial infections. Wiley Interdisciplinary Reviews: Nanomedicine and Nanobiotechnology, 2014, 6, 532-547.	3.3	225
284	High-throughput sequencing for the study of bacterial pathogen biology. Current Opinion in Microbiology, 2014, 19, 106-113.	2.3	43
285	The unseen world: environmental microbial sequencing and identification methods for ecologists. Frontiers in Ecology and the Environment, 2014, 12, 224-231.	1.9	27
286	Comparison of mapping algorithms used in high-throughput sequencing: application to lon Torrent data. BMC Genomics, 2014, 15, 264.	1.2	83
287	Deep sequencing: Becoming a critical tool in clinical virology. Journal of Clinical Virology, 2014, 61, 9-19.	1.6	123
288	Cost-efficient HIV-1 drug resistance surveillance using multiplexed high-throughput amplicon sequencing: implications for use in low- and middle-income countries. Journal of Antimicrobial Chemotherapy, 2014, 69, 3349-3355.	1.3	28
289	Development and Validation of a New HPV Genotyping Assay Based on Next-Generation Sequencing. American Journal of Clinical Pathology, 2014, 141, 796-804.	0.4	53
290	A near-full length genotypic assay for HCV1b. Journal of Virological Methods, 2014, 209, 126-135.	1.0	11
291	A Comparison of Deep Sequencing of <i>TCRG</i> Rearrangements vs Traditional Capillary Electrophoresis for Assessment of Clonality in T-Cell Lymphoproliferative Disorders. American Journal of Clinical Pathology, 2014, 141, 348-359.	0.4	41
292	Metallomics of two microorganisms relevant to heavy metal bioremediation reveal fundamental differences in metal assimilation and utilization. Metallomics, 2014, 6, 1004.	1.0	16
293	Analysis of bacterial communities and bacterial pathogens in a biogas plant by the combination of ethidium monoazide, PCR and Ion Torrent sequencing. Water Research, 2014, 60, 156-163.	5.3	44
294	Microbiomes in bioenergy production: From analysis to management. Current Opinion in Biotechnology, 2014, 27, 65-72.	3.3	60
295	Blue: correcting sequencing errors using consensus and context. Bioinformatics, 2014, 30, 2723-2732.	1.8	68
296	Studying the antibody repertoire after vaccination: practical applications. Trends in Immunology, 2014, 35, 319-331.	2.9	110

#	Article	IF	Citations
297	Development and assessment of an optimized next-generation DNA sequencing approach for the mtgenome using the Illumina MiSeq. Forensic Science International: Genetics, 2014, 13, 20-29.	1.6	99
298	Molecular diagnostics of the HBB gene in an Omani cohort using bench-top DNA Ion Torrent PGM technology. Blood Cells, Molecules, and Diseases, 2014, 53, 133-137.	0.6	4
299	Targeted next-generation sequencing as a comprehensive test for patients with and female carriers of DMD/BMD: a multi-population diagnostic study. European Journal of Human Genetics, 2014, 22, 110-118.	1.4	66
300	Genomics and transcriptomics in drug discovery. Drug Discovery Today, 2014, 19, 126-132.	3.2	54
302	High-Throughput DNA Sequencing Analysis of Antibody Repertoires. Microbiology Spectrum, 2014, 2, .	1.2	24
303	PathoQC: Computationally Efficient Read Preprocessing and Quality Control for High-Throughput Sequencing Data Sets. Cancer Informatics, 2014, 13s1, CIN.S13890.	0.9	5
304	Genetic screening to improve the diagnosis of familial hypercholesterolemia. Clinical Lipidology, 2014, 9, 523-532.	0.4	1
305	Mutation Analysis of the Main Hypertrophic Cardiomyopathy Genes Using Multiplex Amplification and Semiconductor Next-Generation Sequencing. Circulation Journal, 2014, 78, 2963-2971.	0.7	51
306	Can Next-Generation Sequencing Replace Sanger Sequencing for Screening Genetic Variants?. Circulation Journal, 2014, 78, 2845-2847.	0.7	4
308	Library construction for ancient genomics: Single strand or double strand?. BioTechniques, 2014, 56, 289-300.	0.8	64
309	Fast lossless compression via cascading Bloom filters. BMC Bioinformatics, 2014, 15, S7.	1.2	25
310	Targeted high-throughput sequencing for genetic diagnostics of hemophagocytic lymphohistiocytosis. Genome Medicine, 2015, 7, 130.	3.6	37
311	Next Generation Sequencing of Acute Myeloid Leukemia: Influencing Prognosis. BMC Genomics, 2015, 16, S5.	1.2	40
312	Utility of different massive parallel sequencing platforms for mutation profiling in clinical samples and identification of pitfalls using FFPE tissue. International Journal of Molecular Medicine, 2015, 36, 1233-1243.	1.8	12
313	Evaluation of Hybridization Capture Versus Ampliconâ€Based Methods for Wholeâ€Exome Sequencing. Human Mutation, 2015, 36, 903-914.	1.1	206
314	Simultaneous Whole Mitochondrial Genome Sequencing with Short Overlapping Amplicons Suitable for Degraded DNA Using the Ion Torrent Personal Genome Machine. Human Mutation, 2015, 36, 1236-1247.	1.1	51
315	Next generation sequencing of total DNA from sugarcane provides no evidence for chloroplast heteroplasmy. New Negatives in Plant Science, 2015, 1-2, 33-45.	0.9	23
317	Scaffolding of a bacterial genome using MinION nanopore sequencing. Scientific Reports, 2015, 5, 11996.	1.6	70

#	Article	IF	CITATIONS
318	Transcriptome analysis provides insights into the regulatory function of alternative splicing in antiviral immunity in grass carp (Ctenopharyngodon idella). Scientific Reports, 2015, 5, 12946.	1.6	73
319	Rapid genome resequencing of an atoxigenic strain of Aspergillus carbonarius. Scientific Reports, 2015, 5, 9086.	1.6	15
320	Clinical utility of circulating tumor DNA for molecular assessment in pancreatic cancer. Scientific Reports, 2015, 5, 18425.	1.6	164
321	Epidemiological Methods in Microbiology. , 2015, , 277-292.		0
322	Affinity Isolation of Desired Restriction Fragment from Human Genome Using Double-duplex Invasion of Biotin-bound Pseudo-complementary PNA. Chemistry Letters, 2015, 44, 1569-1571.	0.7	5
323	Methods of Targeting Animal Sources of Fecal Pollution in Water. , 2015, , 3.4.4-1-3.4.4-28.		2
324	CADBURE: A generic tool to evaluate the performance of spliced aligners on RNA-Seq data. Scientific Reports, 2015, 5, 13443.	1.6	7
325	<scp>metaxa</scp> 2: improved identification and taxonomic classification of small and large subunit rRNA in metagenomic data. Molecular Ecology Resources, 2015, 15, 1403-1414.	2.2	426
326	Reads2Type: a web application for rapid microbial taxonomy identification. BMC Bioinformatics, 2015, 16, 398.	1.2	5
327	Amplicon sequencing for the quantification of spoilage microbiota in complex foods including bacterial spores. Microbiome, 2015, 3, 30.	4.9	21
328	Artificially designed pathogens – a diagnostic option for future military deployments. Military Medical Research, 2015, 2, 17.	1.9	2
329	Arctic microbial and next-generation sequencing approach for bacteria in snow and frost flowers: selected identification, abundance and freezing nucleation. Atmospheric Chemistry and Physics, 2015, 15, 6183-6204.	1.9	38
330	Differences in mitochondrial DNA inheritance and function align with body conformation in genetically lean and fat sheep1. Journal of Animal Science, 2015, 93, 2083-2093.	0.2	12
331	Introduction to the analysis of next generation sequencing data and its application to venous thromboembolism. Thrombosis and Haemostasis, 2015, 114, 920-932.	1.8	10
332	Towards alleleâ€level human leucocyte antigens genotyping – assessing two nextâ€generation sequencing platforms: Ion Torrent Personal Genome Machine and Illumina MiSeq. International Journal of Immunogenetics, 2015, 42, 346-358.	0.8	20
333	Challenges and opportunities of nextâ \in generation sequencing: a cytopathologist's perspective. Cytopathology, 2015, 26, 271-283.	0.4	76
334	Vertical Distribution of Bacterial Community Diversity and Water Quality during the Reservoir Thermal Stratification. International Journal of Environmental Research and Public Health, 2015, 12, 6933-6945.	1,2	24
335	Genetic Mutations in Human Esophageal and Gastric Cardia Cancers Detected by Ampliseq Sequencing. Journal of Clinical & Medical Genomics, 2015, 3, .	0.1	0

#	ARTICLE	IF	CITATIONS
336	Rational Protein Engineering Guided by Deep Mutational Scanning. International Journal of Molecular Sciences, 2015, 16, 23094-23110.	1.8	18
337	Primer and platform effects on 16S rRNA tag sequencing. Frontiers in Microbiology, 2015, 6, 771.	1.5	435
338	Next-generation sequencing (NGS) for assessment of microbial water quality: current progress, challenges, and future opportunities. Frontiers in Microbiology, 2015, 6, 1027.	1.5	200
339	Quasispecies Analyses of the HIV-1 Near-full-length Genome With Illumina MiSeq. Frontiers in Microbiology, 2015, 6, 1258.	1.5	45
340	From Benchtop to Desktop: Important Considerations when Designing Amplicon Sequencing Workflows. PLoS ONE, 2015, 10, e0124671.	1.1	177
341	High-Throughput, Amplicon-Based Sequencing of the CREBBP Gene as a Tool to Develop a Universal Platform-Independent Assay. PLoS ONE, 2015, 10, e0129195.	1.1	7
342	Targeted Sequencing of the Mitochondrial Genome of Women at High Risk of Breast Cancer without Detectable Mutations in BRCA1/2. PLoS ONE, 2015, 10, e0136192.	1.1	11
343	The Characterization of Novel Tissue Microbiota Using an Optimized 16S Metagenomic Sequencing Pipeline. PLoS ONE, 2015, 10, e0142334.	1.1	155
344	Rare Variants in Transcript and Potential Regulatory Regions Explain a Small Percentage of the Missing Heritability of Complex Traits in Cattle. PLoS ONE, 2015, 10, e0143945.	1.1	16
345	Lung Cancer Prediction Using Neural Network Ensemble with Histogram of Oriented Gradient Genomic Features. Scientific World Journal, The, 2015, 2015, 1-17.	0.8	60
346	Big Data Applications in Health Sciences and Epidemiology. Handbook of Statistics, 2015, , 171-202.	0.4	9
347	An analytical framework for optimizing variant discovery from personal genomes. Nature Communications, 2015, 6, 6275.	5.8	88
348	Sigma: Strain-level inference of genomes from metagenomic analysis for biosurveillance. Bioinformatics, 2015, 31, 170-177.	1.8	90
349	Implementation of Amplicon Parallel Sequencing Leads to Improvement of Diagnosis and Therapy of Lung Cancer Patients. Journal of Thoracic Oncology, 2015, 10, 1049-1057.	0.5	85
350	A single chromosome assembly of Bacteroides fragilis strain BE1 from Illumina and MinION nanopore sequencing data. GigaScience, 2015, 4, 60.	3.3	64
351	NGS-eval: NGS Error analysis and novel sequence VAriant detection tooL. Nucleic Acids Research, 2015, 43, W301-W305.	6.5	16
352	Performance comparison of Next Generation sequencing platforms. , 2015, 2015, 6453-6.		7
353	Novel Phenotype–Genotype Correlations of Restrictive Cardiomyopathy With Myosinâ€Binding Protein C (<i>MYBPC3</i>) Gene Mutations Tested by Nextâ€Generation Sequencing. Journal of the American Heart Association, 2015, 4, .	1.6	36

#	ARTICLE	IF	CITATIONS
354	Deep sequencing in library selection projects: what insight does it bring?. Current Opinion in Structural Biology, 2015, 33, 146-160.	2.6	65
355	Hybrid Vibrio cholerae El Tor Lacking SXT Identified as the Cause of a Cholera Outbreak in the Philippines. MBio, 2015, 6, .	1.8	11
356	Parallel Read Error Correction for Big Genomic Datasets. , 2015, , .		2
357	A Review of Cloud Computing Bioinformatics Solutions for Next-Gen Sequencing Data Analysis and Research. Methods in Next Generation Sequencing, $2015, 2, \ldots$	1.5	5
358	Metagenomic Approaches to Disclose Disease-Associated Pathogens: Detection of Viral Pathogens in Honeybees. Methods in Molecular Biology, 2015, 1247, 491-511.	0.4	4
359	DNA (meta)barcoding of biological invasions: a powerful tool to elucidate invasion processes and help managing aliens. Biological Invasions, 2015, 17, 905-922.	1.2	119
360	Commentaries: Integration of Whole-Genome Sequencing into Infection Control Practices: the Potential and the Hurdles. Journal of Clinical Microbiology, 2015, 53, 1054-1055.	1.8	13
361	High-Throughput Metagenomic Technologies for Complex Microbial Community Analysis: Open and Closed Formats. MBio, 2015, 6, .	1.8	357
362	Prepartum and Postpartum Rumen Fluid Microbiomes: Characterization and Correlation with Production Traits in Dairy Cows. Applied and Environmental Microbiology, 2015, 81, 1327-1337.	1.4	145
363	DNA sequencing using polymerase substrate-binding kinetics. Nature Communications, 2015, 6, 5936.	5.8	7
364	Comparing viral metagenomics methods using a highly multiplexed human viral pathogens reagent. Journal of Virological Methods, 2015, 213, 139-146.	1.0	124
365	Late Pleistocene Australian Marsupial DNA Clarifies the Affinities of Extinct Megafaunal Kangaroos and Wallabies. Molecular Biology and Evolution, 2015, 32, 574-584.	3.5	29
366	Single Nucleotide Variant Detection Using Next Generation Sequencing. , 2015, , 109-127.		10
367	Insertions and Deletions (Indels). , 2015, , 129-150.		12
368	Amplification-Based Methods. , 2015, , 57-67.		3
369	The molecular spectrum and clinical impact of <i><scp>DIS</scp>3</i> mutations in multiple myeloma. British Journal of Haematology, 2015, 169, 57-70.	1.2	61
370	The skin microbiome: Associations between altered microbial communities and disease. Australasian Journal of Dermatology, 2015, 56, 268-274.	0.4	88
371	Next-generation sequencing as a powerful motor for advances in the biological and environmental sciences. Genetica, 2015, 143, 129-132.	0.5	24

#	Article	IF	CITATIONS
372	Less is more: extreme genome complexity reduction with dd <scp>RAD</scp> using Ion Torrent semiconductor technology. Molecular Ecology Resources, 2015, 15, 1145-1152.	2.2	22
373	Pollux: platform independent error correction of single and mixed genomes. BMC Bioinformatics, 2015, 16, 10.	1.2	44
374	Genomic Applications in Hematologic Oncology. , 2015, , 297-319.		0
375	Contact genomics: scaffolding and phasing (meta)genomes using chromosome 3D physical signatures. FEBS Letters, 2015, 589, 2966-2974.	1.3	41
376	Limited Variation in BK Virus T-Cell Epitopes Revealed by Next-Generation Sequencing. Journal of Clinical Microbiology, 2015, 53, 3226-3233.	1.8	19
377	Genomic Tools for the Study of Azospirillum and Other Plant Growth-Promoting Rhizobacteria. , 2015, , 83-97.		1
378	Characterization of human short tandem repeats (STRs) for individual identification using the Ion Torrent. Biochip Journal, 2015, 9, 164-172.	2.5	3
379	Silent mutations at codons 65 and 66 in reverse transcriptase alleviate indel formation and restore fitness in subtype B HIV-1 containing D67N and K70R drug resistance mutations. Nucleic Acids Research, 2015, 43, 3256-3271.	6.5	9
380	STR allele sequence variation: Current knowledge and future issues. Forensic Science International: Genetics, 2015, 18, 118-130.	1.6	155
381	Accurate Whole-Genome Sequencing-Based Epidemiological Surveillance of Mycobacterium Tuberculosis. Methods in Microbiology, 2015, 42, 359-394.	0.4	6
382	Routine Clinical Mutation Profiling of Nonâ€"Small Cell Lung Cancer Using Next-Generation Sequencing. Archives of Pathology and Laboratory Medicine, 2015, 139, 913-921.	1.2	28
383	Rapid draft sequencing and real-time nanopore sequencing in a hospital outbreak of Salmonella. Genome Biology, 2015, 16, 114.	3.8	271
384	New Method for Comparative Functional Genomics and Metagenomics Using KEGG MODULE., 2015,, 525-539.		0
385	Next-Generation Sequencing for Metagenomic Data: Assembling and Binning. , 2015, , 539-544.		0
386	Quantifying ultra-rare pre-leukemic clones via targeted error-corrected sequencing. Leukemia, 2015, 29, 1608-1611.	3.3	77
387	Genomic Applications in the Clinical Management of Infectious Diseases. , 2015, , 581-604.		0
388	Deconvoluting the Composition of Low-Frequency Hepatitis C Viral Quasispecies: Comparison of Genotypes and NS3 Resistance-Associated Variants between HCV/HIV Coinfected Hemophiliacs and HCV Monoinfected Patients in Japan. PLoS ONE, 2015, 10, e0119145.	1.1	12
390	Whole-genome sequencing for prediction of Mycobacterium tuberculosis drug susceptibility and resistance: a retrospective cohort study. Lancet Infectious Diseases, The, 2015, 15, 1193-1202.	4.6	553

#	Article	IF	CITATIONS
391	Next-generation sequencing as an approach to dairy starter selection. Dairy Science and Technology, 2015, 95, 545-568.	2.2	38
392	A labor and cost effective next generation sequencing of PKHD1 in autosomal recessive polycystic kidney disease patients. Gene, 2015, 561, 165-169.	1.0	7
393	Evaluation of the Ion Torrent Personal Genome Machine for Gene-Targeted Studies Using Amplicons of the Nitrogenase Gene <i>nifH</i> . Applied and Environmental Microbiology, 2015, 81, 4536-4545.	1.4	26
394	Mycobiome: Approaches to analysis of intestinal fungi. Journal of Immunological Methods, 2015, 421, 112-121.	0.6	145
395	Whole-Genome Sequencing in Outbreak Analysis. Clinical Microbiology Reviews, 2015, 28, 541-563.	5.7	200
396	Influence of past agricultural fragmentation to the genetic structure of Juniperus oxycedrus in a Mediterranean landscape. Tree Genetics and Genomes, 2015, 11, 1.	0.6	4
397	Analysis of the genetic diversity of influenza A viruses using next-generation DNA sequencing. BMC Genomics, 2015, 16, 79.	1.2	78
398	Ignored sediment fungal populations in water supply reservoirs are revealed by quantitative PCR and 454 pyrosequencing. BMC Microbiology, 2015, 15, 44.	1.3	26
399	lon Torrent sequencing as a tool for mutation discovery in the flax (Linum usitatissimum L.) genome. Plant Methods, 2015, 11, 19.	1.9	18
400	New steady-state microbial community compositions and process performances in biogas reactors induced by temperature disturbances. Biotechnology for Biofuels, 2015, 8, 3.	6.2	68
401	Rapid detection of genetic mutations in individual breast cancer patients by next-generation DNA sequencing. Human Genomics, 2015, 9, 2.	1.4	36
402	Validation of an NGS Approach for Diagnostic BRCA1/BRCA2 Mutation Testing. Molecular Diagnosis and Therapy, 2015, 19, 119-130.	1.6	23
403	Handbook for Azospirillum. , 2015, , .		30
404	Metagenetic tools for the census of marine meiofaunal biodiversity: An overview. Marine Genomics, 2015, 24, 11-20.	0.4	93
405	RNA Nanotechnology and Therapeutics. Methods in Molecular Biology, 2015, , .	0.4	3
406	Doubleâ€digest <scp>RAD</scp> sequencing using <scp>I</scp> on <scp>P</scp> roton semiconductor platform (dd <scp>RAD</scp> seqâ€ion) with nonmodel organisms. Molecular Ecology Resources, 2015, 1316-1329.	2.2	44
407	The impact of quality filter for RNA-Seq. Gene, 2015, 563, 165-171.	1.0	7
408	Insertion and deletion correcting DNA barcodes based on watermarks. BMC Bioinformatics, 2015, 16, 50.	1.2	17

#	Article	IF	CITATIONS
409	Microbial Community Composition and Diversity via 16S rRNA Gene Amplicons: Evaluating the Illumina Platform. PLoS ONE, 2015, 10, e0116955.	1.1	284
410	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
411	Low-Cost, High-Throughput Sequencing of DNA Assemblies Using a Highly Multiplexed Nextera Process. ACS Synthetic Biology, 2015, 4, 860-866.	1.9	49
412	Whole genome sequencing in clinical and public health microbiology. Pathology, 2015, 47, 199-210.	0.3	226
413	Comparison of Next-Generation Sequencing and Mutation-Specific Platforms in Clinical Practice. American Journal of Clinical Pathology, 2015, 143, 573-578.	0.4	41
414	16S rRNA gene high-throughput sequencing data mining of microbial diversity and interactions. Applied Microbiology and Biotechnology, 2015, 99, 4119-4129.	1.7	79
415	Bacterial communities in haloalkaliphilic sulfate-reducing bioreactors under different electron donors revealed by 16S rRNA MiSeq sequencing. Journal of Hazardous Materials, 2015, 295, 176-184.	6.5	37
416	Population Genetics, Evolutionary Genomics, and Genome-Wide Studies of Malaria: A View Across the International Centers of Excellence for Malaria Research. American Journal of Tropical Medicine and Hygiene, 2015, 93, 87-98.	0.6	22
417	Bioinformatic and Statistical Analysis of Adaptive Immune Repertoires. Trends in Immunology, 2015, 36, 738-749.	2.9	178
418	Efficient Identification of Murine M2 Macrophage Peptide Targeting Ligands by Phage Display and Next-Generation Sequencing. Bioconjugate Chemistry, 2015, 26, 1811-1817.	1.8	42
419	Genomic Analysis of Pure Cultures and Communities. Springer Protocols, 2015, , 5-27.	0.1	16
420	Ecotoxicological assessment of antibiotics: A call for improved consideration of microorganisms. Environment International, 2015, 85, 189-205.	4.8	209
421	A novel termini analysis theory using HTS data alone for the identification of Enterococcus phage EF4-like genome termini. BMC Genomics, 2015, 16, 414.	1.2	29
422	Immunoglobulin rearrangement analysis from multiple lesions in the same patient using nextâ€generation sequencing. Histopathology, 2015, 67, 843-858.	1.6	5
423	Distinguishing low frequency mutations from RT-PCR and sequence errors in viral deep sequencing data. BMC Genomics, 2015, 16, 229.	1.2	44
424	Application of Metagenomics in Environmental Anaerobic Technology., 2015,, 73-108.		1
425	The impact of next generation sequencing technologies on haematological research – A review. Pathogenesis, 2015, 2, 9-16.	0.8	19
426	Next generation sequencing under de novo genome assembly. International Journal of Biomathematics, 2015, 08, 1530001.	1.5	8

#	Article	IF	CITATIONS
427	Noncanonical Genomic Imprinting Effects in Offspring. Cell Reports, 2015, 12, 979-991.	2.9	71
428	Advances in the Molecular Analysis of Soft Tissue Tumors and Clinical Implications. Surgical Pathology Clinics, 2015, 8, 525-537.	0.7	14
429	Deletions in a ribosomal protein-coding gene are associated with tigecycline resistance in Enterococcus faecium. International Journal of Antimicrobial Agents, 2015, 46, 572-575.	1.1	32
430	Metagenomics study of endophytic bacteria in Aloe vera using next-generation technology. Genomics Data, 2015, 6, 159-163.	1.3	136
431	Design and evaluation of universal 16S rRNA gene primers for high-throughput sequencing to simultaneously detect DAMO microbes and anammox bacteria. Water Research, 2015, 87, 385-394.	5.3	68
432	Rapid genome sequencing and characterization of novel avian-origin influenza A H7N9 virus directly from clinical sample by semiconductor sequencing. Journal of Clinical Virology, 2015, 73, 84-88.	1.6	3
433	Twenty years of bacterial genome sequencing. Nature Reviews Microbiology, 2015, 13, 787-794.	13.6	246
434	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
435	Sequencing the functional antibody repertoireâ€"diagnostic and therapeutic discovery. Nature Reviews Rheumatology, 2015, 11, 171-182.	3.5	158
436	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
437	Comparative Analysis of Subtyping Methods against a Whole-Genome-Sequencing Standard for Salmonella enterica Serotype Enteritidis. Journal of Clinical Microbiology, 2015, 53, 212-218.	1.8	112
438	Nonâ€invasive prenatal diagnostic testing for βâ€thalassaemia using cellâ€free fetal DNA and next generation sequencing. Prenatal Diagnosis, 2015, 35, 258-265.	1.1	51
439	High-Resolution Taxonomic Profiling of the Subgingival Microbiome for Biomarker Discovery and Periodontitis Diagnosis. Applied and Environmental Microbiology, 2015, 81, 1047-1058.	1.4	94
440	The application of genomics to tracing bacterial pathogen transmission. Current Opinion in Microbiology, 2015, 23, 62-67.	2.3	84
441	Neurofibromatosis type 1 molecular diagnosis: what can NGS do for you when you have a large gene with loss of function mutations?. European Journal of Human Genetics, 2015, 23, 596-601.	1.4	97
442	Analysis of the whole mitochondrial genome: translation of the Ion Torrent Personal Genome Machine system to the diagnostic bench?. European Journal of Human Genetics, 2015, 23, 41-48.	1.4	33
443	A single genus in the gut microbiome reflects host preference and specificity. ISME Journal, 2015, 9, 90-100.	4.4	159
444	Restriction siteâ€associated <scp>DNA</scp> sequencing, genotyping error estimation and <i>de novo</i> assembly optimization for population genetic inference. Molecular Ecology Resources, 2015, 15, 28-41.	2.2	345

#	Article	IF	Citations
446	Overview of Technical Aspects and Chemistries of Next-Generation Sequencing., 2015,, 3-19.		17
447	Comparing Highâ€throughput Platforms for Sequencing the V4 Region of SSUâ€r <scp>DNA</scp> in Environmental Microbial Eukaryotic Diversity Surveys. Journal of Eukaryotic Microbiology, 2015, 62, 338-345.	0.8	53
448	De novo transcriptome characterization of Lilium â€~Sorbonne' and key enzymes related to the flavonoid biosynthesis. Molecular Genetics and Genomics, 2015, 290, 399-412.	1.0	39
449	PCR primers for assessing community structure of aquatic fungi including Chytridiomycota and Cryptomycota. Fungal Ecology, 2015, 13, 33-43.	0.7	24
450	Translating Sanger-Based Routine DNA Diagnostics into Generic Massive Parallel Ion Semiconductor Sequencing. Clinical Chemistry, 2015, 61, 154-162.	1.5	25
451	Sequencing technologies and tools for short tandem repeat variation detection. Briefings in Bioinformatics, 2015, 16, 193-204.	3.2	32
452	Genomic Applications in Pathology. , 2015, , .		1
453	Metagenomic sequencing of activated sludge filamentous bacteria community using the Ion Torrent platform. Desalination and Water Treatment, 2016, 57, 2175-2183.	1.0	12
454	Molecular Methods for Diagnosis of Genetic Diseases Involving the Immune System., 2016,, 5-18.		0
455	Multiple Biological Sequence Alignment: Scoring Functions, Algorithms and Applications. , 2016, , .		9
456	Circulating tumor DNA as a liquid biopsy target for detection of pancreatic cancer. World Journal of Gastroenterology, 2016, 22, 8480.	1.4	41
457	A repetitive sequence assembler based on next-generation sequencing. Genetics and Molecular Research, 2016, 15, .	0.3	1
458	Simultaneous detection of <i>BRCA</i> mutations and large genomic rearrangements in germline DNA and FFPE tumor samples. Oncotarget, 2016, 7, 61845-61859.	0.8	24
459	Slow translation of Tropical Africas wealth in medicinal plants into the clinic: Current biomolecular infrastructural capacity and gaps in sub-Saharan universities. Scientific Research and Essays, 2016, 11, 174-186.	0.1	0
460	Setting Up a Laboratory., 2016,, 409-426.		1
461	Diagnosis of Aquatic Animal Viral Diseases. , 2016, , 49-75.		1
462	Red Algal Mitochondrial Genomes are More Complete than Previously Reported. Genome Biology and Evolution, 2017, 9, evw267.	1.1	19
463	A Multi-Omics Approach to Evaluate the Quality of Milk Whey Used in Ricotta Cheese Production. Frontiers in Microbiology, 2016, 7, 1272.	1.5	24

#	Article	IF	Citations
464	Considerations For Optimizing Microbiome Analysis Using a Marker Gene. Frontiers in Nutrition, 2016, 3, 26.	1.6	40
465	Nanopore-CMOS Interfaces for DNA Sequencing. Biosensors, 2016, 6, 42.	2.3	16
466	Next Generation Sequencing of Actinobacteria for the Discovery of Novel Natural Products. Marine Drugs, 2016, 14, 78.	2.2	118
467	Allelic Imbalance in Regulation of ANRIL through Chromatin Interaction at 9p21 Endometriosis Risk Locus. PLoS Genetics, 2016, 12, e1005893.	1.5	40
468	Targeted Next Generation Sequencing as a Reliable Diagnostic Assay for the Detection of Somatic Mutations in Tumours Using Minimal DNA Amounts from Formalin Fixed Paraffin Embedded Material. PLoS ONE, 2016, 11, e0149405.	1.1	79
469	Building a Robust Tumor Profiling Program: Synergy between Next-Generation Sequencing and Targeted Single-Gene Testing. PLoS ONE, 2016, 11, e0152851.	1.1	9
470	Authentication of Herbal Supplements Using Next-Generation Sequencing. PLoS ONE, 2016, 11, e0156426.	1.1	110
471	De Novo Assembly of Human Herpes Virus Type 1 (HHV-1) Genome, Mining of Non-Canonical Structures and Detection of Novel Drug-Resistance Mutations Using Short- and Long-Read Next Generation Sequencing Technologies. PLoS ONE, 2016, 11, e0157600.	1.1	43
472	Analysis and Visualization Tool for Targeted Amplicon Bisulfite Sequencing on Ion Torrent Sequencers. PLoS ONE, 2016, 11, e0160227.	1.1	24
473	Host-Microbiome Interaction and Cancer: Potential Application in Precision Medicine. Frontiers in Physiology, 2016, 7, 606.	1.3	40
474	Will Benchtop Sequencers Resolve the Sequencing Trade-off in Plant Genetics?. Frontiers in Plant Science, 2016, 7, 433.	1.7	2
475	The new era of genome sequencing using high-throughput sequencing technology: generation of the first version of the Atlantic cod genome., 2016,, 1-20.		1
476	Next-Generation Sequencing — An Overview of the History, Tools, and "Omic―Applications. , 0, , .		94
477	Clinical Genomics: Challenges and Opportunities. Critical Reviews in Eukaryotic Gene Expression, 2016, 26, 97-113.	0.4	12
478	Next-Generation Sequencing Technology: Implications for Barley Genetics and Breeding. , 2016, , 265-280.		0
479	Objective review of <i>de novo</i> standâ€alone error correction methods for <scp>NGS</scp> data. Wiley Interdisciplinary Reviews: Computational Molecular Science, 2016, 6, 111-146.	6.2	21
480	Monitoring disease burden in chronic myeloid leukemia: Past, present, and future. American Journal of Hematology, 2016, 91, 742-746.	2.0	7
481	Genetics of movement disorders in the nextâ€generation sequencing era. Movement Disorders, 2016, 31, 458-470.	2.2	34

#	Article	IF	Citations
482	Targeted gene enrichment and highâ€throughput sequencing for environmental biomonitoring: a case study using freshwater macroinvertebrates. Molecular Ecology Resources, 2016, 16, 1240-1254.	2.2	92
483	The ecologist's field guide to sequenceâ€based identification of biodiversity. Methods in Ecology and Evolution, 2016, 7, 1008-1018.	2.2	316
484	Clinical evaluation of the <scp>IONA</scp> test: a nonâ€invasive prenatal screening test for trisomies 21, 18 and 13. Ultrasound in Obstetrics and Gynecology, 2016, 47, 188-193.	0.9	11
485	Nextâ€Generation Sequencing of the Bacterial 16S <scp>rRNA</scp> Gene for Forensic Soil Comparison: A Feasibility Study. Journal of Forensic Sciences, 2016, 61, 607-617.	0.9	47
486	A Method for Amplicon Deep Sequencing of Drug Resistance Genes in Plasmodium falciparum Clinical Isolates from India. Journal of Clinical Microbiology, 2016, 54, 1500-1511.	1.8	41
487	The E. histolytica Genome Structure and Virulence. Current Tropical Medicine Reports, 2016, 3, 158-163.	1.6	2
489	New insights into the generation and role of de novo mutations in health and disease. Genome Biology, 2016, 17, 241.	3.8	339
491	Identification of microsatellite loci based on BAC sequencing data and their physical mapping into the soft wheat 5B chromosome. Russian Journal of Genetics: Applied Research, 2016, 6, 825-837.	0.4	5
492	Population attenuation in zooplankton communities during transoceanic transfer in ballast water. Ecology and Evolution, 2016, 6, 6170-6177.	0.8	11
493	Linking nitrification characteristic and microbial community structures in integrated fixed film activated sludge reactor by high-throughput sequencing. Water Science and Technology, 2016, 74, 1354-1364.	1.2	7
494	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
495	Resistance-Associated Variants in HCV Subtypes 1a and 1b Detected by Ion Torrent Sequencing Platform. Antiviral Therapy, 2016, 21, 653-660.	0.6	11
496	The role of high performance, grid and cloud computing in high-throughput sequencing. , 2016, , .		1
497	Protist systematics, ecology and next generation sequencing. , 0, , 195-216.		0
498	Computational prospecting the great viral unknown. FEMS Microbiology Letters, 2016, 363, fnw077.	0.7	56
499	Assessment of the clinical application of detecting EGFR, KRAS, PIK3CA and BRAF mutations in patients with non-small cell lung cancer using next-generation sequencing. Scandinavian Journal of Clinical and Laboratory Investigation, 2016, 76, 386-392.	0.6	13
500	Advances in DNA metabarcoding for food and wildlife forensic species identification. Analytical and Bioanalytical Chemistry, 2016, 408, 4615-4630.	1.9	180
501	Coming of age: ten years of next-generation sequencing technologies. Nature Reviews Genetics, 2016, 17, 333-351.	7.7	3,160

#	Article	IF	CITATIONS
502	Structured Low-Rank Matrix Factorization for Haplotype Assembly. IEEE Journal on Selected Topics in Signal Processing, 2016, 10, 647-657.	7.3	19
503	The implications of whole-genome sequencing in the control of tuberculosis. Therapeutic Advances in Infectious Disease, 2016, 3, 47-62.	1.1	28
504	Performance of a new suspended filler biofilter for removal of nitrogen oxides under thermophilic conditions and microbial community analysis. Science of the Total Environment, 2016, 562, 533-541.	3.9	58
505	A Primer on Infectious Disease Bacterial Genomics. Clinical Microbiology Reviews, 2016, 29, 881-913.	5.7	42
506	Microbiome Changes during Tuberculosis and Antituberculous Therapy. Clinical Microbiology Reviews, 2016, 29, 915-926.	5.7	71
507	BRCA to the future: towards best testing practice in the era of personalised healthcare. European Journal of Human Genetics, 2016, 24, S1-S2.	1.4	12
508	The past, present and future of microbiome analyses. Nature Protocols, 2016, 11, 2049-2053.	5.5	59
509	Biogas production from hydrothermal liquefaction wastewater (HTLWW): Focusing on the microbial communities as revealed by high-throughput sequencing of full-length 16S rRNA genes. Water Research, 2016, 106, 98-107.	5. 3	99
510	Seafood Species Identification Using DNA Sequencing. , 2016, , 113-132.		13
511	Illumina MiSeq sequencing reveals the community composition of NirS-Type and NirK-Type denitrifiers in Zhoucun reservoir – a large shallow eutrophic reservoir in northern China. RSC Advances, 2016, 6, 91517-91528.	1.7	33
512	Next-Generation Sequencing in Cancer Diagnostics. Journal of Molecular Diagnostics, 2016, 18, 813-816.	1.2	14
513	The Efficiency of Australian Schools: A Nationwide Analysis Using Gains in Test Scores of Students as Outputs. Economic Papers, 2016, 35, 256-268.	0.4	3
514	Massively parallel sequencing of 10 autosomal STRs in Chinese using the ion torrent personal genome machine (PGM). Forensic Science International: Genetics, 2016, 25, 34-38.	1.6	15
515	<scp>amplisas</scp> : a web server for multilocus genotyping using nextâ€generation amplicon sequencing data. Molecular Ecology Resources, 2016, 16, 498-510.	2.2	110
516	Advances, practice, and clinical perspectives in highâ€ŧhroughput sequencing. Oral Diseases, 2016, 22, 353-364.	1.5	11
517	Metabarcoding Marine Sediments: Preparation of Amplicon Libraries. Methods in Molecular Biology, 2016, 1452, 183-196.	0.4	33
518	Preliminary Evaluation of the Effect of Investigational Ebola Virus Disease Treatments on Viral Genome Sequences. Journal of Infectious Diseases, 2016, 214, S333-S341.	1.9	11
519	Affordable HIV drug-resistance testing for monitoring of antiretroviral therapy in sub-Saharan Africa. Lancet Infectious Diseases, The, 2016, 16, e267-e275.	4.6	54

#	Article	IF	CITATIONS
520	New challenges for BRCA testing: a view from the diagnostic laboratory. European Journal of Human Genetics, 2016, 24, S10-S18.	1.4	73
521	Molecular monitoring of chronic myeloid leukemia: present and future. Expert Review of Molecular Diagnostics, 2016, 16, 1083-1091.	1.5	19
522	Multiplexed next-generation sequencing and de novo assembly to obtain near full-length HIV-1 genome from plasma virus. Journal of Virological Methods, 2016, 236, 98-104.	1.0	19
523	Clinical Versus Research Sequencing. Cold Spring Harbor Perspectives in Medicine, 2016, 6, a025809.	2.9	24
524	Marine Genomics. Methods in Molecular Biology, 2016, , .	0.4	3
525	Human CODIS STR loci profiling from HTS data. , 2016, , .		4
526	Using ultra-sensitive next generation sequencing to dissect DNA damage-induced mutagenesis. Scientific Reports, 2016, 6, 25310.	1.6	10
527	Performance and microbial ecology of a nitritation sequencing batch reactor treating high-strength ammonia wastewater. Scientific Reports, 2016, 6, 35693.	1.6	10
528	Microfluidic Air Sampler for Highly Efficient Bacterial Aerosol Collection and Identification. Analytical Chemistry, 2016, 88, 11504-11512.	3.2	30
529	Carbon Dot-Based Platform for Simultaneous Bacterial Distinguishment and Antibacterial Applications. ACS Applied Materials & Amp; Interfaces, 2016, 8, 32170-32181.	4.0	285
530	Comparison of Next-Generation Sequencing Panels and Platforms for Detection and Verification of Somatic Tumor Variants for Clinical Diagnostics. Journal of Molecular Diagnostics, 2016, 18, 842-850.	1.2	35
531	Research on Robust Relationship Inference in GWAS Parallel Algorithm Based on OpenMP., 2016,,.		0
532	Preanalytic Variables in Cytology: Lessons Learned From Next-Generation Sequencing—The MD Anderson Experience. Archives of Pathology and Laboratory Medicine, 2016, 140, 1191-1199.	1.2	115
533	Deciphering KRAS and NRAS mutated clone dynamics in MLL-AF4 paediatric leukaemia by ultra deep sequencing analysis. Scientific Reports, 2016, 6, 34449.	1.6	20
534	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.	0.5	5
535	Next Generation Sequencing of Pooled Samples: Guideline for Variants' Filtering. Scientific Reports, 2016, 6, 33735.	1.6	81
536	High-throughput sequencing-based analysis of endogenetic fungal communities inhabiting the Chinese Cordyceps reveals unexpectedly high fungal diversity. Scientific Reports, 2016, 6, 33437.	1.6	45
537	Characterization of Viral Populations by Using Circular Sequencing. Journal of Virology, 2016, 90, 8950-8953.	1.5	15

#	Article	IF	Citations
538	Field Guidelines for Genetic Experimental Designs in High-Throughput Sequencing., 2016,,.		6
539	Analysis of Long Noncoding RNAs in RNA-Seq Data. , 2016, , 143-174.		0
540	Toward reliable biomarker signatures in the age of liquid biopsies - how to standardize the small RNA-Seq workflow. Nucleic Acids Research, 2016, 44, 5995-6018.	6.5	97
541	An optimized protocol for generation and analysis of Ion Proton sequencing reads for RNA-Seq. BMC Genomics, 2016, 17, 403.	1.2	26
542	A comparison of tools for the simulation of genomic next-generation sequencing data. Nature Reviews Genetics, 2016, 17, 459-469.	7.7	163
543	Implementation of next generation sequencing in clinical molecular diagnostic laboratories: advantages, challenges and potential. Expert Review of Precision Medicine and Drug Development, 2016, 1, 109-120.	0.4	25
544	Nitrogen removal characteristics of indigenous aerobic denitrifiers and changes in the microbial community of a reservoir enclosure system via in situ oxygen enhancement using water lifting and aeration technology. Bioresource Technology, 2016, 214, 63-73.	4.8	36
545	Effects of the Ion PGMâ,, Hi-Qâ,, sequencing chemistry on sequence data quality. International Journal of Legal Medicine, 2016, 130, 1169-1180.	1.2	28
546	Ultra-precise detection of mutations by droplet-based amplification of circularized DNA. BMC Genomics, 2016, 17, 214.	1.2	11
547	Next-generation genotyping of hypervariable loci in many individuals of a non-model species: technical and theoretical implications. BMC Genomics, 2016, 17, 204.	1.2	21
548	Uncommon nucleotide excision repair phenotypes revealed by targeted high-throughput sequencing. Orphanet Journal of Rare Diseases, 2016, 11, 26.	1.2	32
549	IPED: a highly efficient denoising tool for Illumina MiSeq Paired-end 16S rRNAÂgene amplicon sequencing data. BMC Bioinformatics, 2016, 17, 192.	1.2	30
550	CD4+ T-cell recovery with suppressive ART-induced rapid sequence evolution in hepatitis C virus envelope but not NS3. Aids, 2016, 30, 691-700.	1.0	2
551	Denoising DNA deep sequencing dataâ€"high-throughput sequencing errors and their correction. Briefings in Bioinformatics, 2016, 17, 154-179.	3.2	254
552	Clinical Validation and Implementation of a Targeted Next-Generation Sequencing Assay to Detect Somatic Variants in Non-Small Cell Lung, Melanoma, and Gastrointestinal Malignancies. Journal of Molecular Diagnostics, 2016, 18, 299-315.	1.2	55
553	Bottom-Up Proteomics Methods for Strain-Level Typing and Identification of Bacteria. , 2016, , 83-146.		2
554	Within-host evolution of bacterial pathogens. Nature Reviews Microbiology, 2016, 14, 150-162.	13.6	373
555	A new perspective on microbial landscapes within food production. Current Opinion in Biotechnology, 2016, 37, 182-189.	3.3	100

#	Article	IF	Citations
556	Genomic Epidemiology: Whole-Genome-Sequencing–Powered Surveillance and Outbreak Investigation of Foodborne Bacterial Pathogens. Annual Review of Food Science and Technology, 2016, 7, 353-374.	5.1	152
557	Applications of Mass Spectrometry in Microbiology. , 2016, , .		9
558	The sequence of sequencers: The history of sequencing DNA. Genomics, 2016, 107, 1-8.	1.3	828
559	Genome mining of astaxanthin biosynthetic genes from <i>Sphingomonas </i> sp. ATCC 55669 for heterologous overproduction in <i>Escherichia coli</i> Biotechnology Journal, 2016, 11, 228-237.	1.8	56
560	Conserved rates and patterns of transcription errors across bacterial growth states and lifestyles. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 3311-3316.	3.3	60
561	Molecular Genetic Dissection and Neonatal/Infantile Intrahepatic Cholestasis Using Targeted Next-Generation Sequencing. Journal of Pediatrics, 2016, 171, 171-177.e4.	0.9	88
562	Next-Generation Sequencing: Principles for Clinical Application. , 2016, , 889-909.		0
563	Next-Generation Sequencing for the Analysis of Cancer Specimens. , 2016, , 911-931.		0
564	Decoding DNA, RNA and peptides with quantum tunnelling. Nature Nanotechnology, 2016, 11, 117-126.	15.6	183
565	A novel conceptual approach to read-filtering in high-throughput amplicon sequencing studies. Nucleic Acids Research, 2016, 44, e40-e40.	6.5	35
566	Meta-omics in Inflammatory Bowel Disease Research: Applications, Challenges, and Guidelines. Journal of Crohn's and Colitis, 2016, 10, 735-746.	0.6	37
567	Special Techniques., 2016,, 11-44.		0
568	Self-decontaminating photocatalytic zinc oxide nanorod coatings for prevention of marine microfouling: a mesocosm study. Biofouling, 2016, 32, 383-395.	0.8	38
570	New Methodologies in the Molecular Monitoring of CML. Current Hematologic Malignancy Reports, 2016, 11, 94-101.	1.2	2
571	Molecular evolution of colorectal cancer: from multistep carcinogenesis to the big bang. Cancer and Metastasis Reviews, 2016, 35, 63-74.	2.7	29
572	Current status and recent advances of next generation sequencing techniques in immunological repertoire. Genes and Immunity, 2016, 17, 153-164.	2.2	88
573	Deep Sequencing Reveals Potential Antigenic Variants at Low Frequencies in Influenza A Virus-Infected Humans. Journal of Virology, 2016, 90, 3355-3365.	1.5	101
574	Primary distal renal tubular acidosis: novel findings in patients studied by next-generation sequencing. Pediatric Research, 2016, 79, 496-501.	1.1	25

#	Article	IF	CITATIONS
575	Post-archival genomics and the bulk logistics of DNA sequences. BioSocieties, 2016, 11, 82-105.	0.8	6
576	Performance characteristics of the AmpliSeq Cancer Hotspot panel v2 in combination with the Ion Torrent Next Generation Sequencing Personal Genome Machine. Regulatory Toxicology and Pharmacology, 2016, 74, 178-186.	1.3	18
577	Clinical Evaluation of a Novel Nine-Gene Panel for Ion Torrent PGM Sequencing of Myeloid Malignancies. Molecular Diagnosis and Therapy, 2016, 20, 27-32.	1.6	5
578	Immune repertoire: A potential biomarker and therapeutic for hepatocellular carcinoma. Cancer Letters, 2016, 379, 206-212.	3.2	44
579	Analysis of environmental variables on population dynamic change ofHaliscomenobacter hydrossis, the bulking causative filament in Macau wastewater treatment plant. Desalination and Water Treatment, 2016, 57, 7182-7195.	1.0	11
580	Translating Omics to Food Microbiology. Annual Review of Food Science and Technology, 2017, 8, 113-134.	5.1	82
581	High Interlaboratory Reproducibility and Accuracy of Next-Generation-Sequencing-Based Bacterial Genotyping in a Ring Trial. Journal of Clinical Microbiology, 2017, 55, 908-913.	1.8	75
582	Identification of a novel LMF1 nonsense mutation responsible for severe hypertriglyceridemia by targeted next-generation sequencing. Journal of Clinical Lipidology, 2017, 11, 272-281.e8.	0.6	18
583	Application of high-throughput sequencing (HTS) metabarcoding to diatom biomonitoring: Do DNA extraction methods matter?. Freshwater Science, 2017, 36, 162-177.	0.9	91
584	Optimisation of methods for bacterial skin microbiome investigation: primer selection and comparison of the 454 versus MiSeq platform. BMC Microbiology, 2017, 17, 23.	1.3	133
585	<i>Papaya ringspot virus</i> Populations From East Timorese and Northern Australian Cucurbit Crops: Biological and Molecular Properties, and Absence of Genetic Connectivity. Plant Disease, 2017, 101, 985-993.	0.7	30
586	Nanomaterial Effects on Soil Microorganisms. Soil Biology, 2017, , 137-200.	0.6	12
587	Evaluating Variant Calling Tools for Non-Matched Next-Generation Sequencing Data. Scientific Reports, 2017, 7, 43169.	1.6	185
588	Advances in the application of high-throughput sequencing in invertebrate virology. Journal of Invertebrate Pathology, 2017, 147, 145-156.	1.5	12
589	Describing the diversity of Ag specific receptors in vertebrates: Contribution of repertoire deep sequencing. Developmental and Comparative Immunology, 2017, 75, 28-37.	1.0	32
590	The IONA® Test: Development of an Automated Cell-Free DNA-Based Screening Test for Fetal Trisomies 13, 18, and 21 That Employs the Ion Proton Semiconductor Sequencing Platform. Fetal Diagnosis and Therapy, 2017, 42, 218-224.	0.6	14
591	Developmental validation of the MiSeq FGx Forensic Genomics System for Targeted Next Generation Sequencing in Forensic DNA Casework and Database Laboratories. Forensic Science International: Genetics, 2017, 28, 52-70.	1.6	232
592	Variant call concordance between two laboratory-developed, solid tumor targeted genomic profiling assays using distinct workflows and sequencing instruments. Experimental and Molecular Pathology, 2017, 102, 215-218.	0.9	4

#	Article	IF	CITATIONS
593	Evaluation of applicability of DNA microarray–based characterization of bovine Shiga toxin–producing Escherichia coli isolates using whole genome sequence analysis. Journal of Veterinary Diagnostic Investigation, 2017, 29, 721-724.	0.5	3
595	Next Generation Sequencing uncovers within-host differences in the genetic diversity of Cryptosporidium gp60 subtypes. International Journal for Parasitology, 2017, 47, 601-607.	1.3	38
596	Reprint of "Application of next generation sequencing in clinical microbiology and infection prevention― Journal of Biotechnology, 2017, 250, 2-10.	1.9	34
597	Recent advances in sequence assembly: principles and applications. Briefings in Functional Genomics, 2017, 16, 361-378.	1.3	14
598	High-throughput sequencing of African chikanda cake highlights conservation challenges in orchids. Biodiversity and Conservation, 2017, 26, 2029-2046.	1.2	26
599	Clinical Genomic Testing., 2017,, 247-262.		0
600	Characterization of NIST human mitochondrial DNA SRM-2392 and SRM-2392-I standard reference materials by next generation sequencing. Forensic Science International: Genetics, 2017, 29, 181-192.	1.6	21
601	High precision genome sequencing of engineered Gluconobacter oxydans 621H by combining long nanopore and short accurate Illumina reads. Journal of Biotechnology, 2017, 258, 197-205.	1.9	17
602	Bacterial community dynamics and functional variation during the long-term decomposition of cyanobacterial blooms in-vitro. Science of the Total Environment, 2017, 598, 77-86.	3.9	58
603	Arbuscular Mycorrhizal Fungi: Evolution and Functions in Alleviating Plant Drought Stress. , 2017, , 285-295.		2
604	Altered Gut Microbiota Composition and Immune Response in Experimental Steatohepatitis Mouse Models. Digestive Diseases and Sciences, 2017, 62, 396-406.	1.1	42
605	Targeted next-generation sequencing of the 16S-23S rRNA region for culture-independent bacterial identification - increased discrimination of closely related species. Scientific Reports, 2017, 7, 3434.	1.6	110
607	Precision food safety: A systems approach to food safety facilitated byÂgenomics tools. TrAC - Trends in Analytical Chemistry, 2017, 96, 52-61.	5.8	74
608	Ultrasensitive and high-efficiency screen of de novo low-frequency mutations by o2n-seq. Nature Communications, 2017, 8, 15335.	5.8	20
609	Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. Nature Protocols, 2017, 12, 1261-1276.	5.5	898
610	Adapting Genotyping-by-Sequencing for Rice F2 Populations. G3: Genes, Genomes, Genetics, 2017, 7, 881-893.	0.8	83
612	CTCs and ctDNA: Two Tales of a Complex Biology. Cancer Drug Discovery and Development, 2017, , 119-137.	0.2	1
613	Use of molecular approaches in hydrogeological studies: the case of carbonate aquifers in southern Italy. Hydrogeology Journal, 2017, 25, 1017-1031.	0.9	21

#	Article	IF	CITATIONS
614	Selective Isolation of a Eucalyptus spp. Woodchip Bacterial Community and Its Taxonomic and Metabolic Profiling. Bioenergy Research, 2017, 10, 547-565.	2.2	4
615	Dynamic Succession of Groundwater Sulfate-Reducing Communities during Prolonged Reduction of Uranium in a Contaminated Aquifer. Environmental Science & Environmental Science & 2017, 51, 3609-3620.	4.6	22
616	Guidelines for Validation of Next-Generation Sequencing–Based Oncology Panels. Journal of Molecular Diagnostics, 2017, 19, 341-365.	1.2	524
617	Long-term effects of increasing acidity on low-pH sulfate-reducing bioprocess and bacterial community. Environmental Science and Pollution Research, 2017, 24, 4067-4076.	2.7	10
618	Application of next generation sequencing in clinical microbiology and infection prevention. Journal of Biotechnology, 2017, 243, 16-24.	1.9	414
619	Promises and pitfalls of Illumina sequencing for HIV resistance genotyping. Virus Research, 2017, 239, 97-105.	1.1	27
620	Bioprospecting Soil Metagenomes for Antibiotics. Topics in Biodiversity and Conservation, 2017, , 113-136.	0.3	2
621	Exploring the Plant Microbiome Through Multi-omics Approaches. , 2017, , 233-268.		11
622	High throughput transcriptome analysis of coffee reveals prehaustorial resistance in response to Hemileia vastatrix infection. Plant Molecular Biology, 2017, 95, 607-623.	2.0	25
623	The circadian transcriptome of marine fish (Sparus aurata) larvae reveals highly synchronized biological processes at the whole organism level. Scientific Reports, 2017, 7, 12943.	1.6	54
624	The dynamics of immunoglobulin V-gene usage and clonotype expansion in mice after prime and boost immunizations as analyzed by NGS. Human Vaccines and Immunotherapeutics, 2017, 13, 2987-2995.	1.4	1
625	Accurate immune repertoire sequencing reveals malaria infection driven antibody lineage diversification in young children. Nature Communications, 2017, 8, 531.	5.8	41
626	Environmental <scp>DNA</scp> metabarcoding: Transforming how we survey animal and plant communities. Molecular Ecology, 2017, 26, 5872-5895.	2.0	1,210
627	Whole genome sequencing for the management of drug-resistant TB in low income high TB burden settings: Challenges and implications. Tuberculosis, 2017, 107, 137-143.	0.8	15
628	Microbiome of Pacific Whiteleg shrimp reveals differential bacterial community composition between Wild, Aquacultured and AHPND/EMS outbreak conditions. Scientific Reports, 2017, 7, 11783.	1.6	197
629	Next-generation sequencing reveals novel resistance mechanisms and molecular heterogeneity in EGFR-mutant non-small cell lung cancer with acquired resistance to EGFR-TKIs. Lung Cancer, 2017, 113, 106-114.	0.9	48
630	Metagenomics: An Era of Throughput Gene Mining. , 2017, , 41-54.		0
631	Combined genetic analyses can achieve efficient diagnostic yields for subjects with Alagille syndrome and incomplete Alagille syndrome. Acta Paediatrica, International Journal of Paediatrics, 2017, 106, 1817-1824.	0.7	9

#	Article	IF	CITATIONS
632	Review of Clinical Next-Generation Sequencing. Archives of Pathology and Laboratory Medicine, 2017, 141, 1544-1557.	1.2	253
633	Microbial community response during the treatment of pharmaceutically active compounds (PhACs) in constructed wetland mesocosms. Chemosphere, 2017, 186, 823-831.	4.2	59
634	Metagenome Analysis: a Powerful Tool for Enzyme Bioprospecting. Applied Biochemistry and Biotechnology, 2017, 183, 636-651.	1.4	96
635	Custom Hardware Versus Cloud Computing in Big Data. Advanced Information and Knowledge Processing, 2017, , 175-193.	0.2	2
637	Bacterial Whole Cell Typing by Mass Spectra Pattern Matching with Bootstrapping Assessment. Analytical Chemistry, 2017, 89, 12556-12561.	3.2	28
638	Highly accurate fluorogenic DNA sequencing with information theory–based error correction. Nature Biotechnology, 2017, 35, 1170-1178.	9.4	28
639	The Evolution of Strain Typing in the Mycobacterium tuberculosis Complex. Advances in Experimental Medicine and Biology, 2017, 1019, 43-78.	0.8	43
640	Microarray-Based Gene Expression Analysis for Veterinary Pathologists: A Review. Veterinary Pathology, 2017, 54, 734-755.	0.8	13
641	Selective and High Dynamic Range Assay Format for Multiplex Detection of Pathogenic <i>Pseudomonas aeruginosa</i> , <i>Salmonella typhimurium</i> , and <i>Legionella pneumophila</i> RNAs Using Surface Plasmon Resonance Imaging. Analytical Chemistry, 2017, 89, 7802-7807.	3.2	45
642	Human Genome Sequencing at the Population Scale: A Primer on High-Throughput DNA Sequencing and Analysis. American Journal of Epidemiology, 2017, 186, 1000-1009.	1.6	63
643	Lost in plasmids: next generation sequencing and the complex genome of the tick-borne pathogen Borrelia burgdorferi. BMC Genomics, 2017, 18, 422.	1.2	83
644	Development of a genus-specific next generation sequencing approach for sensitive and quantitative determination of the Legionella microbiome in freshwater systems. BMC Microbiology, 2017, 17, 79.	1.3	32
645	Effects of the dose and viability of Saccharomyces cerevisiae. 1. Diversity of ruminal microbes as analyzed by Illumina MiSeq sequencing and quantitative PCR. Journal of Dairy Science, 2017, 100, 325-342.	1.4	59
646	Genome-scale analysis of the non-cultivable Treponema pallidum reveals extensive within-patient genetic variation. Nature Microbiology, 2017, 2, 16190.	5.9	81
647	Detection of false positive mutations in BRCA gene by next generation sequencing. Familial Cancer, 2017, 16, 311-317.	0.9	14
648	Testing genotyping strategies for ultraâ€deep sequencing of a coâ€amplifying gene family: MHC class I in a passerine bird. Molecular Ecology Resources, 2017, 17, 642-655.	2.2	46
649	Cost-effective Chlorella biomass production from dilute wastewater using a novel photosynthetic microbial fuel cell (PMFC). Water Research, 2017, 108, 356-364.	5. 3	85
650	Monitoring of minimal residual disease in early Tâ€cell precursor acute lymphoblastic leukaemia by nextâ€generation sequencing. British Journal of Haematology, 2017, 176, 318-321.	1.2	7

#	Article	IF	CITATIONS
651	Bacterial Genomes. , 2017, , 62-67.e1.		0
652	Recent advances in inferring viral diversity from high-throughput sequencing data. Virus Research, 2017, 239, 17-32.	1.1	83
653	Epidemiological Surveillance and Typing Methods to Track Antibiotic Resistant Strains Using High Throughput Sequencing. Methods in Molecular Biology, 2017, 1520, 331-356.	0.4	9
654	Nextâ€generation sequencing for blood group genotyping. ISBT Science Series, 2017, 12, 184-190.	1.1	4
656	DNA Barcoding Reveals Habitual Clonal Dominance of Myeloma Plasma Cells in the Bone Marrow Microenvironment. Neoplasia, 2017, 19, 972-981.	2.3	18
657	Application of Next-Generation Sequencing Technologies to Viroids. , 2017, , 401-412.		7
658	Performance Comparison of NextSeq and Ion Proton Platforms for Molecular Diagnosis of Clinical Oncology. Tumori, 2017, 103, 223-230.	0.6	2
660	Salvia Biotechnology., 2017,,.		7
661	A comparison of sequencing platforms and bioinformatics pipelines for compositional analysis of the gut microbiome. BMC Microbiology, 2017, 17, 194.	1.3	196
662	GPU base calling for DNA strand sequencing. , 2017, , .		0
663	22. Microwaves in the omics field., 2017,, 429-451.		1
664	Veronica officinalis Product Authentication Using DNA Metabarcoding and HPLC-MS Reveals Widespread Adulteration with Veronica chamaedrys. Frontiers in Pharmacology, 2017, 8, 378.	1.6	69
665	Genetic Bases of Bicuspid Aortic Valve: The Contribution of Traditional and High-Throughput Sequencing Approaches on Research and Diagnosis. Frontiers in Physiology, 2017, 8, 612.	1.3	57
666	Development and Application of Transcriptome-Derived Microsatellites in Actinidia eriantha (Actinidiaceae). Frontiers in Plant Science, 2017, 8, 1383.	1.7	18
667	Characterization of a Microbial Community in an Anammox Process Using Stored Anammox Sludge. Water (Switzerland), 2017, 9, 829.	1.2	16
668	Assessment of Bifidobacterium Species Using groEL Gene on the Basis of Illumina MiSeq High-Throughput Sequencing. Genes, 2017, 8, 336.	1.0	38
669	Next-Generation Sequencing in the Clinical Laboratory. , 2017, , 25-33.		1
670	Sampling Strategies for Three-Dimensional Spatial Community Structures in IBD Microbiota Research. Frontiers in Cellular and Infection Microbiology, 2017, 7, 51.	1.8	23

#	Article	IF	CITATIONS
671	How B-Cell Receptor Repertoire Sequencing Can Be Enriched with Structural Antibody Data. Frontiers in Immunology, 2017, 8, 1753.	2.2	48
672	High Throughput Sequencing for Detection of Foodborne Pathogens. Frontiers in Microbiology, 2017, 8, 2029.	1.5	88
673	Microbial Communities Shaped by Treatment Processes in a Drinking Water Treatment Plant and Their Contribution and Threat to Drinking Water Safety. Frontiers in Microbiology, 2017, 8, 2465.	1.5	72
674	Screening the Molecular Framework Underlying Local Dendritic mRNA Translation. Frontiers in Molecular Neuroscience, 2017, 10, 45.	1.4	6
675	A comparison of Illumina and Ion Torrent sequencing platforms in the context of differential gene expression. BMC Genomics, 2017, 18, 602.	1.2	57
676	Development of amplicon deep sequencing markers and data analysis pipeline for genotyping multi-clonal malaria infections. BMC Genomics, 2017, 18, 864.	1.2	86
677	Transcriptomics technologies. PLoS Computational Biology, 2017, 13, e1005457.	1.5	677
678	Next-generation sequencing: recent applications to the analysis of colorectal cancer. Journal of Translational Medicine, 2017, 15, 246.	1.8	76
679	A quantitative and qualitative comparison of illumina MiSeq and 454 amplicon sequencing for genotyping the highly polymorphic major histocompatibility complex (MHC) in a non-model species. BMC Research Notes, 2017, 10, 346.	0.6	12
680	Recent Technology of Clinical Microbiology; Whole Genome Sequencing (WGS) and Matrix-Assisted, Laser Desorption Ionization-Time of Flight Mass Spectrometry (MALDI-TOF MS). Journal of Microbial & Biochemical Technology, 2017, 09, .	0.2	1
681	Partners of patients with ulcerative colitis exhibit a biologically relevant dysbiosis in fecal microbial metacommunities. World Journal of Gastroenterology, 2017, 23, 4624.	1.4	23
682	Construction of a multiplex mutation hot spot PCR panel: the first step towards colorectal cancer genotyping on the GS Junior platform. Journal of Cancer, 2017, 8, 162-173.	1.2	7
683	Generations of Sequencing Technologies: From First to Next Generation. Biology and Medicine (Aligarh), $2017,09$, .	0.3	118
684	High Throughput Sequencing Advances and Future Challenges. Journal of Plant Biochemistry & Physiology, 2017, 05, .	0.5	6
685	Targeted Next-Generation Sequencing Newly Identifies Mutations in <i>Exostosin-1</i> and <i>Exostosin-2</i> Genes of Patients with Multiple Osteochondromas. Tohoku Journal of Experimental Medicine, 2017, 242, 173-181.	0.5	1
686	De Novo Assembly of Lucina pectinata Genome using Ion Torrent Reads. , 2017, , .		1
687	Disparities in secondâ€generation <scp>DNA</scp> metabarcoding results exposed with accessible and repeatable workflows. Molecular Ecology Resources, 2018, 18, 590-601.	2.2	23
688	Whole genome sequencing as a typing tool for foodborne pathogens like Listeria monocytogenes – The way towards global harmonisation and data exchange. Trends in Food Science and Technology, 2018, 73, 67-75.	7.8	93

#	Article	IF	Citations
689	Streams of data from drops of water: 21st century molecular microbial ecology. Wiley Interdisciplinary Reviews: Water, 2018, 5, e1280.	2.8	37
690	A Systems Biology Approach to Advancing Adverse Outcome Pathways for Risk Assessment. , 2018, , .		8
691	The Application of Omics Data to the Development of AOPs., 2018,, 177-198.		1
692	Can genomics deliver climate-change ready crops?. Current Opinion in Plant Biology, 2018, 45, 205-211.	3.5	105
693	Comparative analysis of Illumina and Ion Torrent high-throughput sequencing platforms for identification of plant components in herbal teas. Food Control, 2018, 93, 315-324.	2.8	29
694	Do we similarly assess diversity with microscopy and high-throughput sequencing? Case of microalgae in lakes. Organisms Diversity and Evolution, 2018, 18, 51-62.	0.7	46
695	Developmental validation of a Nextera XT mitogenome Illumina MiSeq sequencing method for high-quality samples. Forensic Science International: Genetics, 2018, 34, 25-36.	1.6	35
696	Genotyping strategy matters when analyzing hypervariable major histocompatibility complexâ€xperience from a passerine bird. Ecology and Evolution, 2018, 8, 1680-1692.	0.8	16
697	Bacterial diversity and composition of alfalfa silage as analyzed by Illumina MiSeq sequencing: Effects of Escherichia coli O157:H7 and silage additives. Journal of Dairy Science, 2018, 101, 2048-2059.	1.4	184
698	Data integration and predictive modeling methods for multi-omics datasets. Molecular Omics, 2018, 14, 8-25.	1.4	73
699	geno2pheno[ngs-freq]: a genotypic interpretation system for identifying viral drug resistance using next-generation sequencing data. Nucleic Acids Research, 2018, 46, W271-W277.	6.5	37
700	Methodology challenges in studying human gut microbiota – effects of collection, storage, DNA extraction and next generation sequencing technologies. Scientific Reports, 2018, 8, 5143.	1.6	146
702	What's in the box? Authentication of Echinacea herbal products using DNA metabarcoding and HPTLC. Phytomedicine, 2018, 44, 32-38.	2.3	56
703	Insights of Acute Lymphoblastic Leukemia with Development of Genomic Investigation. Methods in Molecular Biology, 2018, 1754, 387-413.	0.4	1
704	Comparative Transcriptomics Among Four White Pine Species. G3: Genes, Genomes, Genetics, 2018, 8, 1461-1474.	0.8	35
705	Comprehensive analysis of microbial communities in full-scale mesophilic and thermophilic anaerobic digesters treating food waste-recycling wastewater. Bioresource Technology, 2018, 259, 442-450.	4.8	127
706	Circulating tumor DNA and liquid biopsy: opportunities, challenges, and recent advances in detection technologies. Lab on A Chip, 2018, 18, 1174-1196.	3.1	234
707	High-throughput construction of multiple cas9 gene variants via assembly of high-depth tiled and sequence-verified oligonucleotides. Nucleic Acids Research, 2018, 46, e55-e55.	6.5	4

#	Article	IF	Citations
708	SNP typing using the HID-lon AmpliSeqâ,,¢ Identity Panel in a southern Chinese population. International Journal of Legal Medicine, 2018, 132, 997-1006.	1.2	22
709	Application of next-generation sequencing to detect acyclovir-resistant herpes simplex virus type 1 variants at low frequency in thymidine kinase gene of the isolates recovered from patients with hematopoietic stem cell transplantation. Journal of Virological Methods, 2018, 251, 123-128.	1.0	18
710	Microbial transcript and metabolome analysis uncover discrepant metabolic pathways in autotrophic and mixotrophic anammox consortia. Water Research, 2018, 128, 402-411.	5.3	121
711	Biochar and activated carbon act as promising amendments for promoting the microbial debromination of tetrabromobisphenol A. Water Research, 2018, 128, 102-110.	5.3	48
712	Towards a genomics-informed, real-time, global pathogen surveillance system. Nature Reviews Genetics, 2018, 19, 9-20.	7.7	505
713	Bacteriophages. Methods in Molecular Biology, 2018, , .	0.4	21
714	Detection Strategies for Foodborne Salmonella and Prospects for Utilization of Whole Genome Sequencing Approaches., 2018,, 289-308.		2
715	Analyzing Genome Termini of Bacteriophage Through High-Throughput Sequencing. Methods in Molecular Biology, 2018, 1681, 139-163.	0.4	15
716	Sequencing, Assembling, and Finishing Complete Bacteriophage Genomes. Methods in Molecular Biology, 2018, 1681, 109-125.	0.4	212
717	Is the trophosome of Ridgeia piscesae monoclonal?. Symbiosis, 2018, 74, 55-65.	1.2	7
718	Illumina MiSeq sequencing investigation of Chanhua (Cordyceps cicadae Shing) fungal community structures in different regions. Journal of Traditional Chinese Medical Sciences, 2018, 5, 206-212.	0.1	1
719	Variations in microbial community during nitrogen removal by in situ oxygen-enhanced indigenous nitrogen-removal bacteria. Water Science and Engineering, 2018, 11, 276-287.	1.4	8
720	Phylotranscriptomics suggests the jawed vertebrate ancestor could generate diverse helper and regulatory T cell subsets. BMC Evolutionary Biology, 2018, 18, 169.	3.2	27
721	Implications of Targeted Next Generation Sequencing in Forensic Science. Journal of Forensics Research, 2018, 09, .	0.1	0
722	High-throughput sequencing for the molecular diagnosis of Usher syndrome reveals 42 novel mutations and consolidates CEP250 as Usher-like disease causative. Scientific Reports, 2018, 8, 17113.	1.6	30
723	Formal description of sequence-based voucherless Fungi: promises and pitfalls, and how to resolve them. IMA Fungus, 2018, 9, 143-165.	1.7	42
724	Ancestry informative alleles captured with reduced representation library sequencing in Theobroma cacao. PLoS ONE, 2018, 13, e0203973.	1.1	5
725	Colombia, an unknown genetic diversity in the era of Big Data. BMC Genomics, 2018, 19, 859.	1.2	15

#	ARTICLE	IF	CITATIONS
726	Whole exome sequencing for the identification of CYP3A7 variants associated with tacrolimus concentrations in kidney transplant patients. Scientific Reports, 2018, 8, 18064.	1.6	13
727	An alternative storage method for characterization of the intestinal microbiota through next generation sequencing. Revista Do Instituto De Medicina Tropical De Sao Paulo, 2018, 60, e77.	0.5	8
728	Evaluating metabarcoding to analyse diet composition of species foraging in anthropogenic landscapes using Ion Torrent and Illumina sequencing. Scientific Reports, 2018, 8, 17091.	1.6	29
729	Triterpene Functional Genomics in Ocimum. Compendium of Plant Genomes, 2018, , 111-126.	0.3	0
730	Progress of analytical tools and techniques for human gut microbiome research. Journal of Microbiology, 2018, 56, 693-705.	1.3	49
731	Genome-wide SNP analyses reveal high gene flow and signatures of local adaptation among the scalloped spiny lobster (Panulirus homarus) along the Omani coastline. BMC Genomics, 2018, 19, 690.	1.2	22
732	Duplex Proximity Sequencing (Pro-Seq): A method to improve DNA sequencing accuracy without the cost of molecular barcoding redundancy. PLoS ONE, 2018, 13, e0204265.	1.1	12
734	Predicting B cell receptor substitution profiles using public repertoire data. PLoS Computational Biology, 2018, 14, e1006388.	1.5	8
735	Genome-Wide Analysis on the Landscape of Transcriptomes and Their Relationship With DNA Methylomes in the Hypothalamus Reveals Genes Related to Sexual Precocity in Jining Gray Goats. Frontiers in Endocrinology, 2018, 9, 501.	1.5	30
736	Pseudomonas-Specific NGS Assay Provides Insight Into Abundance and Dynamics of Pseudomonas Species Including P. aeruginosa in a Cooling Tower. Frontiers in Microbiology, 2018, 9, 1958.	1.5	17
737	Genomic repeats, misassembly and reannotation: a case study with long-read resequencing of Porphyromonas gingivalis reference strains. BMC Genomics, 2018, 19, 54.	1.2	28
738	Symposium review: Understanding diet–microbe interactions to enhance productivity of dairy cows. Journal of Dairy Science, 2018, 101, 7661-7679.	1.4	22
739	HLA Typing. Methods in Molecular Biology, 2018, , .	0.4	4
740	AmpliSAS and AmpliHLA: Web Server Tools for MHC Typing of Non-Model Species and Human Using NGS Data. Methods in Molecular Biology, 2018, 1802, 249-273.	0.4	4
741	appreci8: a pipeline for precise variant calling integrating 8 tools. Bioinformatics, 2018, 34, 4205-4212.	1.8	26
742	Validation and Implementation of BRCA1/2 Variant Screening in Ovarian Tumor Tissue. Journal of Molecular Diagnostics, 2018, 20, 600-611.	1.2	18
743	Distinct Oceanic Microbiomes From Viruses to Protists Located Near the Antarctic Circumpolar Current. Frontiers in Microbiology, 2018, 9, 1474.	1.5	23
744	Genome Analysis of Multidrug-Resistant Shewanella algae Isolated From Human Soft Tissue Sample. Frontiers in Pharmacology, 2018, 9, 419.	1.6	20

#	ARTICLE	IF	CITATIONS
745	Insect-specific viruses: from discovery to potential translational applications. Current Opinion in Virology, 2018, 33, 33-41.	2.6	73
746	Benchmarking of Amplicon-Based Next-Generation Sequencing Panels Combined with Bioinformatics Solutions for Germline BRCA1 and BRCA2 Alteration Detection. Journal of Molecular Diagnostics, 2018, 20, 754-764.	1.2	9
747	Evaluation of the precision ID mtDNA whole genome panel on two massively parallel sequencing systems. Forensic Science International: Genetics, 2018, 36, 213-224.	1.6	35
748	Updating Plakobranchus cf. ianthobapsus (Gastropoda, Sacoglossa) host use: Diverse algal-animal interactions revealed by NGS with implications for invasive species management. Molecular Phylogenetics and Evolution, 2018, 128, 172-181.	1.2	16
749	Analyzing Immunoglobulin Repertoires. Frontiers in Immunology, 2018, 9, 462.	2.2	89
750	16S rRNA Gene Sequencing for Deciphering the Colorectal Cancer Gut Microbiome: Current Protocols and Workflows. Frontiers in Microbiology, 2018, 9, 767.	1.5	39
751	Deep-Coverage MPS Analysis of Heteroplasmic Variants within the mtGenome Allows for Frequent Differentiation of Maternal Relatives. Genes, 2018, 9, 124.	1.0	30
752	Endophytic Microbes as a Novel Source for Producing Anticancer Compounds as Multidrug Resistance Modulators., 2018,, 343-381.		1
753	RNA-Seq as an Emerging Tool for Marine Dinoflagellate Transcriptome Analysis: Process and Challenges. Processes, 2018, 6, 5.	1.3	36
754	Applying Unique Molecular Identifiers in Next Generation Sequencing Reveals a Constrained Viral Quasispecies Evolution under Cross-Reactive Antibody Pressure Targeting Long Alpha Helix of Hemagglutinin. Viruses, 2018, 10, 148.	1.5	4
755	Genomes of two archaeal endosymbionts show convergent adaptations to an intracellular lifestyle. ISME Journal, 2018, 12, 2655-2667.	4.4	26
756	Targeted sequencing reveals complex, phenotype-correlated genotypes in cystic fibrosis. BMC Medical Genomics, 2018, 11, 13.	0.7	24
757	Species classifier choice is a key consideration when analysing low-complexity food microbiome data. Microbiome, 2018, 6, 50.	4.9	65
758	Defoliation intensity and elevated precipitation effects on microbiome and interactome depend on site type in northern mixed-grass prairie. Soil Biology and Biochemistry, 2018, 122, 163-172.	4.2	23
759	Impact of Human Immunodeficiency Virus Type 1 Minority Variants on the Virus Response to a Rilpivirine-Based First-line Regimen. Clinical Infectious Diseases, 2018, 66, 1588-1594.	2.9	15
760	Performance comparison of deep sequencing platforms for detecting HIVâ€1 variants in the pol gene. Journal of Medical Virology, 2018, 90, 1486-1492.	2.5	5
761	Enhanced response rate to pegylated liposomal doxorubicin in high grade serous ovarian carcinomas harbouring BRCA1 and BRCA2 aberrations. BMC Cancer, 2018, 18, 16.	1.1	13
762	Phylogenomics and barcoding of Panax: toward the identification of ginseng species. BMC Evolutionary Biology, 2018, 18, 44.	3.2	45

#	Article	IF	Citations
763	Analyses of microbial community of naturally homemade soybean pastes in Liaoning Province of China by Illumina Miseq Sequencing. Food Research International, 2018, 111, 50-57.	2.9	45
764	Implementation of next generation sequencing technology for somatic mutation detection in routine laboratory practice. Pathology, 2018, 50, 389-401.	0.3	30
765	Assessment of the physicochemical properties and bacterial composition of Lactobacillus plantarum and Enterococcus faecium-fermented Astragalus membranaceus using single molecule, real-time sequencing technology. Scientific Reports, 2018, 8, 11862.	1.6	11
766	PIK3CA mutation is a favorable prognostic factor in esophageal cancer: molecular profile by next-generation sequencing using surgically resected formalin-fixed, paraffin-embedded tissue. BMC Cancer, 2018, 18, 826.	1.1	11
767	Analytical "bake-off―of whole genome sequencing quality for the Genome Russia project using a small cohort for autoimmune hepatitis. PLoS ONE, 2018, 13, e0200423.	1.1	7
768	Bayesian reconstruction of transmission within outbreaks using genomic variants. PLoS Computational Biology, 2018, 14, e1006117.	1.5	69
769	Validation of the Oncomineâ,,¢ focus panel for next-generation sequencing of clinical tumour samples. Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, 2018, 473, 489-503.	1.4	66
770	Deciphering Endodontic Microbial Communities by Next-generation Sequencing. Journal of Endodontics, 2018, 44, 1080-1087.	1.4	54
771	Assessment of an Organ-Specific <i>de Novo</i> Transcriptome of the Nematode Trap-Crop, <i>Solanum sisymbriifolium</i> G3: Genes, Genomes, Genetics, 2018, 8, 2135-2143.	0.8	4
772	Genetic stability of foot-and-mouth disease virus during long-term infections in natural hosts. PLoS ONE, 2018, 13, e0190977.	1.1	8
773	Review of applications of high-throughput sequencing in personalized medicine: barriers and facilitators of future progress in research and clinical application. Briefings in Bioinformatics, 2019, 20, 1795-1811.	3.2	112
774	Genome-Wide Scanning of Gene Expression. , 2019, , 452-462.		O
775	Immunoglobulin Clonotype and Ontogeny Inference. , 2019, , 972-983.		0
776	Using Large Datasets to Understand Nanotechnology. Advanced Materials, 2019, 31, e1902798.	11.1	45
777	Metagenomic insights into the diversity and functions of microbial assemblages in lakes. , 2019, , $175-223$.		3
778	Can Targeting Non-Contiguous V-Regions With Paired-End Sequencing Improve 16S rRNA-Based Taxonomic Resolution of Microbiomes?: An In Silico Evaluation. Frontiers in Genetics, 2019, 10, 653.	1.1	7
779	Germline mismatch repair gene variants analyzed by universal sequencing in Japanese cancer patients. Cancer Medicine, 2019, 8, 5534-5543.	1.3	10
780	The evolution and characterization of influenza A(H7N9) virus under the selective pressure of peramivir. Virology, 2019, 536, 58-67.	1.1	1

#	ARTICLE	IF	CITATIONS
781	The importance of genome sequence quality to microbial comparative genomics. BMC Genomics, 2019, 20, 662.	1.2	35
782	Genome Sequencing Technologies in Livestock Health System. , 2019, , 339-348.		1
783	Next-Generation Sequencing Vis-Ã-Vis Veterinary Health Management. , 2019, , 463-470.		0
784	Next-generation sequencing for the clinical management of hepatitis C virus infections: does one test fits all purposes?. Critical Reviews in Clinical Laboratory Sciences, 2019, 56, 420-434.	2.7	8
785	Multidimensional Tunability of Nucleic Acids Enables Sensing over Unknown Backgrounds. Analytical Chemistry, 2019, 91, 14275-14280.	3.2	4
786	Bioinformatics Strategies, Challenges, and Opportunities for Next Generation Sequencing-Based HLA Genotyping. Transfusion Medicine and Hemotherapy, 2019, 46, 312-325.	0.7	44
787	Variations of bacterial community during the decomposition of Microcystis under different temperatures and biomass. BMC Microbiology, 2019, 19, 207.	1.3	9
788	Clinical metagenomics for infection diagnosis. , 2019, , 35-60.		1
789	RACS: rapid analysis of ChIP-Seq data for contig based genomes. BMC Bioinformatics, 2019, 20, 533.	1.2	4
790	Application of different DNA extraction procedures, library preparation protocols and sequencing platforms: impact on sequencing results. Heliyon, 2019, 5, e02745.	1.4	12
791	Diatom DNA Metabarcoding for Biomonitoring: Strategies to Avoid Major Taxonomical and Bioinformatical Biases Limiting Molecular Indices Capacities. Frontiers in Ecology and Evolution, 2019, 7, .	1.1	58
792	Tumor BRCA Test for Patients with Epithelial Ovarian Cancer: The Role of Molecular Pathology in the Era of PARP Inhibitor Therapy. Cancers, 2019, 11, 1641.	1.7	22
793	Endophytic Bacteria in in planta Organopollutant Detoxification in Crops. Reviews of Environmental Contamination and Toxicology, 2019, 252, 1-50.	0.7	1
794	Cancer Panel Assay for Precision Oncology Clinic: Results from a 1-Year Study. Translational Oncology, 2019, 12, 1488-1495.	1.7	6
795	Next-generation sequencing reveals fecal contamination and potentially pathogenic bacteria in a major inflow river of Taihu Lake. Environmental Pollution, 2019, 254, 113108.	3.7	37
796	The Influence on Contaminant Bioavailability and Microbial Abundance of Lake Hongze by the South-to-North Water Diversion Project. International Journal of Environmental Research and Public Health, 2019, 16, 3068.	1.2	11
797	A Deep-Sequencing Workflow for the Fast and Efficient Generation of High-Quality African Swine Fever Virus Whole-Genome Sequences. Viruses, 2019, 11, 846.	1.5	41
798	Application of next-generation sequencing for the identification of herbal products. Biotechnology Advances, 2019, 37, 107450.	6.0	37

#	Article	IF	CITATIONS
799	CGGBP1 regulates CTCF occupancy at repeats. Epigenetics and Chromatin, 2019, 12, 57.	1.8	14
800	A Metataxonomic Tool to Investigate the Diversity of Treponema. Frontiers in Microbiology, 2019, 10, 2094.	1.5	13
801	Evaluation of the Performance of AmpliSeq and SureSelect Exome Sequencing Libraries for Ion Proton. Frontiers in Genetics, 2019, 10, 856.	1.1	8
802	Reply to â€~Errors in long-read assemblies can critically affect protein prediction'. Nature Biotechnology, 2019, 37, 127-128.	9.4	29
803	Non-invasive prenatal sequencing for multiple Mendelian monogenic disorders using circulating cell-free fetal DNA. Nature Medicine, 2019, 25, 439-447.	15.2	160
804	Comparison of the oral microbiome of patients with generalized aggressive periodontitis and periodontitis-free subjects. Archives of Oral Biology, 2019, 99, 169-176.	0.8	62
805	Physicochemical properties and bacterial community dynamics of hongeo, a Korean traditional fermented skate product, during fermentation at 10â€Â°C. LWT - Food Science and Technology, 2019, 104, 109-119.	2.5	20
806	DNA Sequencing Historical Lichen Specimens. Frontiers in Ecology and Evolution, 2019, 7, .	1.1	11
807	Recovery of mtDNA from unfired metallic ammunition components with an assessment of sequence profile quality and DNA damage through MPS analysis. Forensic Science International: Genetics, 2019, 39, 86-96.	1.6	29
808	Functional Gene Array-Based Ultrasensitive and Quantitative Detection of Microbial Populations in Complex Communities. MSystems, 2019, 4, .	1.7	54
809	Nanopore metagenomics enables rapid clinical diagnosis of bacterial lower respiratory infection. Nature Biotechnology, 2019, 37, 783-792.	9.4	396
810	<i>De novo</i> genotyping of the major histocompatibility complex in an Australian dragon lizard, <i>Ctenophorus decresii</i> Transactions of the Royal Society of South Australia, 2019, 143, 97-117.	0.1	0
811	Advances in Molecular Diagnostic Approaches for Biothreat Agents. , 2019, , 281-310.		3
812	Mendelian Inconsistent Signatures from 1314 Ancestrally Diverse Family Trios Distinguish Biological Variation from Sequencing Error. Journal of Computational Biology, 2019, 26, 405-419.	0.8	7
813	Next-generation sequencing of <i>BRCA1</i> and <i>BRCA2</i> genes for rapid detection of germline mutations in hereditary breast/ovarian cancer. PeerJ, 2019, 7, e6661.	0.9	21
814	Investigating targetâ€site resistance mechanism to the PPOâ€inhibiting herbicide fomesafen in waterhemp and interspecific hybridization of <i>Amaranthus</i> species using next generation sequencing. Pest Management Science, 2019, 75, 3235-3244.	1.7	21
815	Teaching an Old Virus New Tricks: A Review on New Approaches to Study Age-Old Questions in Influenza Biology. Journal of Molecular Biology, 2019, 431, 4247-4258.	2.0	3
816	Defense Against Biological Attacks. , 2019, , .		2

#	ARTICLE	IF	CITATIONS
817	A breast one-patient panel of heterogeneous genomes reveals genetic alterations driving DCIS into invasive lesions. Future Oncology, 2019, 15, 1565-1576.	1.1	6
818	Conidae phylogenomics and evolution. Zoologica Scripta, 2019, 48, 194-214.	0.7	21
820	Selection of reference genes for the quantitative real-time PCR normalization of gene expression in Isatis indigotica fortune. BMC Molecular Biology, 2019, 20, 9.	3.0	32
821	Fast and Quantitative Identification of Ex Vivo Precise Genome Targeting-Induced Indel Events by IDAA. Methods in Molecular Biology, 2019, 1961, 45-66.	0.4	3
822	Natural, incidental, and engineered nanomaterials and their impacts on the Earth system. Science, 2019, 363, .	6.0	479
823	Next-generation sequencing-guided identification and reconstruction of antibody CDR combinations from phage selection outputs. Nucleic Acids Research, 2019, 47, e50-e50.	6.5	35
824	Sequencing Framework for the Sensitive Detection and Precise Mapping of Defective Interfering Particle-Associated Deletions across Influenza A and B Viruses. Journal of Virology, 2019, 93, .	1.5	50
825	Next-generation sequencing for hypothesis-free genomic detection of invasive tropical infections in poly-microbially contaminated, formalin-fixed, paraffin-embedded tissue samples – a proof-of-principle assessment. BMC Microbiology, 2019, 19, 75.	1.3	23
826	Next-generation sequencing of HIV-1 single genome amplicons. Biomolecular Detection and Quantification, 2019, 17, 100080.	7.0	7
827	Enhanced CHO Clone Screening: Application of Targeted Locus Amplification and Nextâ€Generation Sequencing Technologies for Cell Line Development. Biotechnology Journal, 2019, 14, 1800371.	1.8	11
828	Challenges of next-generation sequencing targeting anaerobes. Anaerobe, 2019, 58, 47-52.	1.0	17
829	Identification and evaluation of the microbiome in the female and male reproductive tracts. Human Reproduction Update, 2019, 25, 298-325.	5.2	115
830	Sequencing of animal viruses: quality data assurance for NGS bioinformatics. Virology Journal, 2019, 16, 140.	1.4	18
831	Microbial Genomics in Sustainable Agroecosystems. , 2019, , .		5
832	Operational models and criteria for incorporating microbial whole genome sequencing in hospital microbiology – A systematic literature review. Clinical Microbiology and Infection, 2019, 25, 1086-1095.	2.8	16
833	The impact of OTU sequence similarity threshold on diatomâ€based bioassessment: A case study of the rivers of Mayotte (France, Indian Ocean). Ecology and Evolution, 2019, 9, 166-179.	0.8	55
834	Impact of the mutational load on the virological response to a first-line rilpivirine-based regimen. Journal of Antimicrobial Chemotherapy, 2019, 74, 718-721.	1.3	4
835	Composition of the cutaneous bacterial community of a cave amphibian, <i>Proteus anguinus </i> Microbiology Ecology, 2019, 95, .	1.3	7

#	Article	IF	CITATIONS
836	Recent Trends in the Development of Paper-Based Diagnostic Chips for the Detection of Human Viruses., 2019,, 349-361.		4
837	Introduction: Special issue on species interactions, ecological networks and community dynamics – Untangling the entangled bank using molecular techniques. Molecular Ecology, 2019, 28, 157-164.	2.0	20
838	Accurate and Sensitive Analysis of Minimal Residual Disease in Acute Myeloid Leukemia Using Deep Sequencing of Single Nucleotide Variations. Journal of Molecular Diagnostics, 2019, 21, 149-162.	1.2	14
839	Practical guide for the comparison of two next-generation sequencing systems for solid tumour analysis in a universal healthcare system. Journal of Clinical Pathology, 2019, 72, 225-231.	1.0	7
840	Bi-Level Error Correction for PacBio Long Reads. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 899-905.	1.9	0
841	An Efficient Trimming Algorithm based on Multi-Feature Fusion Scoring Model for NGS Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2020, 17, 728-738.	1.9	14
842	Transcriptomic analysis to affirm the regulatory role of long non-coding RNA in horn cancer of Indian zebu cattle breed Kankrej (Bos indicus). Functional and Integrative Genomics, 2020, 20, 75-87.	1.4	5
843	Segregation, linkage, GWAS, and sequencing. , 2020, , 7-23.		0
844	Whole mitochondrial genome analysis of highland Tibetan ethnicity using massively parallel sequencing. Forensic Science International: Genetics, 2020, 44, 102197.	1.6	18
845	Analysis of bacterial diversity and biogenic amines content during fermentation of farmhouse sauce from Northeast China. Food Control, 2020, 108, 106861.	2.8	35
846	Bioinformatic strategies to address limitations of 16rRNA short-read amplicons from different sequencing platforms. Journal of Microbiological Methods, 2020, 169, 105811.	0.7	12
847	Metagenomic insights into bioaugmentation and biovalorization of oily industrial wastes by lipolytic oleaginous yeast <i>Yarrowia lipolytica</i> during successive batch fermentation. Biotechnology and Applied Biochemistry, 2020, 67, 1020-1029.	1.4	7
848	Effects of commercial microbial biostimulants on soil and root microbial communities and sugarcane yield. Biology and Fertility of Soils, 2020, 56, 565-580.	2.3	20
849	Targeting the 16S rRNA Gene for Bacterial Identification in Complex Mixed Samples: Comparative Evaluation of Second (Illumina) and Third (Oxford Nanopore Technologies) Generation Sequencing Technologies. International Journal of Molecular Sciences, 2020, 21, 298.	1.8	117
850	RNA sequencing data of tobacco inoculated with Apple stem pitting virus. Data in Brief, 2020, 29, 105106.	0.5	1
851	High-throughput sequencing and food microbiology. Advances in Food and Nutrition Research, 2020, 91, 275-300.	1.5	21
852	High-throughput omics in the precision medicine ecosystem. , 2020, , 19-31.		1
853	Long walk to genomics: History and current approaches to genome sequencing and assembly. Computational and Structural Biotechnology Journal, 2020, 18, 9-19.	1.9	171

#	Article	IF	CITATIONS
854	Searching the undetected mtDNA variants in forensic MPS data. Forensic Science International: Genetics, 2020, 49, 102399.	1.6	7
855	Microbial Community Dynamics During the Non-filamentous Fungi Growth-Based Fermentation Process of Miang, a Traditional Fermented Tea of North Thailand and Their Product Characterizations. Frontiers in Microbiology, 2020, 11, 1515.	1.5	17
856	Diversity of Gut Microbiota and Bifidobacterial Community of Chinese Subjects of Different Ages and from Different Regions. Microorganisms, 2020, 8, 1108.	1.6	15
857	Patient specific circulating tumor DNA fingerprints to monitor treatment response across multiple tumors. Journal of Translational Medicine, 2020, 18, 293.	1.8	20
858	Dysbiosis in intestinal microbiome linked to fecal blood determined by direct hybridization. 3 Biotech, 2020, 10, 358.	1.1	5
859	Platinum-Quality Mitogenome Haplotypes from United States Populations. Genes, 2020, 11, 1290.	1.0	17
860	An innovative and affordable quantitative assessment of human TCR repertoire. EBioMedicine, 2020, 61, 103021.	2.7	1
861	Deep Mining of Human Antibody Repertoires: Concepts, Methodologies, and Applications. Small Methods, 2020, 4, 2000451.	4.6	5
862	Advances in Viral Diagnostic Technologies for Combating COVID-19 and Future Pandemics. SLAS Technology, 2020, 25, 513-521.	1.0	15
863	Performance and Application of 16S rRNA Gene Cycle Sequencing for Routine Identification of Bacteria in the Clinical Microbiology Laboratory. Clinical Microbiology Reviews, 2020, 33, .	5.7	116
864	Multiple Rare Risk Coding Variants in Postsynaptic Density-Related Genes Associated With Schizophrenia Susceptibility. Frontiers in Genetics, 2020, 11, 524258.	1.1	3
865	Uncovering fungal community composition in natural habitat of Ophiocordyceps sinensis using high-throughput sequencing and culture-dependent approaches. BMC Microbiology, 2020, 20, 331.	1.3	9
866	Marine Microbial Community Composition During the Upwelling Season in the Southern Benguela. Frontiers in Marine Science, 2020, 7, .	1.2	8
867	Next-Generation Sequencing in High-Sensitive Detection of Mutations in Tumors. Journal of Molecular Diagnostics, 2020, 22, 994-1007.	1.2	46
868	The application of a heatâ€inducible CRISPR/Cas12b (C2c1) genome editing system in tetraploid cotton (<i>G.Âhirsutum</i>) plants. Plant Biotechnology Journal, 2020, 18, 2436-2443.	4.1	58
869	Bacterial community dissimilarity in soils is driven by longâ€ŧerm landâ€useÂpractices. , 2020, 3, e20031.		15
870	Improvement of gibberellin production by a newly isolated <i>Fusarium fujikuroi </i> mutant. Journal of Applied Microbiology, 2020, 129, 1620-1632.	1.4	9
871	The fragmentation patterns of maternal plasma cellâ€free DNA and its applications in nonâ€invasive prenatal testing. Prenatal Diagnosis, 2020, 40, 911-917.	1.1	11

#	Article	IF	CITATIONS
872	Comparative analyses of Ion Torrent V4 and Illumina V3-V4 16S rRNA gene metabarcoding methods for characterization of cervical microbiota: taxonomic and functional profiling. Scientific African, 2020, 7, e00278.	0.7	12
873	Second-Generation Sequencing with Deep Reinforcement Learning for Lung Infection Detection. Journal of Healthcare Engineering, 2020, 2020, 1-9.	1.1	6
874	The Impact of Exogenous Aerobic Bacteria on Sustainable Methane Production Associated with Municipal Solid Waste Biodegradation: Revealed by High-Throughput Sequencing. Sustainability, 2020, 12, 1815.	1.6	5
875	MinION-in-ARMS: Nanopore Sequencing to Expedite Barcoding of Specimen-Rich Macrofaunal Samples From Autonomous Reef Monitoring Structures. Frontiers in Marine Science, 2020, 7, .	1.2	32
876	Systematic comparison of somatic variant calling performance among different sequencing depth and mutation frequency. Scientific Reports, 2020, 10, 3501.	1.6	44
877	Adaptive immune receptor repertoires, an overview of this exciting field. Immunology Letters, 2020, 221, 49-55.	1.1	4
878	PCR inhibition in qPCR, dPCR and MPS—mechanisms and solutions. Analytical and Bioanalytical Chemistry, 2020, 412, 2009-2023.	1.9	135
879	Cationic Organic Nanoaggregates as AIE Luminogens for Wash-Free Imaging of Bacteria and Broad-Spectrum Antimicrobial Application. ACS Applied Materials & Samp; Interfaces, 2020, 12, 5389-5402.	4.0	42
880	Comprehensive comparison of cloud-based NGS data analysis and alignment tools. Informatics in Medicine Unlocked, 2020, 18, 100296.	1.9	10
881	Phylogenetic conservation of soil bacterial responses to simulated global changes. Philosophical Transactions of the Royal Society B: Biological Sciences, 2020, 375, 20190242.	1.8	46
882	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
883	Stochasticity in microbiology: managing unpredictability to reach the Sustainable Development Goals. Microbial Biotechnology, 2020, 13, 829-843.	2.0	26
884	Metabolic versatility of freshwater sedimentary archaea feeding on different organic carbon sources. PLoS ONE, 2020, 15, e0231238.	1.1	6
885	On conflict free DNA codes. Cryptography and Communications, 2021, 13, 143-171.	0.9	12
886	Extending the knowledge of Phyllosticta citricarpa population structure in USA with re-sequencing and genome wide analysis. Physiological and Molecular Plant Pathology, 2021, 113, 101591.	1.3	3
887	Benthic algae assessments in the EU and the US: Striving for consistency in the face of great ecological diversity. Ecological Indicators, 2021, 121, 107082.	2.6	37
888	Cyanobacterial blooms in wastewater treatment facilities: Significance and emerging monitoring strategies. Journal of Microbiological Methods, 2021, 180, 106123.	0.7	11
889	Function score-based technological trend analysis. Technovation, 2021, 101, 102199.	4.2	12

#	Article	IF	Citations
890	Role of Tumor Mutation Burden Analysis in Detecting Lynch Syndrome in Precision Medicine: Analysis of 2,501 Japanese Cancer Patients. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 166-174.	1.1	8
891	Variation of volatile fatty acid oxidation and methane production during the bioaugmentation of anaerobic digestion system: Microbial community analysis revealing the influence of microbial interactions on metabolic pathways. Science of the Total Environment, 2021, 754, 142425.	3.9	29
892	How can accumulated organics and salts deteriorate the biological treatment unit in the printing and dyeing wastewater recycling system?. Chemical Engineering Journal, 2021, 413, 127528.	6.6	15
893	The methods and advances of adaptive immune receptors repertoire sequencing. Theranostics, 2021, 11 , $8945-8963$.	4.6	22
894	Sustainable Cultivation of GM Crops in the Age of Climate Change: A Global Perspective. , 2021, , 237-271.		0
895	Detection of Bacteriophages: Sequence-Based Systems. , 2021, , 621-644.		3
896	Next-Generation Sequencing (NGS)., 2021,, 305-327.		3
897	Advances in Biotechnological Tools and Techniques for Metatranscriptomics. , 2021, , 567-579.		0
898	Computational intelligence for genomic data. , 2021, , 247-260.		0
899	Assessment of Illumina \hat{A}^{\otimes} Human mtDNA Genome assay: workflow evaluation with development of analysis and interpretation guidelines. International Journal of Legal Medicine, 2021, 135, 1161-1178.	1.2	6
900	Next-generation omics technologies to explore microbial diversity., 2021,, 541-563.		1
901	Phylogenomics of Foodborne Pathogens: The Case of Listeria monocytogenes. , 2021, , 138-146.		0
902	Is Oxford Nanopore sequencing ready for analyzing complex microbiomes?. FEMS Microbiology Ecology, 2021, 97, .	1.3	31
903	Current Achievements and Applications of Transcriptomics in Personalized Cancer Medicine. International Journal of Molecular Sciences, 2021, 22, 1422.	1.8	64
904	Microbiome Analysis Using 16S Amplicon Sequencing: From Samples to ASVs. Methods in Molecular Biology, 2021, 2243, 123-141.	0.4	0
905	Next Generation Sequencing in Cytopathology: Focus on Non-Small Cell Lung Cancer. Frontiers in Medicine, 2021, 8, 633923.	1.2	26
906	Rare deleterious germline variants and risk of lung cancer. Npj Precision Oncology, 2021, 5, 12.	2.3	19
907	Mining indigenous honeybee gut microbiota for Lactobacillus with probiotic potential. Microbiology (United Kingdom), 2021, 167 , .	0.7	4

#	Article	IF	CITATIONS
908	Comprehensive Pathogen Identification, Antibiotic Resistance, and Virulence Genes Prediction Directly From Simulated Blood Samples and Positive Blood Cultures by Nanopore Metagenomic Sequencing. Frontiers in Genetics, 2021, 12, 620009.	1.1	16
909	Methods for exploring the faecal microbiome of premature infants: a review. Maternal Health, Neonatology and Perinatology, 2021, 7, 11.	1.0	3
910	Bias in RNA-seq Library Preparation: Current Challenges and Solutions. BioMed Research International, 2021, 2021, 1-11.	0.9	31
911	Four novel BRCA variants found in Chinese hereditary breast cancer patients by next-generation sequencing. Clinica Chimica Acta, 2021, 516, 55-63.	0.5	3
912	Molecular characterization of a new highly divergent Mobala related arenavirus isolated from Praomys sp. rodents. Scientific Reports, 2021, 11, 10188.	1.6	2
913	Metabolic patterns reveal enhanced anammox activity at low nitrogen conditions in the integrated lâ€ABR. Water Environment Research, 2021, 93, 1455-1465.	1.3	8
914	Strategies for Natural Products Discovery from Uncultured Microorganisms. Molecules, 2021, 26, 2977.	1.7	8
915	Low-Abundant Microorganisms: The Human Microbiome's Dark Matter, a Scoping Review. Frontiers in Cellular and Infection Microbiology, 2021, 11, 689197.	1.8	34
916	The time is now for ubiquitous forensic <scp>mtMPS</scp> analysis. Wiley Interdisciplinary Reviews Forensic Science, 2022, 4, .	1.2	7
917	DNA Metabarcoding for Quality Control of Basil, Oregano, and Paprika. Frontiers in Plant Science, 2021, 12, 665618.	1.7	14
919	cfDNA Sequencing: Technological Approaches and Bioinformatic Issues. Pharmaceuticals, 2021, 14, 596.	1.7	31
920	Syntrophic butyrate-oxidizing methanogenesis promoted by anthraquinone-2-sulfonate and cysteine: Distinct tendencies towards the enrichment of methanogens and syntrophic fatty-acid oxidizing bacteria. Bioresource Technology, 2021, 332, 125074.	4.8	8
921	Genomic Mosaicism Formed by Somatic Variation in the Aging and Diseased Brain. Genes, 2021, 12, 1071.	1.0	17
922	High prevalence of tryptophan-truncated S quasispecies in treatment-na \tilde{A} -ve chronic hepatitis B patients. Journal of General Virology, 2021, 102, .	1.3	0
923	Pervasive transcription of the mitochondrial genome in <i>Candida albicans</i> is revealed in mutants lacking the mtEXO RNase complex. RNA Biology, 2021, 18, 303-317.	1.5	3
925	Multiomic Approach to Analyze Infant Gut Microbiota: Experimental and Analytical Method Optimization. Biomolecules, 2021, 11, 999.	1.8	3
926	AlEgens for Bacterial Imaging and Ablation. Advanced Healthcare Materials, 2021, 10, e2100877.	3.9	19
927	Trends and Applications of Omics Technologies to Functional Characterisation of Enzymes and Protein Metabolites Produced by Fungi. Journal of Fungi (Basel, Switzerland), 2021, 7, 700.	1.5	3

#	Article	IF	CITATIONS
928	Singleâ€molecule, hybridizationâ€based strategies for short nucleic acids detection and recognition with nanopores. Proteomics, 2022, 22, e2100046.	1.3	6
929	Bridging the academia-to-industry gap: organ-on-a-chip platforms for safety and toxicology assessment. Trends in Pharmacological Sciences, 2021, 42, 715-728.	4.0	26
930	Internal validation and improvement of mitochondrial genome sequencing using the Precision ID mtDNA Whole Genome Panel. International Journal of Legal Medicine, 2021, 135, 2295-2306.	1.2	9
931	APC mutations are common in adenomas but infrequent in adenocarcinomas of the non-ampullary duodenum. Journal of Gastroenterology, 2021, 56, 988-998.	2.3	6
932	The <i>Bacillus subtilis</i> Minimal Genome Compendium. ACS Synthetic Biology, 2021, 10, 2767-2771.	1.9	23
933	Fish intended for human consumption: from DNA barcoding to a next-generation sequencing (NGS)-based approach. Current Opinion in Food Science, 2021, 42, 86-92.	4.1	10
934	A new Trypanosoma cruzi genotyping method enables high resolution evolutionary analyses. Memorias Do Instituto Oswaldo Cruz, 2021, 116, e200538.	0.8	3
936	Full-length 16S rRNA gene amplicon analysis of human gut microbiota using MinlONâ,,¢ nanopore sequencing confers species-level resolution. BMC Microbiology, 2021, 21, 35.	1.3	146
937	Next-Generation Sequencing in Veterinary Medicine: How Can the Massive Amount of Information Arising from High-Throughput Technologies Improve Diagnosis, Control, and Management of Infectious Diseases?. Methods in Molecular Biology, 2015, 1247, 415-436.	0.4	33
938	Origin and Evolution of Human Immunodeficiency Viruses. , 2015, , 587-611.		3
939	Profiling Short Tandem Repeats from Short Reads. Methods in Molecular Biology, 2013, 1038, 113-135.	0.4	5
940	DNA Profiling and Characterization of Animal Cell Lines. Methods in Molecular Biology, 2014, 1104, 57-73.	0.4	4
941	Pulsed Field Gel Electrophoresis of Staphylococcus epidermidis. Methods in Molecular Biology, 2014, 1106, 55-60.	0.4	7
942	Functional Microbial Composition. Handbook of Environmental Chemistry, 2016, , 387-450.	0.2	1
943	Cancer Genomics in Precision Oncology: Applications, Challenges, and Prospects., 2020,, 453-499.		9
944	Next-Generation Sequencing (NGS) Platforms: An Exciting Era of Genome Sequence Analysis. , 2019, , 89-109.		14
945	An easy and robust method for isolation and validation of single-nucleotide polymorphic markers from a first Erysiphe alphitoides draft genome. Mycological Progress, 2020, 19, 615-628.	0.5	6
946	High-throughput sequencing (HTS) for the analysis of viral populations. Infection, Genetics and Evolution, 2020, 80, 104208.	1.0	35

#	Article	IF	CITATIONS
947	Next-generation sequencing analysis of new genotypes appearing during antiviral treatment of chronic hepatitis C reveals that these are selected from pre-existing minor strains. Journal of General Virology, 2018, 99, 1633-1642.	1.3	4
948	Phase variable DNA repeats in Neisseria gonorrhoeae influence transcription, translation, and protein sequence variation. Microbial Genomics, 2016, 2, e000078.	1.0	11
949	mlplasmids: a user-friendly tool to predict plasmid- and chromosome-derived sequences for single species. Microbial Genomics, $2018,4,.$	1.0	121
967	High-Throughput DNA Sequencing Analysis of Antibody Repertoires. , 0, , 345-362.		6
968	Clonal relationships of CSF B cells in treatment-naive multiple sclerosis patients. JCI Insight, 2017, 2, .	2.3	84
969	Applying clinical metagenomics for the detection and characterisation of respiratory infections. , 2019, , 35-49.		3
971	Chapter 1 Molecular Community Ecology of Arbuscular Mycorrhizal Fungi. Mycology, 2017, , 1-26.	0.5	8
973	Revising a Personal Genome by Comparing and Combining Data from Two Different Sequencing Platforms. PLoS ONE, 2013, 8, e60585.	1.1	5
974	Next-Generation Sequencing of the Chrysanthemum nankingense (Asteraceae) Transcriptome Permits Large-Scale Unigene Assembly and SSR Marker Discovery. PLoS ONE, 2013, 8, e62293.	1.1	107
975	A Microfluidic Device for Preparing Next Generation DNA Sequencing Libraries and for Automating Other Laboratory Protocols That Require One or More Column Chromatography Steps. PLoS ONE, 2013, 8, e64084.	1.1	33
976	Choosing a Benchtop Sequencing Machine to Characterise Helicobacter pylori Genomes. PLoS ONE, 2013, 8, e67539.	1.1	22
977	Massively Parallel DNA Sequencing Successfully Identifies New Causative Mutations in Deafness Genes in Patients with Cochlear Implantation and EAS. PLoS ONE, 2013, 8, e75793.	1.1	83
978	Impact of Technical Sources of Variation on the Hand Microbiome Dynamics of Healthcare Workers. PLoS ONE, 2014, 9, e88999.	1.1	20
979	Massively Parallel DNA Sequencing Facilitates Diagnosis of Patients with Usher Syndrome Type 1. PLoS ONE, 2014, 9, e90688.	1.1	36
980	Performance Comparison between Rapid Sequencing Platforms for Ultra-Low Coverage Sequencing Strategy. PLoS ONE, 2014, 9, e92192.	1.1	23
981	Is DNA Barcoding Actually Cheaper and Faster than Traditional Morphological Methods: Results from a Survey of Freshwater Bioassessment Efforts in the United States?. PLoS ONE, 2014, 9, e95525.	1.1	116
982	The Mitochondrial Genome of the Leaf-Cutter Ant Atta laevigata: A Mitogenome with a Large Number of Intergenic Spacers. PLoS ONE, 2014, 9, e97117.	1.1	37
983	HIV-1 Quasispecies Delineation by Tag Linkage Deep Sequencing. PLoS ONE, 2014, 9, e97505.	1.1	25

#	Article	IF	CITATIONS
984	OTG-snpcaller: An Optimized Pipeline Based on TMAP and GATK for SNP Calling from Ion Torrent Data. PLoS ONE, 2014, 9, e97507.	1.1	32
985	Reporting Tumor Molecular Heterogeneity in Histopathological Diagnosis. PLoS ONE, 2014, 9, e104979.	1.1	35
986	PCR Primers to Study the Diversity of Expressed Fungal Genes Encoding Lignocellulolytic Enzymes in Soils Using High-Throughput Sequencing. PLoS ONE, 2014, 9, e116264.	1.1	33
987	Chlamydia trachomatis In Vivo to In Vitro Transition Reveals Mechanisms of Phase Variation and Down-Regulation of Virulence Factors. PLoS ONE, 2015, 10, e0133420.	1.1	14
988	Robustness of Massively Parallel Sequencing Platforms. PLoS ONE, 2015, 10, e0138259.	1.1	3
989	Transcriptome Analysis of Blunt Snout Bream (Megalobrama amblycephala) Reveals Putative Differential Expression Genes Related to Growth and Hypoxia. PLoS ONE, 2015, 10, e0142801.	1.1	20
990	Comparing Apples and Oranges?: Next Generation Sequencing and Its Impact on Microbiome Analysis. PLoS ONE, 2016, 11, e0148028.	1.1	234
991	Molecular Heterogeneity of Ewing Sarcoma as Detected by Ion Torrent Sequencing. PLoS ONE, 2016, 11, e0153546.	1.1	12
992	Variability of Bacterial Communities in the Moth Heliothis virescens Indicates Transient Association with the Host. PLoS ONE, 2016, 11, e0154514.	1.1	89
993	Genome Sequencing and Comparative Analysis of Saccharomyces cerevisiae Strains of the Peterhof Genetic Collection. PLoS ONE, 2016, 11, e0154722.	1.1	27
994	Transcriptome Analysis of the Innate Immunity-Related Complement System in Spleen Tissue of Ctenopharyngodon idella Infected with Aeromonas hydrophila. PLoS ONE, 2016, 11, e0157413.	1.1	85
995	Characterization and Adaptation of Anaerobic Sludge Microbial Communities Exposed to Tetrabromobisphenol A. PLoS ONE, 2016, 11, e0157622.	1.1	25
996	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
997	GLM-based optimization of NGS data analysis: A case study of Roche 454, Ion Torrent PGM and Illumina NextSeq sequencing data. PLoS ONE, 2017, 12, e0171983.	1.1	7
998	Identification of key contributors in complex population structures. PLoS ONE, 2017, 12, e0177638.	1.1	13
999	Evaluation of metagenetic community analysis of planktonic copepods using Illumina MiSeq: Comparisons with morphological classification and metagenetic analysis using Roche 454. PLoS ONE, 2017, 12, e0181452.	1.1	20
1000	Evaluating the number of different genomes in a metagenome by means of the compositional spectra approach. PLoS ONE, 2020, 15, e0237205.	1.1	1
1001	Next generation sequencing applications for breast cancer research. Medicine and Pharmacy Reports, 2015, 88, 278-287.	0.2	6

#	Article	IF	CITATIONS
1002	RNA-SEQ: A GLANCE AT TECHNOLOGIES AND METHODOLOGIES. Acta Biologica Colombiana, 2015, 20, .	0.1	9
1003	Analysis of Microbial Composition Associated with Freshwater and Seawater. Biomedical Science Letters, 2016, 22, 150-159.	0.0	37
1004	OutLyzer: software for extracting low-allele-frequency tumor mutations from sequencing background noise in clinical practice. Oncotarget, 2016, 7, 79485-79493.	0.8	19
1005	Validation and optimization of the Ion Torrent S5 XL sequencer and Oncomine workflow for <i>BRCA1</i> and <i>BRCA2</i> genetic testing. Oncotarget, 2017, 8, 34858-34866.	0.8	29
1006	Analytic validation and real-time clinical application of an amplicon-based targeted gene panel for advanced cancer. Oncotarget, 2017, 8, 75822-75833.	0.8	6
1007	High-throughput sequencing of murine immunoglobulin heavy chain repertoires using single side unique molecular identifiers on an Ion Torrent PGM. Oncotarget, 2018, 9, 30225-30239.	0.8	4
1008	Next-generation sequencing workflows in veterinary infection biology: towards validation and quality assurance. OIE Revue Scientifique Et Technique, 2016, 35, 67-81.	0.5	9
1009	Genomics and outbreaks: foot and mouth disease. OIE Revue Scientifique Et Technique, 2016, 35, 175-189.	0.5	19
1010	Biological properties of African swine fever virus Odintsovo 02/14 isolate and its genome analysis. International Journal of Environmental & Agriculture Research, 2017, 3, 26-37.	0.0	5
1011	Epidemiological investigation of Pseudomonas aeruginosa isolates from a six-year-long hospital outbreak using high-throughput whole genome sequencing. Eurosurveillance, 2013, 18 , .	3.9	57
1012	Current application and future perspectives of molecular typing methods to study Clostridium difficile infections. Eurosurveillance, 2013, 18, 20381.	3.9	110
1013	From theory to practice: molecular strain typing for the clinical and public health setting. Eurosurveillance, 2013, 18, 20383.	3.9	16
1014	Effect of exogenous nitrogen and phosphorus inputs on the microbe-soil interaction in the secondary Castanopsis sclerophylla forest in east China. IForest, 2018, 11, 794-801.	0.5	5
1015	Using next generation sequencing to tackle non-typhoidal Salmonella infections. Journal of Infection in Developing Countries, 2013, 7, 001-005.	0.5	25
1016	Bioinformatics for Viral Metagenomics. Journal of Data Mining in Genomics & Proteomics, 2013, 04, .	0.5	14
1017	Efficiency of Corynebacterium pseudotuberculosis Cp31 Genome Assembly with the Hi-Q Enzyme on an Ion Torrent PGM Sequencing Platform. Journal of Proteomics and Bioinformatics, 2014, 7, .	0.4	3
1018	Molecular predictive markers in tumors of the gastrointestinal tract. World Journal of Gastrointestinal Oncology, 2016, 8, 772.	0.8	6
1019	Value of a newly sequenced bacterial genome. World Journal of Biological Chemistry, 2014, 5, 161-8.	1.7	10

#	Article	IF	CITATIONS
1021	Next-generation sequencing in clinical virology: Discovery of new viruses. World Journal of Virology, 2015, 4, 265.	1.3	72
1022	The potential of High-Throughput Sequencing (HTS) of natural samples as a source of primary taxonomic information for reference libraries of diatom barcodes. Fottea, 2018, 18, 37-54.	0.4	40
1023	A Primer for Disease Gene Prioritization Using Next-Generation Sequencing Data. Genomics and Informatics, 2013, 11, 191.	0.4	11
1024	Changes in the intestinal microbiota of superobese patients after bariatric surgery. Clinics, 2019, 74, e1198.	0.6	13
1025	A comparison of rumen microbial profiles in dairy cows as retrieved by 454 Roche and Ion Torrent (PGM) sequencing platforms. PeerJ, 2016, 4, e1599.	0.9	17
1026	Assessing Illumina technology for the high-throughput sequencing of bacteriophage genomes. PeerJ, 2016, 4, e2055.	0.9	38
1027	Greater than <i>X</i> kb: a quantitative assessment of preservation conditions on genomic DNA quality, and a proposed standard for genome-quality DNA. PeerJ, 2016, 4, e2528.	0.9	23
1028	Culture-independent detection and characterisation of <i>Mycobacterium tuberculosis </i> africanum in sputum samples using shotgun metagenomics on a benchtop sequencer. Peerl, 2014, 2, e585.	0.9	113
1029	An evaluation of alternative methods for constructing phylogenies from whole genome sequence data: a case study with <i>Salmonella </i> . PeerJ, 2014, 2, e620.	0.9	45
1031	Novel Approaches to Pathogen Discovery in Metagenomes. , 2012, , 1-8.		0
1032	Genome Assembly Algorithms: A Survey. Hans Journal of Computational Biology, 2013, 03, 7-14.	0.0	0
1033	12.ÂMolecular Typing and Differentiation. , 2015, , .		0
1034	Pathology, Biomarkers, and Molecular Diagnostics. , 2014, , 226-252.e6.		1
1035	Diagnosis, Discovery and Dissection of Viral Diseases. , 2014, , 39-45.		1
1036	Current Massively Parallel Sequencing Technologies: Platforms and Reporting Considerations. , 2015, , 3-17.		0
1037	Tandem Mass Spectrometry Analysis as an Approach to Delineate Genetically Related Taxa, with Specific Implication for Differentiating Escherichia coli from amongst the Complex Enterobacteriaceae Family. Journal of Proteomics & Enzymology, 2015, 04, .	0.5	0
1038	Mapping RNA Interactions to Proteins in Virions Using CLIP-Seq. Methods in Molecular Biology, 2015, 1297, 213-224.	0.4	0
1040	Genetic Diagnosis of Renal Diseases: Basic Concepts and Testing. , 2016, , 107-149.		0

#	Article	IF	CITATIONS
1041	DNA Sequencing for Clinical and Public Health Virology: Some Assembly Required., 0,, 173-199.		0
1043	Next-Generation Sequencing., 2016,, 229-241.		0
1044	Molecular Taxonomy of Environmental Prokaryotes. , 2016, , 3-35.		0
1045	Freeze-drying feces reduces illumina-derived artefacts on 16S rRNA-based microbial community analysis. Journal of Applied Biological Chemistry, 2016, 59, 299-304.	0.2	0
1046	Bioinformatics Aspects of Foodborne Pathogen Research. , 2017, , 51-64.		0
1049	Existing and Emerging Molecular Technologies in Myeloid Neoplasms. Molecular Pathology Library, 2018, , 369-412.	0.1	O
1055	Detection of Bacteriophages: Sequence-Based Systems. , 2019, , 1-25.		1
1056	Current Massively Parallel Sequencing Technologies: Platforms and Reporting Considerations. , 2019, , 11-21.		O
1057	Genomic Applications in Hematologic Oncology. , 2019, , 269-287.		0
1058	Recent Advances in Microbial Genome Sequencing. , 2019, , 131-144.		4
1060	The use of preimplantation genetic testing for aneuploidy and mitochondrial DNA scoring helps in improving assisted reproductive techniques outcome. The Onco Fertility Journal, 2019, 2, 66.	0.3	0
1063	Pre-analytics, Current Testing Technologies, and Limitations of Testing. , 2020, , 3-23.		O
1064	La microbiota del tracto digestivo de camarones peneidos: una perspectiva hist \tilde{A}^3 rica y estado del arte//The gut microbiota of penaeid shrimp: a historical perspective and state of the art. Biotecnia, 2019, 22, 5-16.	0.1	0
1067	Development of EST-SSR markers based on transcriptome and its validation in ginger (Zingiber) Tj ETQq1 1 0.784	314 rgBT	/Overlock I
1068	Evaluation of Ion Torrent next-generation sequencing for thalassemia diagnosis. Journal of International Medical Research, 2020, 48, 030006052096777.	0.4	5
1069	OBSOLETE: Phylogenomics of Foodborne Pathogens: The Case of Listeria monocytogenes. , 2020, , .		O
1070	A comparison between SOLiD 5500XLand Ion Torrent PGM-derived miRNA expression profiles in two breast cell lines. Genetics and Molecular Biology, 2020, 43, e20180351.	0.6	1
1072	Identification of Campylobacter jejuni and Chlamydia psittaci from cockatiel (Nymphicus hollandicus) using metagenomics. BMC Genomics, 2021, 22, 797.	1.2	2

#	Article	IF	Citations
1074	Liquid Biopsy in Thyroid Cancer: New Insight. International Journal of Hematology-Oncology and Stem Cell Research, 2018, 12, 235-248.	0.3	25
1075	TP53, PIK3CA, FBXW7 and KRAS Mutations in Esophageal Cancer Identified by Targeted Sequencing. Cancer Genomics and Proteomics, 2016, 13, 231-8.	1.0	14
1076	The storm of NGS in NSCLC diagnostic-therapeutic pathway: How to sun the real clinical practice. Critical Reviews in Oncology/Hematology, 2022, 169, 103561.	2.0	16
1077	Improved quantitative microbiome profiling for environmental antibiotic resistance surveillance. Environmental Microbiomes, 2021, 16, 21.	2.2	4
1078	Deciphering Multidrug-Resistant Acinetobacter baumannii from a Pediatric Cancer Hospital in Egypt. MSphere, 2021, 6, e0072521.	1.3	10
1079	Longitudinal analysis of FcRL5 expression and clonal relationships among classical and atypical memory B cells following malaria. Malaria Journal, 2021, 20, 435.	0.8	8
1080	The methodological challenge in highâ€throughput profiling and quantifying microRNAs. Quantitative Biology, 2022, 10, 321-332.	0.3	0
1081	Bacterial Diversity, Organic Acid, and Flavor Analysis of Dacha and Ercha Fermented Grains of Fen Flavor Baijiu. Frontiers in Microbiology, 2021, 12, 769290.	1.5	7
1082	Exploring large-scale protein function using systematic mutant analysis., 2022,, 575-588.		0
1083	Genomic Mutations Within the Host Microbiome: Adaptive Evolution or Purifying Selection. Engineering, 2023, 20, 96-102.	3.2	5
1084	Tatajuba: exploring the distribution of homopolymer tracts. NAR Genomics and Bioinformatics, 2022, 4, Iqac003.	1.5	1
1085	Chimeric chromosome landscapes of human somatic cell cultures show dependence on stress and regulation of genomic repeats by CGGBP1. Oncotarget, 2022, 13, 136-155.	0.8	1
1086	Next-Generation DNA Sequencing: Ion Torrent Sequencers Versus Nanopore Technology. , 2022, , 651-666.		0
1087	Bulge-loop tuned entropy-driven catalytic reaction and tag-encoded barcodes for multiplexed mutation detection. Sensors and Actuators B: Chemical, 2022, 358, 131462.	4.0	8
1088	eDNA in subterranean ecosystems: Applications, technical aspects, and future prospects. Science of the Total Environment, 2022, 820, 153223.	3.9	38
1089	Towards comprehensive understanding of bacterial genetic diversity: large-scale amplifications in Bordetella pertussis and Mycobacterium tuberculosis. Microbial Genomics, 2022, 8, .	1.0	0
1090	Tool evaluation for the detection of variably sized indels from next generation whole genome and targeted sequencing data. PLoS Computational Biology, 2022, 18, e1009269.	1.5	13
1091	Exploring statistical weight estimates for mitochondrial DNA matches involving heteroplasmy. International Journal of Legal Medicine, 2022, 136, 671-685.	1.2	5

#	Article	IF	Citations
1092	Application of Next Generation Sequencing for Diagnosis and Clinical Management of Drug-Resistant Tuberculosis: Updates on Recent Developments in the Field. Frontiers in Microbiology, 2022, 13, 775030.	1.5	22
1093	Massively parallel sequencing of Cannabis sativa chloroplast hotspots for forensic typing. Journal of Cannabis Research, 2022, 4, 13.	1.5	3
1094	Comparison of Different Carriers to Maintain a Stable Partial Nitrification Process for Low-Strength Wastewater Treatment. Frontiers in Bioengineering and Biotechnology, 2022, 10, 851565.	2.0	1
1095	An accessible, efficient and global approach for the large-scale sequencing of bacterial genomes. Genome Biology, 2021, 22, 349.	3.8	20
1096	SARS-CoV-2 genetic variations associated with COVID-19 pathogenicity. Microbial Genomics, 2021, 7, .	1.0	10
1097	Use of Proteomics and Transcriptomics to Identify Proteins for Cold Adaptation in Microbes. , 2022, , 285-319.		0
1098	Mining for NRPS and PKS Genes in Actinobacteria Using Whole-Genome Sequencing and Bioinformatic Tools., 2022,, 393-410.		1
1100	Evaluation of the correctable decoding sequencing as a new powerful strategy for DNA sequencing. Life Science Alliance, 2022, 5, e202101294.	1.3	4
1163	Variants minoritaires du VIH-1Â: détection, quantification et implications cliniques. Virologie, 2012, 16, 276-285.	0.1	0
1164	Best practices for reporting throughput in biomedical research. Nature Methods, 2022, 19, 633-634.	9.0	9
1165	Archaeal Communities of South China Mangroves and Their Potential Roles in the Nitrogen Cycle. Geomicrobiology Journal, 2022, 39, 697-704.	1.0	5
1166	A New Computational Deconvolution Algorithm for the Analysis of Forensic DNA Mixtures with SNP Markers. Genes, 2022, 13, 884.	1.0	1
1167	FRAGTE2: An Enhanced Algorithm to Pre-Select Closely Related Genomes for Bacterial Species Demarcation. Frontiers in Microbiology, 2022, 13, .	1.5	0
1168	Proof of concept for multiplex amplicon sequencing for mutation identification using the MinION nanopore sequencer. Scientific Reports, 2022, 12, .	1.6	13
1169	A Review of Next Generation Sequencing Methods and its Applications in Laboratory Diagnosis. Journal of Pure and Applied Microbiology, 0, , .	0.3	2
1170	The Revolution of Omics Technology in Plant Science. , 2022, , 23-56.		1
1171	High-throughput method for the hybridisation-based targeted enrichment of long genomic fragments for PacBio third-generation sequencing. NAR Genomics and Bioinformatics, 2022, 4, .	1.5	7
1172	Tumor-on-a-chip model for advancement of anti-cancer nano drug delivery system. Journal of Nanobiotechnology, 2022, 20, .	4.2	13

#	Article	IF	CITATIONS
1174	Development of two 410-cancer-gene panel tests for solid tumors and liquid biopsy based on genome data of 5,143 Japanese cancer patients. Biomedical Research, 2022, 43, 115-126.	0.3	1
1177	Next Generation and Other Sequencing Technologies in Diagnostic Microbiology and Infectious Diseases. Genes, 2022, 13, 1566.	1.0	32
1178	Comparison of 16S rRNA Gene Primers on Studying Microbial Community Composition in Bottom Water and Sediment of Artificial Reefs in Laoshan Bay, China. Journal of Ocean University of China, 2022, 21, 1313-1322.	0.6	0
1179	Performance Comparison of Different Approaches in Genotyping MHC-DRB: The Contrast between Single-Locus and Multi-Locus Species. Animals, 2022, 12, 2452.	1.0	O
1180	Connectivity and divergence of symbiotic bacteria of deep-sea hydrothermal vent mussels in relation to the structure and dynamics of mid-ocean ridges. Frontiers in Marine Science, 0, 9, .	1.2	2
1182	Human transcriptome profiling: applications in health and disease. , 2023, , 373-395.		0
1183	Bioinformatic Analysis of Natively Paired VH:VL Antibody Repertoires for Antibody Discovery. Methods in Molecular Biology, 2023, , 447-463.	0.4	1
1185	The formation of double metalimnetic oxygen minima in a drinking water reservoir and its influence on bacterial community. Science of the Total Environment, 2023, 860, 160540.	3.9	4
1186	Influence of Sex on the Microbiota of the Human Face. Microorganisms, 2022, 10, 2470.	1.6	7
1187	Molecular Profiling of Gynaecological Cancer and Breast Cancer. , 2022, , 9-24.		0
1188	De Novo Transcriptome Assembly and EST-SSR Marker Development and Application in Chrysosplenium macrophyllum. Genes, 2023, 14, 279.	1.0	2
1189	Which technology performs better? From sample volume to extraction and molecular profiling. , 2023, , 119-202.		0
1190	Methods to improve the accuracy of next-generation sequencing. Frontiers in Bioengineering and Biotechnology, 0, 11 , .	2.0	15
1191	Beyond genomics and proteomics., 2023,, 191-243.		0
1193	Molecular Accounting and Profiling of Human Respiratory Microbial Communities: Toward Precision Medicine by Targeting the Respiratory Microbiome for Disease Diagnosis and Treatment. International Journal of Molecular Sciences, 2023, 24, 4086.	1.8	11
1194	Full-Length 16S rRNA Gene Analysis Using Long-Read Nanopore Sequencing for Rapid Identification of Bacteria from Clinical Specimens. Methods in Molecular Biology, 2023, , 193-213.	0.4	4
1195	Comparison of four DNA extraction kits efficiency for 16SrDNA microbiota profiling of diverse human samples. Future Science OA, 2023, 9, .	0.9	2
1196	AlEgen-Based Nanomaterials for Bacterial Imaging and Antimicrobial Applications: Recent Advances and Perspectives. Molecules, 2023, 28, 2863.	1.7	2

#	Article	IF	Citations
1197	The Wildâ€Type tRNA Adenosine Deaminase Enzyme TadA Is Capable of Sequenceâ€Specific DNA Base Editing. ChemBioChem, 2023, 24, .	1.3	2
1199	Molecular Diagnosis of Genetic Diseases of the Kidney: Primer for Pediatric Nephrologists. , 2023, , 119-169.		0
1200	In-house homologous recombination deficiency testing in ovarian cancer: a multi-institutional Italian pilot study. Journal of Clinical Pathology, 0, , jcp-2023-208852.	1.0	4
1204	Establishing Phylogenetic Profile and Identification of Function and Ligands for Mycobacterium Ulcerans Microbiome., 2023,, 65-78.		0
1207	Comparison of VCFs Generated from Different Software in the Evaluation of Variants in Genes Responsible for Rare Thrombophilic Conditions. Lecture Notes in Computer Science, 2023, , 456-462.	1.0	0
1211	Next-Generation Sequencing in Plant Breeding: Challenges and Possibilities. , 2023, , 507-535.		0
1212	Direct Transposition Interleaving Technique for DNA Data Storage., 2023,,.		0
1213	SIUrO best practice recommendations to optimize BRCA $1/2$ gene testing from DNA extracted from bone biopsy in mCRPC patients (BRCA Optimal Bone Biopsy Procedure: BOP). Virchows Archiv Fur Pathologische Anatomie Und Physiologie Und Fur Klinische Medizin, $0, , .$	1.4	1
1220	Single-Cell Sequencing Technology and Its Application in the Study of Central Nervous System Diseases. Cell Biochemistry and Biophysics, 0, , .	0.9	0