NCBI Reference Sequences (RefSeq): current status, nev policy

Nucleic Acids Research

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Citation Report

#	Article	IF	Citations
1	â€œOn the Power of Penetrating into Spaceâ€\ The Telescopes of William Herschel. Journal for the History of Astronomy, 1976, 7, 75-108.	0.1	38
2	Virus Pathogen Database and Analysis Resource (ViPR): A Comprehensive Bioinformatics Database and Analysis Resource for the Coronavirus Research Community. Viruses, 2012, 4, 3209-3226.	1.5	156
3	Nebulaâ€”a web-server for advanced ChIP-seq data analysis. Bioinformatics, 2012, 28, 2517-2519.	1.8	42
4	A Response Regulator Interfaces between the Frz Chemosensory System and the MglA/MglB GTPase/GAP Module to Regulate Polarity in Myxococcus xanthus. PLoS Genetics, 2012, 8, e1002951.	1.5	60
5	MBGD update 2013: the microbial genome database for exploring the diversity of microbial world. Nucleic Acids Research, 2012, 41, D631-D635.	6.5	37
6	Update on activities at the Universal Protein Resource (UniProt) in 2013. Nucleic Acids Research, 2012, 41, D43-D47.	6.5	620
7	GGRNA: an ultrafast, transcript-oriented search engine for genes and transcripts. Nucleic Acids Research, 2012, 40, W592-W596.	6.5	9
8	Tracking and coordinating an international curation effort for the CCDS Project. Database: the Journal of Biological Databases and Curation, 2012, 2012, bas008-bas008.	1.4	48
9	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2012, 41, D8-D20.	6.5	459
10	Improvements in the protein identifier cross-reference service. Nucleic Acids Research, 2012, 40, W276-W280.	6.5	27
11	EcoGene 3.0. Nucleic Acids Research, 2012, 41, D613-D624.	6.5	180
12	ClusterMine360: a database of microbial PKS/NRPS biosynthesis. Nucleic Acids Research, 2012, 41, D402-D407.	6.5	113
13	MicrobeDB: a locally maintainable database of microbial genomic sequences. Bioinformatics, 2012, 28, 1947-1948.	1.8	15
14	A Novel Computational Strategy to Identify A-to-I RNA Editing Sites by RNA-Seq Data: De Novo Detection in Human Spinal Cord Tissue. PLoS ONE, 2012, 7, e44184.	1.1	19
15	Reference-independent comparative metagenomics using cross-assembly: crAss. Bioinformatics, 2012, 28, 3225-3231.	1.8	87
16	Draft Genome Sequence of the Extremely Halophilic Archaeon Halogranum salarium B-1 ^T. Journal of Bacteriology, 2012, 194, 6659-6659.	1.0	4
17	The effect of human genome annotation complexity on RNA-Seq gene expression quantification. , 2012, 2012, 712-717.		7
18	SAVoR: a server for sequencing annotation and visualization of RNA structures. Nucleic Acids Research, 2012, 40, W59-W64.	6.5	14

#	ARTICLE	IF	CITATIONS
19	Clone DB: an integrated NCBI resource for clone-associated data. Nucleic Acids Research, 2012, 41, D1070-D1078.	6.5	14
20	Bioinformatic <scp>Databases</scp> and <scp>Resources</scp> in the public domain to aid <scp>HLA</scp> research. Tissue Antigens, 2012, 80, 295-304.	1.0	7
21	Online Tools for Bioinformatics Analyses in Nutrition Sciences. Advances in Nutrition, 2012, 3, 654-665.	2.9	13
22	Genomic determinants of sporulation in <i>Bacilli</i> and <i>Clostridia</i>: towards the minimal set of sporulationâ€specific genes. Environmental Microbiology, 2012, 14, 2870-2890.	1.8	235
23	The <i>Escherichia coli</i> RlmN methyltransferase is a dual-specificity enzyme that modifies both rRNA and tRNA and controls translational accuracy. Rna, 2012, 18, 1783-1795.	1.6	81
24	The Rice Genome Knowledgebase (RGKbase): an annotation database for rice comparative genomics and evolutionary biology. Nucleic Acids Research, 2012, 41, D1199-D1205.	6.5	25
25	GENCODE: The reference human genome annotation for The ENCODE Project. Genome Research, 2012, 22, 1760-1774.	2.4	4,217
26	The NIH genetic testing registry: a new, centralized database of genetic tests to enable access to comprehensive information and improve transparency. Nucleic Acids Research, 2012, 41, D925-D935.	6.5	146
27	Affymetrix&#x00AE; Mismatch (MM) Probes: Useful after All. , 2012, , .		2
28	Design and Implementation of an Integrated PPI System. , 2012, , .		0
29	MonarchBase: the monarch butterfly genome database. Nucleic Acids Research, 2012, 41, D758-D763.	6.5	91
30	Mining Data from National Center for Biotechnology Information System. , 2012, , .		0
31	Extracting Top Hot Hits in Biomedicine from PubMed. , 2012, , .		0
32	Ensembl 2013. Nucleic Acids Research, 2012, 41, D48-D55.	6.5	856
33	Computational Analysis of Cysteine and Methionine Metabolism and Its Regulation in Dairy Starter and Related Bacteria. Journal of Bacteriology, 2012, 194, 3522-3533.	1.0	29
34	CerealsDB 2.0: an integrated resource for plant breeders and scientists. BMC Bioinformatics, 2012, 13, 219.	1.2	194
35	Transcriptome analysis at four developmental stages of grape berry (Vitis vinifera cv. Shiraz) provides insights into regulated and coordinated gene expression. BMC Genomics, 2012, 13, 691.	1.2	125
36	Comparative genomic analysis of the DUF71/COG2102 family predicts roles in diphthamide biosynthesis and B12 salvage. Biology Direct, 2012, 7, 32.	1.9	19

#	ARTICLE	IF	CITATIONS
37	Thousands of missed genes found in bacterial genomes and their analysis with COMBREX. Biology Direct, 2012, 7, 37.	1.9	28
38	The genome of the ammoniaâ€oxidizing <i><scp>C</scp>andidatus</i><scp>N</scp>itrososphaera gargensis: insights into metabolic versatility and environmental adaptations. Environmental Microbiology, 2012, 14, 3122-3145.	1.8	332
39	The UCSC Genome Browser. Current Protocols in Bioinformatics, 2012, 40, Unit1.4.	25.8	86
40	Using the KEGG Database Resource. Current Protocols in Bioinformatics, 2012, 38, Unit1.12.	25.8	232
41	Personalizing rare disease research: how genomics is revolutionizing the diagnosis and treatment of rare disease. Personalized Medicine, 2012, 9, 805-819.	0.8	8
42	Long-Range Interactions in Nonsense-Mediated mRNA Decay Are Mediated by Intrinsically Disordered Protein Regions. Journal of Molecular Biology, 2012, 424, 125-131.	2.0	7
43	Using ProHits to Store, Annotate, and Analyze Affinity Purificationâ€“Mass Spectrometry (APâ€MS) Data. Current Protocols in Bioinformatics, 2012, 39, Unit8.16.	25.8	19
44	Genomic Resources for Evolutionary Studies in the Large, Diverse, Tropical Genus, Begonia. Tropical Plant Biology, 2012, 5, 261-276.	1.0	16
45	CD19: a biomarker for B cell development, lymphoma diagnosis and therapy. Experimental Hematology and Oncology, 2012, 1, 36.	2.0	398
46	CBS: an open platform that integrates predictive methods and epigenetics information to characterize conserved regulatory features in multiple Drosophila genomes. BMC Genomics, 2012, 13, 688.	1.2	1
47	PMRD: a curated database for genes and mutants involved in plant male reproduction. BMC Plant Biology, 2012, 12, 215.	1.6	21
48	PCDq: human protein complex database with quality index which summarizes different levels of evidences of protein complexes predicted from H-Invitational protein-protein interactions integrative dataset. BMC Systems Biology, 2012, 6, S7.	3.0	61
49	Discovery of Novel MicroRNAs in Rat Kidney Using Next Generation Sequencing and Microarray Validation. PLoS ONE, 2012, 7, e34394.	1.1	19
50	The Human Homolog of Escherichia coli Endonuclease V Is a Nucleolar Protein with Affinity for Branched DNA Structures. PLoS ONE, 2012, 7, e47466.	1.1	23
51	Expanded Functional Diversity of Shaker K+ Channels in Cnidarians Is Driven by Gene Expansion. PLoS ONE, 2012, 7, e51366.	1.1	29
52	Multiple Strategies for Translesion Synthesis in Bacteria. Cells, 2012, 1, 799-831.	1.8	25
53	A post-assembly genome-improvement toolkit (PAGIT) to obtain annotated genomes from contigs. Nature Protocols, 2012, 7, 1260-1284.	5.5	167
54	Molecular probe technology detects bacteria without culture. BMC Microbiology, 2012, 12, 29.	1.3	10

#	ARTICLE	IF	CITATIONS
55	Viral categorization and discovery in human circulation by transcriptome sequencing. Biochemical and Biophysical Research Communications, 2013, 436, 525-529.	1.0	4
56	The CRAPome: a contaminant repository for affinity purificationâ€“mass spectrometry data. Nature Methods, 2013, 10, 730-736.	9.0	1,353
57	Human housekeeping genes, revisited. Trends in Genetics, 2013, 29, 569-574.	2.9	1,091
58	Metaproteomics to unravel major microbial players in leaf litter and soil environments: <scp>C</scp>hallenges and perspectives. Proteomics, 2013, 13, 2895-2909.	1.3	51
59	Disease Co-Morbidity and the Human Wnt Signaling Pathway: A Network-Wise Study. OMICS A Journal of Integrative Biology, 2013, 17, 318-337.	1.0	5
60	iSeeRNA: identification of long intergenic non-coding RNA transcripts from transcriptome sequencing data. BMC Genomics, 2013, 14, S7.	1.2	141
61	A gene expression restriction network mediated by sense and antisense Alu sequences located on protein-coding messenger RNAs. BMC Genomics, 2013, 14, 325.	1.2	9
62	MGcV: the microbial genomic context viewer for comparative genome analysis. BMC Genomics, 2013, 14, 209.	1.2	53
63	RNAseq versus genome-predicted transcriptomes: a large population of novel transcripts identified in an Illumina-454 Hydra transcriptome. BMC Genomics, 2013, 14, 204.	1.2	61
64	dbNSFP v2.0: A Database of Human Non-synonymous SNVs and Their Functional Predictions and Annotations. Human Mutation, 2013, 34, E2393-E2402.	1.1	546
65	Getting the most out of parasitic helminth transcriptomes using HelmDB: Implications for biology and biotechnology. Biotechnology Advances, 2013, 31, 1109-1119.	6.0	23
66	Accuracy and coverage assessment of Oryctolagus cuniculus (rabbit) genes encoding immunoglobulins in the whole genome sequence assembly (OryCun2.0) and localization of the IGH locus to chromosome 20. Immunogenetics, 2013, 65, 749-762.	1.2	19
67	Recurrent mutations in multiple components of the cohesin complex in myeloid neoplasms. Nature Genetics, 2013, 45, 1232-1237.	9.4	334
68	Characterization of the DNA methylome and its interindividual variation in human peripheral blood monocytes. Epigenomics, 2013, 5, 255-269.	1.0	19
69	CELFish ways to modulate mRNA decay. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 695-707.	0.9	43
70	Role of protein farnesylation events in the ABA-mediated regulation of the Pinoresinolâ€“Lariciresinol Reductase 1 (LuPLR1) gene expression and lignan biosynthesis in flax (Linum usitatissimum L.). Plant Physiology and Biochemistry, 2013, 72, 96-111.	2.8	25
71	Condensin I associates with structural and gene regulatory regions in vertebrate chromosomes. Nature Communications, 2013, 4, 2537.	5.8	70
72	Expression and regulation of intergenic long noncoding RNAs during T cell development and differentiation. Nature Immunology, 2013, 14, 1190-1198.	7.0	414

#	Article	IF	Citations
73	A genomic update on clostridial phylogeny: <scp>G</scp>ramâ€negative spore formers and other misplaced clostridia. Environmental Microbiology, 2013, 15, 2631-2641.	1.8	771
74	Automated interpretation of metabolic capacity from genome and metagenome sequences. Quantitative Biology, 2013, 1, 192-200.	0.3	1
75	Translational Repression and eIF4A2 Activity Are Critical for MicroRNA-Mediated Gene Regulation. Science, 2013, 340, 82-85.	6.0	290
76	Screening metatranscriptomes for toxin genes as functional drivers of human colorectal cancer. Bailliere's Best Practice and Research in Clinical Gastroenterology, 2013, 27, 85-99.	1.0	36
77	The Genome of the Alga-Associated Marine Flavobacterium Formosa agariphila KMM 3901 ^T Reveals a Broad Potential for Degradation of Algal Polysaccharides. Applied and Environmental Microbiology, 2013, 79, 6813-6822.	1.4	222
78	Computational Largeâ€Scale Mapping of Proteinâ€Protein Interactions Using Structural Complexes. Current Protocols in Protein Science, 2013, 73, 3.9.1-3.9.9.	2.8	2
79	Transparency tools in gene patenting for informing policy and practice. Nature Biotechnology, 2013, 31, 1086-1093.	9.4	22
80	Organization and regulation of the arsenite oxidase operon of the moderately acidophilic and facultative chemoautotrophic Thiomonas arsenitoxydans. Extremophiles, 2013, 17, 911-920.	0.9	18
81	Web Apollo: a web-based genomic annotation editing platform. Genome Biology, 2013, 14, R93.	13.9	329
82	Role of conserved cis-regulatory elements in the post-transcriptional regulation of the human MECP2 gene involved in autism. Human Genomics, 2013, 7, 19.	1.4	11
83	Large-scale study of long non-coding RNA functions based on structure and expression features. Science China Life Sciences, 2013, 56, 953-959.	2.3	8
84	Comparison of RefSeq protein-coding regions in human and vertebrate genomes. BMC Genomics, 2013, 14, 654.	1.2	27
85	Genome resolved analysis of a premature infant gut microbial community reveals a Varibaculum cambriense genome and a shift towards fermentation-based metabolism during the third week of life. Microbiome, 2013, 1, 30.	4.9	50
86	Rapid construction of metabolic models for a family of Cyanobacteria using a multiple source annotation workflow. BMC Systems Biology, 2013, 7, 142.	3.0	28
87	Statistics for approximate gene clusters. BMC Bioinformatics, 2013, 14, S14.	1.2	11
88	Genome-wide analyses implicate 33 loci in heritable dog osteosarcoma, including regulatory variants near CDKN2A/B. Genome Biology, 2013, 14, R132.	13.9	132
89	STaRRRT: a table of short tandem repeats in regulatory regions of the human genome. BMC Genomics, 2013, 14, 795.	1.2	33
90	Simple and Efficient Identification of Rare Recessive Pathologically Important Sequence Variants from Next Generation Exome Sequence Data. Human Mutation, 2013, 34, 945-952.	1.1	4

#	Article	IF	Citations
91	Towards Precision Medicine: Advances in Computational Approaches for the Analysis of Human Variants. Journal of Molecular Biology, 2013, 425, 4047-4063.	2.0	122
92	Cycles in spatial and temporal chromosomal organization driven by the circadian clock. Nature Structural and Molecular Biology, 2013, 20, 1206-1213.	3.6	110
93	Genome-wide sequencing of<i>Phytophthora lateralis</i>reveals genetic variation among isolates from Lawson cypress (<i>Chamaecyparis lawsoniana</i>) in Northern Ireland. FEMS Microbiology Letters, 2013, 344, 179-185.	0.7	47
94	The humankind genome: from genetic diversity to the origin of human diseases. Genome, 2013, 56, 705-716.	0.9	18
95	Whole-Genome Sequencing of the Akata and Mutu Epstein-Barr Virus Strains. Journal of Virology, 2013, 87, 1172-1182.	1.5	98
96	Proteomics-Based Methods for Discovery, Quantification, and Validation of Proteinâ€“Protein Interactions. Analytical Chemistry, 2013, 85, 749-768.	3.2	85
97	Gene expression analysis of novel genes in the prefrontal cortex of major depressive disorder subjects. Progress in Neuro-Psychopharmacology and Biological Psychiatry, 2013, 43, 126-133.	2.5	59
98	A library of TAL effector nucleases spanning the human genome. Nature Biotechnology, 2013, 31, 251-258.	9.4	344
99	VariBench: A Benchmark Database for Variations. Human Mutation, 2013, 34, 42-49.	1.1	129
100	Density peaks of paralog pairs in human and mouse genomes. Gene, 2013, 527, 55-61.	1.0	3
101	Sost and its paralog Sostdc1 coordinate digit number in a Gli3-dependent manner. Developmental Biology, 2013, 383, 90-105.	0.9	47
102	Identification of a possible respiratory arsenate reductase in Denitrovibrio acetiphilus, a member of the phylum Deferribacteres. Archives of Microbiology, 2013, 195, 661-670.	1.0	11
103	Development of an ELISA for the quantification of the C-terminal decapeptide prothymosin Î±(100â€“109) in sera of mice infected with bacteria. Journal of Immunological Methods, 2013, 395, 54-62.	0.6	10
104	SNVDis: A Proteome-wide Analysis Service for Evaluating nsSNVs in Protein Functional Sites and Pathways. Genomics, Proteomics and Bioinformatics, 2013, 11, 122-126.	3.0	15
105	A new family of proteins related to the HEAT-like repeat DNA glycosylases with affinity for branched DNA structures. Journal of Structural Biology, 2013, 183, 66-75.	1.3	8
106	Regulation of glycogen synthase from mammalian skeletal muscle â€“ a unifying view of allosteric and covalent regulation. FEBS Journal, 2013, 280, 2-27.	2.2	39
107	Cyclic di-GMP: the First 25 Years of a Universal Bacterial Second Messenger. Microbiology and Molecular Biology Reviews, 2013, 77, 1-52.	2.9	1,479
108	Detecting and visualizing gene fusions. Methods, 2013, 59, S24-S28.	1.9	13

#	ARTICLE	IF	CITATIONS
109	General Framework for Meta-analysis of Rare Variants in Sequencing Association Studies. American Journal of Human Genetics, 2013, 93, 42-53.	2.6	211
110	Computational meta'omics for microbial community studies. Molecular Systems Biology, 2013, 9, 666.	3.2	253
111	Mutations in Interaction Surfaces Differentially Impact E. coli Hfq Association with Small RNAs and Their mRNA Targets. Journal of Molecular Biology, 2013, 425, 3678-3697.	2.0	127
112	Ribosome Profiling Provides Evidence that Large Noncoding RNAs Do Not Encode Proteins. Cell, 2013, 154, 240-251.	13.5	678
113	lincRNAs: Genomics, Evolution, and Mechanisms. Cell, 2013, 154, 26-46.	13.5	2,337
114	Analyses of the general rule on residue pair frequencies in local amino acid sequences of soluble, ordered proteins. Protein Science, 2013, 22, 725-733.	3.1	2
115	Natural Selection in a Bangladeshi Population from the Cholera-Endemic Ganges River Delta. Science Translational Medicine, 2013, 5, 192ra86.	5.8	77
116	Epigenomic Analysis of Multilineage Differentiation of Human Embryonic Stem Cells. Cell, 2013, 153, 1134-1148.	13.5	689
117	Genome-wide association study for backfat thickness in Canchim beef cattle using Random Forest approach. BMC Genetics, 2013, 14, 47.	2.7	32
118	Small, Highly Active DNAs That Hydrolyze DNA. Journal of the American Chemical Society, 2013, 135, 9121-9129.	6.6	134
119	Whole genome sequencing in the prevention and control of Staphylococcus aureus infection. Journal of Hospital Infection, 2013, 83, 14-21.	1.4	59
120	AVISPA: a web tool for the prediction and analysis of alternative splicing. Genome Biology, 2013, 14, R114.	13.9	37
122	Full-length Transcriptome-based H-InvDB Throws a New Light on Chromosome-centric Proteomics. Journal of Proteome Research, 2013, 12, 62-66.	1.8	7
123	Many human accelerated regions are developmental enhancers. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20130025.	1.8	188
124	Genomeâ€Scale Sequencing to Identify Genes Involved in Mendelian Disorders. Current Protocols in Human Genetics, 2013, 79, Unit 6.13..	3.5	4
125	Viral Metagenome Annotation Pipeline. , 2013, , 1-12.		1
126	Transcriptome analyses of the human retina identify unprecedented transcript diversity and 3.5 Mb of novel transcribed sequence via significant alternative splicing and novel genes. BMC Genomics, 2013, 14, 486.	1.2	151
127	Novel Burkholderia mallei Virulence Factors Linked to Specific Host-Pathogen Protein Interactions. Molecular and Cellular Proteomics, 2013, 12, 3036-3051.	2.5	38

#	ARTICLE	IF	CITATIONS
128	Updating RNA-Seq analyses after re-annotation. Bioinformatics, 2013, 29, 1631-1637.	1.8	23
129	Clinical analysis of genome next-generation sequencing data using the Omicia platform. Expert Review of Molecular Diagnostics, 2013, 13, 529-540.	1.5	31
130	Deep mutational scanning of an RRM domain of the <i>Saccharomyces cerevisiae</i> poly(A)-binding protein. Rna, 2013, 19, 1537-1551.	1.6	207
131	HMGN1 Modulates Nucleosome Occupancy and DNase I Hypersensitivity at the CpG Island Promoters of Embryonic Stem Cells. Molecular and Cellular Biology, 2013, 33, 3377-3389.	1.1	68
132	Computational analysis of bacterial RNA-Seq data. Nucleic Acids Research, 2013, 41, e140-e140.	6.5	573
133	Autoreactivity and Exceptional CDR Plasticity (but Not Unusual Polyspecificity) Hinder Elicitation of the Anti-HIV Antibody 4E10. PLoS Pathogens, 2013, 9, e1003639.	2.1	44
134	Viral Proteins Originated De Novo by Overprinting Can Be Identified by Codon Usage: Application to the â€œGene Nurseryâ€• of Deltaretroviruses. PLoS Computational Biology, 2013, 9, e1003162.	1.5	61
135	Isoforms of elongation factor eEF1A may be differently regulated at post-transcriptional level in breast cancer progression. Biopolymers and Cell, 2013, 29, 55-63.	0.1	4
136	The Complete Exosome Workflow Solution: From Isolation to Characterization of RNA Cargo. BioMed Research International, 2013, 2013, 1-15.	0.9	142
137	The COMBREX Project: Design, Methodology, and Initial Results. PLoS Biology, 2013, 11, e1001638.	2.6	54
138	Detecting and Comparing Non-Coding RNAs in the High-Throughput Era. International Journal of Molecular Sciences, 2013, 14, 15423-15458.	1.8	22
139	Differences in Gastric Carcinoma Microenvironment Stratify According to EBV Infection Intensity: Implications for Possible Immune Adjuvant Therapy. PLoS Pathogens, 2013, 9, e1003341.	2.1	140
140	H-InvDB in 2013: an omics study platform for human functional gene and transcript discovery. Nucleic Acids Research, 2013, 41, D915-D919.	6.5	22
141	Molecular detection of bacterial contamination in gnotobiotic rodent units. Gut Microbes, 2013, 4, 361-370.	4.3	39
142	EBARDenovo: highly accurate <i>de novo</i> assembly of RNA-Seq with efficient chimera-detection. Bioinformatics, 2013, 29, 1004-1010.	1.8	33
143	Characterization of the human ESC transcriptome by hybrid sequencing. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, E4821-30.	3.3	316
144	Explaining microbial phenotypes on a genomic scale: GWAS for microbes. Briefings in Functional Genomics, 2013, 12, 366-380.	1.3	57
145	Long non-coding RNA identification over mouse brain development by integrative modeling of chromatin and genomic features. Nucleic Acids Research, 2013, 41, 10044-10061.	6.5	65

#	ARTICLE	IF	CITATIONS
146	MicroScopeâ€"an integrated microbial resource for the curation and comparative analysis of genomic and metabolic data. Nucleic Acids Research, 2013, 41, D636-D647.	6.5	406
147	Epstein-Barr Virus and Human Herpesvirus 6 Detection in a Non-Hodgkin's Diffuse Large B-Cell Lymphoma Cohort by Using RNA Sequencing. Journal of Virology, 2013, 87, 13059-13062.	1.5	35
148	The Mouse Genome Database: Genotypes, Phenotypes, and Models of Human Disease. Nucleic Acids Research, 2013, 41, D885-D891.	6.5	61
149	Accurate Identification and Analysis of Human mRNA Isoforms Using Deep Long Read Sequencing. G3: Genes, Genomes, Genetics, 2013, 3, 387-397.	0.8	59
150	Non-redundant compendium of human ncRNA genes in GeneCards. Bioinformatics, 2013, 29, 255-261.	1.8	41
151	Laser capture microdissectionâ€"reduced representation bisulfite sequencing (LCM-RRBS) maps changes in DNA methylation associated with gonadectomy-induced adrenocortical neoplasia in the mouse. Nucleic Acids Research, 2013, 41, e116-e116.	6.5	38
152	Rfam 11.0: 10 years of RNA families. Nucleic Acids Research, 2013, 41, D226-D232.	6.5	745
153	JBioWH: an open-source Java framework for bioinformatics data integration. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat051-bat051.	1.4	8
154	Incorporating the human gene annotations in different databases significantly improved transcriptomic and genetic analyses. Rna, 2013, 19, 479-489.	1.6	29
155	Evolutionary history of the TBP-domain superfamily. Nucleic Acids Research, 2013, 41, 2832-2845.	6.5	27
156	Gene Expression Signatures of Coronary Heart Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2013, 33, 1418-1426.	1.1	105
157	RhesusBase: a knowledgebase for the monkey research community. Nucleic Acids Research, 2013, 41, D892-D905.	6.5	27
158	Specificity between Lactobacilli and Hymenopteran Hosts Is the Exception Rather than the Rule. Applied and Environmental Microbiology, 2013, 79, 1803-1812.	1.4	75
159	EcoGene-RefSeq: EcoGene tools applied to the RefSeq prokaryotic genomes. Bioinformatics, 2013, 29, 1917-1918.	1.8	10
160	Photosystem II Photochemistry and Phycobiliprotein of the Red AlgaeKappaphycus alvareziiand Their Implications for Light Adaptation. BioMed Research International, 2013, 2013, 1-9.	0.9	7
161	YY1TargetDB: an integral information resource for Yin Yang 1 target loci. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat007.	1.4	8
162	Mineralogical Study of a Biologically-Based Treatment System That Removes Arsenic, Zinc and Copper from Landfill Leachate. Minerals (Basel, Switzerland), 2013, 3, 427-449.	0.8	11
163	Evidence for a host role in thermotolerance divergence between populations of the mustard hill coral (<i><scp>P</scp>orites astreoides</i>) from different reef environments. Molecular Ecology, 2013, 22, 4335-4348.	2.0	158

#	ARTICLE	IF	CITATIONS
164	How many signal peptides are there in bacteria?. Environmental Microbiology, 2013, 15, 983-990.	1.8	29
165	A meta-analysis of the genomic and transcriptomic composition of complex life. Cell Cycle, 2013, 12, 2061-2072.	1.3	134
166	MitoFish and MitoAnnotator: A Mitochondrial Genome Database of Fish with an Accurate and Automatic Annotation Pipeline. Molecular Biology and Evolution, 2013, 30, 2531-2540.	3.5	651
167	The expanding superfamily of gelsolin homology domain proteins. Cytoskeleton, 2013, 70, 775-795.	1.0	39
168	eALPS: Estimating Abundance Levels in Pooled Sequencing Using Available Genotyping Data. Journal of Computational Biology, 2013, 20, 861-877.	0.8	4
169	Rice Annotation Project Database (RAP-DB): An Integrative and Interactive Database for Rice Genomics. Plant and Cell Physiology, 2013, 54, e6-e6.	1.5	614
170	OrtholugeDB: a bacterial and archaeal orthology resource for improved comparative genomic analysis. Nucleic Acids Research, 2013, 41, D366-D376.	6.5	73
171	The Complexity of Thyroid Transcription Factor 1 with Both Pro- and Anti-oncogenic Activities. Journal of Biological Chemistry, 2013, 288, 24992-25000.	1.6	29
172	Polymorphisms affecting miRNA regulation: a new level of genetic variation affecting disorders and diseases of the human CNS. Future Neurology, 2013, 8, 411-431.	0.9	3
173	Exploring nucleo-cytoplasmic large DNA viruses in Tara Oceans microbial metagenomes. ISME Journal, 2013, 7, 1678-1695.	4.4	185
174	CNCTDISCRIMINATOR: CODING AND NONCODING TRANSCRIPT DISCRIMINATOR â€" AN EXCURSION THROUGH HYPOTHESIS LEARNING AND ENSEMBLE LEARNING APPROACHES. Journal of Bioinformatics and Computational Biology, 2013, 11, 1342002.	0.3	6
175	YM500: a small RNA sequencing (smRNA-seq) database for microRNA research. Nucleic Acids Research, 2013, 41, D285-D294.	6.5	60
176	GenomeRNAi: a database for cell-based and in vivo RNAi phenotypes, 2013 update. Nucleic Acids Research, 2013, 41, D1021-D1026.	6.5	135
177	Early bioenergetic evolution. Philosophical Transactions of the Royal Society B: Biological Sciences, 2013, 368, 20130088.	1.8	199
179	Genome sequence of the moderately halophilic bacterium Salinicoccus carnicancri type strain CrmT (= DSM 23852T). Standards in Genomic Sciences, 2013, 8, 255-263.	1.5	11
180	Genome Diversity of Spore-Forming <i>Firmicutes</i>. Microbiology Spectrum, 2013, 1, .	1.2	153
181	Transcription-factor occupancy at HOT regions quantitatively predicts RNA polymerase recruitment in five human cell lines. BMC Genomics, 2013, 14, 720.	1.2	35
182	Whole Genome Sequencing and Comparative Analysis of Bartonella bacilliformis Strain INS, the Causative Agent of Carrion's Disease. Genome Announcements, 2013, 1, .	0.8	6

#	ARTICLE	IF	CITATIONS
183	MisPred: a resource for identification of erroneous protein sequences in public databases. Database: the Journal of Biological Databases and Curation, 2013, 2013, bat053.	1.4	17
184	Analysis of long non-coding RNA expression profiles in gastric cancer. World Journal of Gastroenterology, 2013, 19, 3658.	1.4	177
185	Next-Generation Sequencing Identifies Transportin 3 as the Causative Gene for LGMD1F. PLoS ONE, 2013, 8, e63536.	1.1	69
186	Identification and Characterization of Long Non-Coding RNAs Related to Mouse Embryonic Brain Development from Available Transcriptomic Data. PLoS ONE, 2013, 8, e71152.	1.1	55
187	A Metastable Equilibrium Model for the Relative Abundances of Microbial Phyla in a Hot Spring. PLoS ONE, 2013, 8, e72395.	1.1	23
188	INDIGO â€" INtegrated Data Warehouse of MIcrobial GenOmes with Examples from the Red Sea Extremophiles. PLoS ONE, 2013, 8, e82210.	1.1	83
189	Prioritization of Copy Number Variation Loci Associated with Autism from AutDBâ€"An Integrative Multi-Study Genetic Database. PLoS ONE, 2013, 8, e66707.	1.1	13
190	Ceruloplasmin Is a Novel Adipokine Which Is Overexpressed in Adipose Tissue of Obese Subjects and in Obesity-Associated Cancer Cells. PLoS ONE, 2014, 9, e80274.	1.1	50
191	C2orf62 and TTC17 Are Involved in Actin Organization and Ciliogenesis in Zebrafish and Human. PLoS ONE, 2014, 9, e86476.	1.1	19
192	Structural Properties of Prokaryotic Promoter Regions Correlate with Functional Features. PLoS ONE, 2014, 9, e88717.	1.1	22
193	Transcriptional Regulation of YWHAZ, the Gene Encoding 14-3-3Î¶. PLoS ONE, 2014, 9, e93480.	1.1	17
194	Deep-Sequencing Method for Quantifying Background Abundances of Symbiodinium Types: Exploring the Rare Symbiodinium Biosphere in Reef-Building Corals. PLoS ONE, 2014, 9, e94297.	1.1	135
195	Deep Sequencing Reveals New Aspects of Progesterone Receptor Signaling in Breast Cancer Cells. PLoS ONE, 2014, 9, e98404.	1.1	12
196	A Pseudomonas aeruginosa EF-Hand Protein, EfhP (PA4107), Modulates Stress Responses and Virulence at High Calcium Concentration. PLoS ONE, 2014, 9, e98985.	1.1	39
197	dbCerEx: A Web-Based Database for the Analysis of Cervical Cancer Transcriptomes. PLoS ONE, 2014, 9, e99834.	1.1	2
198	Novel Insights into the Regulatory Architecture of CD4+ T Cells in Rheumatoid Arthritis. PLoS ONE, 2014, 9, e100690.	1.1	22
199	Detection Theory in Identification of RNA-DNA Sequence Differences Using RNA-Sequencing. PLoS ONE, 2014, 9, e112040.	1.1	7
200	High-Performance Integrated Virtual Environment (HIVE) Tools and Applications for Big Data Analysis. Genes, 2014, 5, 957-981.	1.0	76

#	Article	IF	Citations
201	Long noncoding RNAs in spermatogenesis: insights from recent high-throughput transcriptome studies. Reproduction, 2014, 147, R131-R141.	1.1	106
202	Investigating co-evolution of functionally associated phosphosites in human. Molecular Genetics and Genomics, 2014, 289, 1217-1223.	1.0	0
203	PATRIC, the bacterial bioinformatics database and analysis resource. Nucleic Acids Research, 2014, 42, D581-D591.	6.5	1,222
204	Ensembl 2014. Nucleic Acids Research, 2014, 42, D749-D755.	6.5	1,211
205	Identification of non-coding RNAs with a new composite feature in the Hybrid Random Forest Ensemble algorithm. Nucleic Acids Research, 2014, 42, e93-e93.	6.5	42
206	Pleiotropic Mutations Are Subject to Strong Stabilizing Selection. Genetics, 2014, 197, 1051-1062.	1.2	38
207	Unraveling the clonal hierarchy of somatic genomic aberrations. Genome Biology, 2014, 15, 439.	3.8	80
208	MotorPlex provides accurate variant detection across large muscle genes both in single myopathic patients and in pools of DNA samples. Acta Neuropathologica Communications, 2014, 2, 100.	2.4	76
209	Prediction of DNA binding motifs from 3D models of transcription factors; identifying TLX3 regulated genes. Nucleic Acids Research, 2014, 42, 13500-13512.	6.5	74
210	Current status and new features of the Consensus Coding Sequence database. Nucleic Acids Research, 2014, 42, D865-D872.	6.5	140
211	Development of an experimental model to assess the bioavailability of zinc in practical piglet diets. Archives of Animal Nutrition, 2014, 68, 73-92.	0.9	30
212	Filovirus RefSeq Entries: Evaluation and Selection of Filovirus Type Variants, Type Sequences, and Names. Viruses, 2014, 6, 3663-3682.	1.5	49
213	A framework for organizing cancer-related variations from existing databases, publications and NGS data using a High-performance Integrated Virtual Environment (HIVE). Database: the Journal of Biological Databases and Curation, 2014, 2014, bau022.	1.4	62
214	PeptideManager: a peptide selection tool for targeted proteomic studies involving mixed samples from different species. Frontiers in Genetics, 2014, 5, 305.	1.1	18
215	The Proceedings of the Second International Conference on Communications, Signal Processing, and Systems. Lecture Notes in Electrical Engineering, 2014, , .	0.3	6
216	FixPred: a resource for correction of erroneous protein sequences. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau032.	1.4	9
217	Ecological Consistency of SSU rRNA-Based Operational Taxonomic Units at a Global Scale. PLoS Computational Biology, 2014, 10, e1003594.	1.5	85
218	Long Non-Coding RNA and Alternative Splicing Modulations in Parkinson's Leukocytes Identified by RNA Sequencing. PLoS Computational Biology, 2014, 10, e1003517.	1.5	167

#	ARTICLE	IF	CITATIONS
219	Comparison of REST Cistromes across Human Cell Types Reveals Common and Context-Specific Functions. PLoS Computational Biology, 2014, 10, e1003671.	1.5	40
220	Methods of Molecular Study. , 2014, , 77-90.		3
221	Microbial Contamination in Next Generation Sequencing: Implications for Sequence-Based Analysis of Clinical Samples. PLoS Pathogens, 2014, 10, e1004437.	2.1	159
222	Applying the ResFinder and VirulenceFinder web-services for easy identification of acquired antibiotic resistance and<i>E. coli</i>virulence genes in bacteriophage and prophage nucleotide sequences. Bacteriophage, 2014, 4, e27943.	1.9	313
223	Forty-Four Novel Protein-Coding Loci Discovered Using a Proteomics Informed by Transcriptomics (PIT) Approach in Rat Male Germ Cells1. Biology of Reproduction, 2014, 91, 123.	1.2	20
224	Complete Genome Sequence of Pluralibacter gergoviae FB2, an <i>N</i> -Acyl Homoserine Lactone-Degrading Strain Isolated from Packed Fish Paste. Genome Announcements, 2014, 2, .	0.8	5
225	High-Resolution Profiling of Novel Transcribed Regions During Rat Spermatogenesis1. Biology of Reproduction, 2014, 91, 5.	1.2	50
226	Gene Prediction and Annotation inPenstemon(Plantaginaceae): A Workflow for Marker Development from Extremely Low-Coverage Genome Sequencing. Applications in Plant Sciences, 2014, 2, 1400044.	0.8	15
227	Beyond genomic variation - comparison and functional annotation of three Brassica rapagenomes: a turnip, a rapid cycling and a Chinese cabbage. BMC Genomics, 2014, 15, 250.	1.2	87
228	The transcriptome of human pluripotent stem cells. Current Opinion in Genetics and Development, 2014, 28, 71-77.	1.5	14
229	Subcellular transcriptomicsâ€"Dissection of the mRNA composition in the axonal compartment of sensory neurons. Developmental Neurobiology, 2014, 74, 365-381.	1.5	104
230	A Comprehensive Phylogenetic and Structural Analysis of the Carcinoembryonic Antigen (CEA) Gene Family. Genome Biology and Evolution, 2014, 6, 1314-1326.	1.1	26
231	Global discovery of erythroid long noncoding RNAs reveals novel regulators of red cell maturation. Blood, 2014, 123, 570-581.	0.6	181
232	Whole-genome analyses resolve early branches in the tree of life of modern birds. Science, 2014, 346, 1320-1331.	6.0	1,583
233	Genome-wide transcriptome analysis of human epidermal melanocytes. Genomics, 2014, 104, 482-489.	1.3	35
234	Molecular diagnostics on the toxigenic potential of <i> <scp>F</scp> usarium </i> spp. plant pathogens. Journal of Applied Microbiology, 2014, 116, 1607-1620.	1.4	25
235	Hybrid Data Acquisition and Processing Strategies with Increased Throughput and Selectivity: pSMART Analysis for Global Qualitative and Quantitative Analysis. Journal of Proteome Research, 2014, 13, 5415-5430.	1.8	43
236	Choice of transcripts and software has a large effect on variant annotation. Genome Medicine, 2014, 6, 26.	3.6	158

#	ARTICLE	IF	CITATIONS
237	RiceWiki: a wiki-based database for community curation of rice genes. Nucleic Acids Research, 2014, 42, D1222-D1228.	6.5	19
238	Explaining the correlations among properties of mammalian promoters. Nucleic Acids Research, 2014, 42, 4823-4832.	6.5	7
239	NONCODEv4: exploring the world of long non-coding RNA genes. Nucleic Acids Research, 2014, 42, D98-D103.	6.5	398
240	Locus Reference Genomic: reference sequences for the reporting of clinically relevant sequence variants. Nucleic Acids Research, 2014, 42, D873-D878.	6.5	73
241	The Genome Database for Rosaceae (GDR): year 10 update. Nucleic Acids Research, 2014, 42, D1237-D1244.	6.5	195
242	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
243	Diversification of MIF immune regulators in aphids: link with agonistic and antagonistic interactions. BMC Genomics, 2014, 15, 762.	1.2	20
244	High-resolution functional annotation of human transcriptome: predicting isoform functions by a novel multiple instance-based label propagation method. Nucleic Acids Research, 2014, 42, e39-e39.	6.5	45
245	The Transporter Classification Database. Nucleic Acids Research, 2014, 42, D251-D258.	6.5	437
246	GWIPS-viz: development of a ribo-seq genome browser. Nucleic Acids Research, 2014, 42, D859-D864.	6.5	223
247	NGSmethDB: an updated genome resource for high quality, single-cytosine resolution methylomes. Nucleic Acids Research, 2014, 42, D53-D59.	6.5	22
248	NCG 4.0: the network of cancer genes in the era of massive mutational screenings of cancer genomes. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau015.	1.4	50
249	Multiple novel promoter-architectures revealed by decoding the hidden heterogeneity within the genome. Nucleic Acids Research, 2014, 42, 12388-12403.	6.5	14
250	COLOMBOS v2.0: an ever expanding collection of bacterial expression compendia: Table 1.. Nucleic Acids Research, 2014, 42, D649-D653.	6.5	38
251	SIMAPâ€"the database of all-against-all protein sequence similarities and annotations with new interfaces and increased coverage. Nucleic Acids Research, 2014, 42, D279-D284.	6.5	24
252	TargetRNA2: identifying targets of small regulatory RNAs in bacteria. Nucleic Acids Research, 2014, 42, W124-W129.	6.5	177
253	Differential Expression Analysis of Complex RNA-seq Experiments Using edgeR. , 2014, , 51-74.		119
254	Rare mutations associating with serum creatinine and chronic kidney disease. Human Molecular Genetics, 2014, 23, 6935-6943.	1.4	52

#	Article	IF	Citations
256	EXPANDS: expanding ploidy and allele frequency on nested subpopulations. Bioinformatics, 2014, 30, 50-60.	1.8	125
257	FusoBase: an online Fusobacterium comparative genomic analysis platform. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau082-bau082.	1.4	5
258	Vespucci: a system for building annotated databases of nascent transcripts. Nucleic Acids Research, 2014, 42, 2433-2447.	6.5	18
259	RNA CoMPASS: A Dual Approach for Pathogen and Host Transcriptome Analysis of RNA-Seq Datasets. PLoS ONE, 2014, 9, e89445.	1.1	38
260	sRNAbench: profiling of small RNAs and its sequence variants in single or multi-species high-throughput experiments. Methods in Next Generation Sequencing, 2014, 1, .	1.5	44
261	NPInter v2.0: an updated database of ncRNA interactions. Nucleic Acids Research, 2014, 42, D104-D108.	6.5	141
262	DPRP: a database of phenotype-specific regulatory programs derived from transcription factor binding data. Nucleic Acids Research, 2014, 42, D178-D183.	6.5	2
263	Differential protein occupancy profiling of the mRNA transcriptome. Genome Biology, 2014, 15, R15.	13.9	72
264	Kraken: ultrafast metagenomic sequence classification using exact alignments. Genome Biology, 2014, 15, R46.	13.9	3,540
265	CollecTF: a database of experimentally validated transcription factor-binding sites in Bacteria. Nucleic Acids Research, 2014, 42, D156-D160.	6.5	93
266	Lynx: a database and knowledge extraction engine for integrative medicine. Nucleic Acids Research, 2014, 42, D1007-D1012.	6.5	40
267	eggNOG v4.0: nested orthology inference across 3686 organisms. Nucleic Acids Research, 2014, 42, D231-D239.	6.5	526
268	IMG 4 version of the integrated microbial genomes comparative analysis system. Nucleic Acids Research, 2014, 42, D560-D567.	6.5	555
269	Integrating Pathways of Parkinson's Disease in a Molecular Interaction Map. Molecular Neurobiology, 2014, 49, 88-102.	1.9	231
270	Chemical Allergen Induced Perturbations of the Mouse Lymph Node DNA Methylome. Toxicological Sciences, 2014, 139, 350-361.	1.4	9
271	Diagnostic gene expression biomarkers of coral thermal stress. Molecular Ecology Resources, 2014, 14, 667-678.	2.2	65
272	Impact of human pathogenic micro-insertions and micro-deletions on post-transcriptional regulation. Human Molecular Genetics, 2014, 23, 3024-3034.	1.4	27
273	Computational Approaches and Resources in Single Amino Acid Substitutions Analysis Toward Clinical Research. Advances in Protein Chemistry and Structural Biology, 2014, 94, 365-423.	1.0	22

#	ARTICLE	IF	CITATIONS
274	Identification of low-frequency and rare sequence variants associated with elevated or reduced risk of type 2 diabetes. Nature Genetics, 2014, 46, 294-298.	9.4	294
275	CapR: revealing structural specificities of RNA-binding protein target recognition using CLIP-seq data. Genome Biology, 2014, 15, R16.	13.9	80
276	Non-synonymous variations in cancer and their effects on the human proteome: workflow for NGS data biocuration and proteome-wide analysis of TCGA data. BMC Bioinformatics, 2014, 15, 28.	1.2	12
277	A survey of software for genome-wide discovery of differential splicing in RNA-Seq data. Human Genomics, 2014, 8, 3.	1.4	66
278	Subtelomeric CTCF and cohesin binding site organization using improved subtelomere assemblies and a novel annotation pipeline. Genome Research, 2014, 24, 1039-1050.	2.4	64
279	Sailfish enables alignment-free isoform quantification from RNA-seq reads using lightweight algorithms. Nature Biotechnology, 2014, 32, 462-464.	9.4	594
280	Phylogenomic reconstruction of archaeal fatty acid metabolism. Environmental Microbiology, 2014, 16, 907-918.	1.8	67
281	Further Steps in TANGO: improved taxonomic assignment in metagenomics. Bioinformatics, 2014, 30, 17-23.	1.8	22
282	Transcriptomics of salinity tolerance capacity in Arctic charr (<i>Salvelinus alpinus</i>): a comparison of gene expression profiles between divergent QTL genotypes. Physiological Genomics, 2014, 46, 123-137.	1.0	32
283	Comparison of CAGE and RNA-seq transcriptome profiling using clonally amplified and single-molecule next-generation sequencing. Genome Research, 2014, 24, 708-717.	2.4	99
284	Jannovar: A Java Library for Exome Annotation. Human Mutation, 2014, 35, 548-555.	1.1	63
285	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2014, 42, D7-D17.	6.5	349
286	Emerging novel roles of neuropeptide Y in the retina: From neuromodulation to neuroprotection. Progress in Neurobiology, 2014, 112, 70-79.	2.8	23
287	Metaâ€analysis of deepâ€sequenced fungal communities indicates limited taxon sharing between studies and the presence of biogeographic patterns. New Phytologist, 2014, 201, 623-635.	3.5	106
288	Geochemical, metagenomic and metaproteomic insights into trace metal utilization by methaneâ€oxidizing microbial consortia in sulphidic marine sediments. Environmental Microbiology, 2014, 16, 1592-1611.	1.8	47
289	Plant and Animal Glycolate Oxidases Have a Common Eukaryotic Ancestor and Convergently Duplicated to Evolve Long-Chain 2-Hydroxy Acid Oxidases. Molecular Biology and Evolution, 2014, 31, 1089-1101.	3.5	51
290	featureCounts: an efficient general purpose program for assigning sequence reads to genomic features. Bioinformatics, 2014, 30, 923-930.	1.8	16,839
291	RNA viruses can hijack vertebrate microRNAs to suppress innate immunity. Nature, 2014, 506, 245-248.	13.7	195

#	Article	IF	Citations
292	Tools to Covisualize and Coanalyze Proteomic Data with Genomes and Transcriptomes: Validation of Genes and Alternative mRNA Splicing. Journal of Proteome Research, 2014, 13, 84-98.	1.8	40
293	Epigenetic Regulation of the DLK1-MEG3 MicroRNA Cluster in Human Type 2 Diabetic Islets. Cell Metabolism, 2014, 19, 135-145.	7.2	304
294	Evolutionary dynamics and tissue specificity of human long noncoding RNAs in six mammals. Genome Research, 2014, 24, 616-628.	2.4	318
295	<scp>exonsampler</scp>: a computer program for genomeâ€wide and candidate gene exon sampling for targeted nextâ€generation sequencing. Molecular Ecology Resources, 2014, 14, 1296-1301.	2.2	2
296	Average oxidation state of carbon in proteins. Journal of the Royal Society Interface, 2014, 11, 20131095.	1.5	33
297	Klebsormidium flaccidum genome reveals primary factors for plant terrestrial adaptation. Nature Communications, 2014, 5, 3978.	5.8	532
298	The tumor promoting activity of the EP4 receptor forÂprostaglandin E₂ in murine skin. Molecular Oncology, 2014, 8, 1626-1639.	2.1	16
299	Analysis of the Human Tissue-specific Expression by Genome-wide Integration of Transcriptomics and Antibody-based Proteomics. Molecular and Cellular Proteomics, 2014, 13, 397-406.	2.5	2,819
300	Cardiovascular Transcriptomics and Epigenomics Using Next-Generation Sequencing. Circulation: Cardiovascular Genetics, 2014, 7, 701-710.	5.1	14
301	Discovery of Novel Genes and Gene Isoforms by Integrating Transcriptomic and Proteomic Profiling from Mouse Liver. Journal of Proteome Research, 2014, 13, 2409-2419.	1.8	25
302	Comprehensive High-Throughput RNA Sequencing Analysis Reveals Contamination of Multiple Nasopharyngeal Carcinoma Cell Lines with HeLa Cell Genomes. Journal of Virology, 2014, 88, 10696-10704.	1.5	87
303	Genome Sequence-Based Discriminator for Vancomycin-Intermediate Staphylococcus aureus. Journal of Bacteriology, 2014, 196, 940-948.	1.0	29
304	RefSeq microbial genomes database: new representation and annotation strategy. Nucleic Acids Research, 2014, 42, D553-D559.	6.5	423
305	Structural analysis of atovaquone-inhibited cytochrome bc1 complex reveals the molecular basis of antimalarial drug action. Nature Communications, 2014, 5, 4029.	5.8	151
306	Clinical PathoScope: rapid alignment and filtration for accurate pathogen identification in clinical samples using unassembled sequencing data. BMC Bioinformatics, 2014, 15, 262.	1.2	55
307	Discovery and validation of novel and distinct RNA regulators for ribosomal protein S15 in diverse bacterial phyla. BMC Genomics, 2014, 15, 657.	1.2	21
308	Evolutionary and sequence-based relationships in bacterial AdoMet-dependent non-coding RNA methyltransferases. BMC Research Notes, 2014, 7, 440.	0.6	13
309	A systems biology approach reveals a link between systemic cytokines and skeletal muscle energy metabolism in a rodent smoking model and human COPD. Genome Medicine, 2014, 6, 59.	3.6	20

#	ARTICLE	IF	CITATIONS
310	A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32, 903-914.	9.4	883
311	The plastid ancestor originated among one of the major cyanobacterial lineages. Nature Communications, 2014, 5, 4937.	5.8	83
312	p53 haploinsufficiency and functional abnormalities in multiple myeloma. Leukemia, 2014, 28, 2066-2074.	3.3	72
313	Candidate genes and functional noncoding variants identified in a canine model of obsessive-compulsive disorder. Genome Biology, 2014, 15, R25.	13.9	78
314	Single Molecule Fluorescence Approaches Shed Light on Intracellular RNAs. Chemical Reviews, 2014, 114, 3224-3265.	23.0	73
315	Strategies to Design and Analyze Targeted Sequencing Data. Circulation: Cardiovascular Genetics, 2014, 7, 335-343.	5.1	18
316	Identification and characterization of long intergenic non-coding RNAs related to mouse liver development. Molecular Genetics and Genomics, 2014, 289, 1225-1235.	1.0	28
317	CDSbank: taxonomy-aware extraction, selection, renaming and formatting of protein-coding DNA or amino acid sequences. BMC Bioinformatics, 2014, 15, 61.	1.2	2
318	Microbiota diversity and gene expression dynamics in human oral biofilms. BMC Genomics, 2014, 15, 311.	1.2	142
319	Genetic distance as an alternative to physical distance for definition of gene units in association studies. BMC Genomics, 2014, 15, 408.	1.2	6
320	A community-based resource for automatic exome variant-calling and annotation in Mendelian disorders. BMC Genomics, 2014, 15, S5.	1.2	17
321	Sources of Individual Variability: Mirnas That Predispose to Neuropathic Pain Identified Using Genome-Wide Sequencing. Molecular Pain, 2014, 10, 1744-8069-10-22.	1.0	41
322	Frequent, independent transfers of a catabolic gene from bacteria to contrasted filamentous eukaryotes. Proceedings of the Royal Society B: Biological Sciences, 2014, 281, 20140848.	1.2	35
323	Meta-Analysis of Sequencing Studies With Heterogeneous Genetic Associations. Genetic Epidemiology, 2014, 38, 389-401.	0.6	27
324	Sequence determinants of prokaryotic gene expression level under heat stress. Gene, 2014, 551, 92-102.	1.0	2
325	An insight into the exploration of druggable genome of Streptococcus gordonii for the identification of novel therapeutic candidates. Genomics, 2014, 104, 203-214.	1.3	36
326	Serum proteomics for gastric cancer. Clinica Chimica Acta, 2014, 431, 179-184.	0.5	32
327	Structure activity relationship studies of 3-arylsulfonyl-pyrido[1,2-a]pyrimidin-4-imines as potent 5-HT6 antagonists. Bioorganic and Medicinal Chemistry, 2014, 22, 1782-1790.	1.4	13

#	Article	IF	Citations
328	Decoding complex patterns of genomic rearrangement in hepatocellular carcinoma. Genomics, 2014, 103, 189-203.	1.3	49
329	High-throughput transcription profiling identifies putative epigenetic regulators of hematopoiesis. Blood, 2014, 123, e46-e57.	0.6	21
330	MetaRef: a pan-genomic database for comparative and community microbial genomics. Nucleic Acids Research, 2014, 42, D617-D624.	6.5	51
331	Signatures of Natural Selection on Mutations of Residues with Multiple Posttranslational Modifications. Molecular Biology and Evolution, 2014, 31, 1641-1645.	3.5	10
332	AroER Tri-Screen Is a Biologically Relevant Assay for Endocrine Disrupting Chemicals Modulating the Activity of Aromatase and/or the Estrogen Receptor. Toxicological Sciences, 2014, 139, 198-209.	1.4	27
333	GC skew and mitochondrial origins of replication. Mitochondrion, 2014, 17, 56-66.	1.6	35
334	Integrative analysis of many RNA-seq datasets to study alternative splicing. Methods, 2014, 67, 313-324.	1.9	18
335	Open source libraries and frameworks for mass spectrometry based proteomics: A developer's perspective. Biochimica Et Biophysica Acta - Proteins and Proteomics, 2014, 1844, 63-76.	1.1	67
336	A distributed computational search strategy for the identification of diagnostics targets: Application to finding aptamer targets for methicillin-resistant staphylococci. Journal of Integrative Bioinformatics, 2014, 11, 80-92.	1.0	2
337	Dynamics of enhancers in myeloid antigen presenting cells upon LPS stimulation. BMC Genomics, 2014, 15, S4.	1.2	2
338	BCL2DB: database of BCL-2 family members and BH3-only proteins. Database: the Journal of Biological Databases and Curation, 2014, 2014, bau013-bau013.	1.4	17
339	â—¾ Quality Control and Preprocessing. , 2014, , 66-87.		1
340	Epigenomic Reprogramming of Adult Cardiomyocyte-Derived Cardiac Progenitor Cells. Scientific Reports, 2015, 5, 17686.	1.6	25
341	Methods for biological data integration: perspectives and challenges. Journal of the Royal Society Interface, 2015, 12, 20150571.	1.5	196
342	Fundamentals of protein interaction network mapping. Molecular Systems Biology, 2015, 11, 848.	3.2	226
343	Ancient pathogen DNA in archaeological samples detected with a Microbial Detection Array. Scientific Reports, 2014, 4, 4245.	1.6	48
344	Marine amoebae with cytoplasmic and perinuclear symbionts deeply branching in the Gammaproteobacteria. Scientific Reports, 2015, 5, 13381.	1.6	36
345	Sequence variants from whole genome sequencing a large group of Icelanders. Scientific Data, 2015, 2, 150011.	2.4	59

#	ARTICLE	IF	CITATIONS
346	Metagenomics: Assigning Functional Status to Community Gene Content. , 2015, , 2.4.4-1-2.4.4-7.		0
347	Comprehensive comparative homeobox gene annotation in human and mouse. Database: the Journal of Biological Databases and Curation, 2015, 2015, .	1.4	12
348	Identification of the relationship between the variability of the expression of signaling pathway genes in the human brain and the affinity of TATA-binding protein to their promoters. Russian Journal of Genetics: Applied Research, 2015, 5, 626-634.	0.4	6
349	Modeling of interaction between cytochrome c and the WD domains of Apaf-1: bifurcated salt bridges underlying apoptosome assembly. Biology Direct, 2015, 10, 29.	1.9	19
350	Draft genome sequences of Chrysoporthe austroafricana, Diplodia scrobiculata, Fusarium nygamai, Leptographium lundbergii, Limonomyces culmigenus, Stagonosporopsis tanaceti, and Thielaviopsis punctulata. IMA Fungus, 2015, 6, 233-248.	1.7	46
351	Complete genome sequence of Salinicoccus halodurans H3B36, isolated from the Qaidam Basin in China. Standards in Genomic Sciences, 2015, 10, 116.	1.5	7
352	IIIDB: a database for isoform-isoform interactions and isoform network modules. BMC Genomics, 2015, 16, S10.	1.2	31
353	Accurate inference of isoforms from multiple sample RNA-Seq data. BMC Genomics, 2015, 16, S15.	1.2	11
354	Using host-pathogen protein interactions to identify and characterize Francisella tularensis virulence factors. BMC Genomics, 2015, 16, 1106.	1.2	33
355	An interactive web application for the dissemination of human systems immunology data. Journal of Translational Medicine, 2015, 13, 196.	1.8	49
356	Use of semantic workflows to enhance transparency and reproducibility in clinical omics. Genome Medicine, 2015, 7, 73.	3.6	16
359	Metazoan Remaining Genes for Essential Amino Acid Biosynthesis: Sequence Conservation and Evolutionary Analyses. Nutrients, 2015, 7, 1-16.	1.7	9
360	Similar Microbial Communities Found on Two Distant Seafloor Basalts. Frontiers in Microbiology, 2015, 6, 1409.	1.5	14
361	Metagenomic Profiling of Known and Unknown Microbes with MicrobeGPS. PLoS ONE, 2015, 10, e0117711.	1.1	23
362	Complete Genome Sequence of Borrelia afzelii K78 and Comparative Genome Analysis. PLoS ONE, 2015, 10, e0120548.	1.1	16
363	Network-Based Isoform Quantification with RNA-Seq Data for Cancer Transcriptome Analysis. PLoS Computational Biology, 2015, 11, e1004465.	1.5	17
364	A Novel Quality Measure and Correction Procedure for the Annotation of Microbial Translation Initiation Sites. PLoS ONE, 2015, 10, e0133691.	1.1	4
365	Nucleosome Organization in Human Embryonic Stem Cells. PLoS ONE, 2015, 10, e0136314.	1.1	22

#	ARTICLE	IF	CITATIONS
366	An Efficient Approach for the Development of Locus Specific Primers in Bread Wheat (Triticum) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 74 10, e0142746.	1.1	5
367	ReprOlive: a database with linked data for the olive tree (Olea europaea L.) reproductive transcriptome. Frontiers in Plant Science, 2015, 6, 625.	1.7	58
368	Predicting effective microRNA target sites in mammalian mRNAs. ELife, 2015, 4, .	2.8	5,779
369	Update on RefSeq microbial genomes resources. Nucleic Acids Research, 2015, 43, D599-D605.	6.5	125
370	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2015, 43, D6-D17.	6.5	275
371	GenBank. Nucleic Acids Research, 2015, 43, D30-D35.	6.5	371
372	Sigma: Strain-level inference of genomes from metagenomic analysis for biosurveillance. Bioinformatics, 2015, 31, 170-177.	1.8	90
373	Integrative structural annotation of de novo RNA-Seq provides an accurate reference gene set of the enormous genome of the onion (Allium cepa L.). DNA Research, 2015, 22, 19-27.	1.5	59
374	New insight into the gut microbiome through metagenomics. Advances in Genomics and Genetics, 0, , 77.	0.8	10
375	BEACON: automated tool for Bacterial GEnome Annotation ComparisON. BMC Genomics, 2015, 16, 616.	1.2	26
376	Duplex stem-loop-containing quadruplex motifs in the human genome: a combined genomic and structural study. Nucleic Acids Research, 2015, 43, 5630-5646.	6.5	66
377	LSD1 is essential for oocyte meiotic progression by regulating CDC25B expression in mice. Nature Communications, 2015, 6, 10116.	5.8	38
378	miR-17-92 fine-tunes MYC expression and function to ensure optimal B cell lymphoma growth. Nature Communications, 2015, 6, 8725.	5.8	88
379	Whole-Genome Sequence of Stenotrophomonas maltophilia ZBG7B Reveals Its Biotechnological Potential. Genome Announcements, 2015, 3, .	0.8	4
380	Genome-wide discovery of miRNAs using ensembles of machine learning algorithms and logistic regression. International Journal of Data Mining and Bioinformatics, 2015, 13, 338.	0.1	2
381	Biochemical analysis of pistol self-cleaving ribozymes. Rna, 2015, 21, 1852-1858.	1.6	59
382	Identification of 4438 novel lincRNAs involved in mouse pre-implantation embryonic development. Molecular Genetics and Genomics, 2015, 290, 685-697.	1.0	24
383	Comparison of sister species identifies factors underpinning plastid compatibility in green sea slugs. Proceedings of the Royal Society B: Biological Sciences, 2015, 282, 20142519.	1.2	44

#	ARTICLE	IF	CITATIONS
384	Cross-talk between ER and HER2 regulates c-MYC-mediated glutamine metabolism in aromatase inhibitor resistant breast cancer cells. Journal of Steroid Biochemistry and Molecular Biology, 2015, 149, 118-127.	1.2	71
385	Building a Pan-Genome Reference for a Population. Journal of Computational Biology, 2015, 22, 387-401.	0.8	48
386	Tissue-based map of the human proteome. Science, 2015, 347, 1260419.	6.0	10,802
387	Curation, integration and visualization of bacterial virulence factors in PATRIC. Bioinformatics, 2015, 31, 252-258.	1.8	58
388	Ether-Ã-go-go family voltage-gated K+ channels evolved in an ancestral metazoan and functionally diversified in a cnidarianâ€"bilaterian ancestor. Journal of Experimental Biology, 2015, 218, 526-536.	0.8	29
389	Research Resource: The Dynamic Transcriptional Profile of Sertoli Cells During the Progression of Spermatogenesis. Molecular Endocrinology, 2015, 29, 627-642.	3.7	74
390	Expression and regulation of long noncoding RNAs in TLR4 signaling in mouse macrophages. BMC Genomics, 2015, 16, 45.	1.2	76
391	Identification of indels in next-generation sequencing data. BMC Bioinformatics, 2015, 16, 42.	1.2	42
392	Amplification of pico-scale DNA mediated by bacterial carrier DNA for small-cell-number transcription factor ChIP-seq. BMC Genomics, 2015, 16, 46.	1.2	27
393	Distribution on Contingency of Alignment of Two Literal Sequences Under Constrains. Acta Biotheoretica, 2015, 63, 55-69.	0.7	0
394	REBASEâ€"a database for DNA restriction and modification: enzymes, genes and genomes. Nucleic Acids Research, 2015, 43, D298-D299.	6.5	748
395	RNA-Binding Protein Musashi1 Is a Central Regulator of Adhesion Pathways in Glioblastoma. Molecular and Cellular Biology, 2015, 35, 2965-2978.	1.1	51
396	Genomic Tools for the Study of Azospirillum and Other Plant Growth-Promoting Rhizobacteria. , 2015, , 83-97.		1
397	Whole genome sequence of Pseudomonas aeruginosa F9676, an antagonistic bacterium isolated from rice seed. Journal of Biotechnology, 2015, 211, 77-78.	1.9	5
398	Databases for Microbiologists. Journal of Bacteriology, 2015, 197, 2458-2467.	1.0	39
399	Genenames.org: the HGNC resources in 2015. Nucleic Acids Research, 2015, 43, D1079-D1085.	6.5	463
400	Loss-of-function variants in ATM confer risk of gastric cancer. Nature Genetics, 2015, 47, 906-910.	9.4	155
401	Lysoplex: An efficient toolkit to detect DNA sequence variations in the autophagy-lysosomal pathway. Autophagy, 2015, 11, 928-938.	4.3	47

#	Article	IF	Citations
402	Differential Promoter Methylation of Macrophage Genes Is Associated With Impaired Vascular Growth in Ischemic Muscles of Hyperlipidemic and Type 2 Diabetic Mice. Circulation Research, 2015, 117, 289-299.	2.0	60
403	RNA and DNA Diagnostics. RNA Technologies, 2015, , .	0.2	5
404	Circular RNA is enriched and stable in exosomes: a promising biomarker for cancer diagnosis. Cell Research, 2015, 25, 981-984.	5.7	1,777
405	Re-annotation of presumed noncoding disease/trait-associated genetic variants by integrative analyses. Scientific Reports, 2015, 5, 9453.	1.6	13
406	Genomics data curation roles, skills and perception of data quality. Library and Information Science Research, 2015, 37, 10-20.	1.2	7
407	Genome sequence of Pseudomonas parafulva CRS01-1, an antagonistic bacterium isolated from rice field. Journal of Biotechnology, 2015, 206, 89-90.	1.9	10
408	Genome sequence of Xanthomonas sacchari R1, a biocontrol bacterium isolated from the rice seed. Journal of Biotechnology, 2015, 206, 77-78.	1.9	19
409	Characterization of Actinobacteria Associated with Three Antâ€"Plant Mutualisms. Microbial Ecology, 2015, 69, 192-203.	1.4	39
410	Identification of horizontally transferred genes in the genus Colletotrichum reveals a steady tempo of bacterial to fungal gene transfer. BMC Genomics, 2015, 16, 2.	1.2	49
411	Analysis of RNA decay factor mediated RNA stability contributions on RNA abundance. BMC Genomics, 2015, 16, 154.	1.2	36
412	Comparative analysis of sugarcane bagasse metagenome reveals unique and conserved biomass-degrading enzymes among lignocellulolytic microbial communities. Biotechnology for Biofuels, 2015, 8, 16.	6.2	92
413	RNA-Seq analysis and annotation of a draft blueberry genome assembly identifies candidate genes involved in fruit ripening, biosynthesis of bioactive compounds, and stage-specific alternative splicing. GigaScience, 2015, 4, 5.	3.3	138
414	Whole genome sequence of Enterobacter ludwigii type strain EN-119T, isolated from clinical specimens. FEMS Microbiology Letters, 2015, 362, .	0.7	8
415	Identification of microRNA Genes in Three Opisthorchiids. PLoS Neglected Tropical Diseases, 2015, 9, e0003680.	1.3	24
416	Pma1 is an alkali/alkaline earth metal cation ATPase that preferentially transports Na+ and K+ across the Mycobacterium smegmatis plasma membrane. Microbiological Research, 2015, 176, 1-6.	2.5	7
417	Neuropeptide Y system in the retina: From localization to function. Progress in Retinal and Eye Research, 2015, 47, 19-37.	7.3	25
418	Identification of a large set of rare complete human knockouts. Nature Genetics, 2015, 47, 448-452.	9.4	214
419	Large-scale whole-genome sequencing of the Icelandic population. Nature Genetics, 2015, 47, 435-444.	9.4	663

#	ARTICLE	IF	CITATIONS
420	CiVi: circular genome visualization with unique features to analyze sequence elements. Bioinformatics, 2015, 31, 2867-2869.	1.8	36
421	Metagenomic analysis reveals adaptations to a cold-adapted lifestyle in a low-temperature acid mine drainage stream. FEMS Microbiology Ecology, 2015, 91, .	1.3	75
422	A comparative study of RNA-seq analysis strategies. Briefings in Bioinformatics, 2015, 16, 932-940.	3.2	23
423	Exploring population size changes using SNP frequency spectra. Nature Genetics, 2015, 47, 555-559.	9.4	332
424	The lncRNA DEANR1 Facilitates Human Endoderm Differentiation by Activating FOXA2 Expression. Cell Reports, 2015, 11, 137-148.	2.9	127
425	Neuronal Kmt2a/Mll1 Histone Methyltransferase Is Essential for Prefrontal Synaptic Plasticity and Working Memory. Journal of Neuroscience, 2015, 35, 5097-5108.	1.7	126
426	Probing the Missing Human Proteome: A Computational Perspective. Journal of Proteome Research, 2015, 14, 4949-4958.	1.8	6
427	Eight proteins play critical roles in RCC with bone metastasis via mitochondrial dysfunction. Clinical and Experimental Metastasis, 2015, 32, 605-622.	1.7	18
428	Complete genome sequence of Kibdelosporangium phytohabitans KLBMP 1111T, a plant growth promoting endophytic actinomycete isolated from oil-seed plant Jatropha curcas L.. Journal of Biotechnology, 2015, 216, 129-130.	1.9	9
429	Methane metabolism in the archaeal phylum Bathyarchaeota revealed by genome-centric metagenomics. Science, 2015, 350, 434-438.	6.0	677
430	Complete genome sequence of Deinococcus swuensis, a bacterium resistant to radiation toxicity. Molecular and Cellular Toxicology, 2015, 11, 315-321.	0.8	32
431	Identification of linc-NeD125, a novel long non coding RNA that hosts miR-125b-1 and negatively controls proliferation of human neuroblastoma cells. RNA Biology, 2015, 12, 1323-1337.	1.5	23
432	HPMV: Human protein mutation viewer â€" relating sequence mutations to protein sequence architecture and function changes. Journal of Bioinformatics and Computational Biology, 2015, 13, 1550028.	0.3	2
433	The Histone Demethylase Jumonji Coordinates Cellular Senescence Including Secretion of Neural Stem Cellâ€"Attracting Cytokines. Molecular Cancer Research, 2015, 13, 636-650.	1.5	40
434	Limits to robustness and reproducibility in the demarcation of operational taxonomic units. Environmental Microbiology, 2015, 17, 1689-1706.	1.8	95
435	Identification of cancerâ€related genes and motifs in the human gene regulatory network. IET Systems Biology, 2015, 9, 128-134.	0.8	6
436	Identification of<i>in vivo</i>DNA-binding mechanisms of Pax6 and reconstruction of Pax6-dependent gene regulatory networks during forebrain and lens development. Nucleic Acids Research, 2015, 43, 6827-6846.	6.5	102
437	Reevaluating Emx gene phylogeny: homopolymeric amino acid tracts as a potential factor obscuring orthology signals in cyclostome genes. BMC Evolutionary Biology, 2015, 15, 78.	3.2	11

#	Article	IF	Citations
438	Characterization of fusion genes and the significantly expressed fusion isoforms in breast cancer by hybrid sequencing. Nucleic Acids Research, 2015, 43, e116-e116.	6.5	104
439	Defects of Lipid Synthesis Are Linked to the Age-Dependent Demyelination Caused by Lamin B1 Overexpression. Journal of Neuroscience, 2015, 35, 12002-12017.	1.7	51
440	Meta-analysis of shared genetic architecture across ten pediatric autoimmune diseases. Nature Medicine, 2015, 21, 1018-1027.	15.2	212
441	Bioinformatics Annotation of Human Y Chromosome-Encoded Protein Pathways and Interactions. Journal of Proteome Research, 2015, 14, 3503-3518.	1.8	9
442	Towards a comprehensive picture of alloacceptor tRNA remolding in metazoan mitochondrial genomes. Nucleic Acids Research, 2015, 43, 8044-8056.	6.5	22
443	Evolution of selenophosphate synthetases: emergence and relocation of function through independent duplications and recurrent subfunctionalization. Genome Research, 2015, 25, 1256-1267.	2.4	46
444	NCBI Viral Genomes Resource. Nucleic Acids Research, 2015, 43, D571-D577.	6.5	541
445	Epsteinâ€“Barr virus transcription factor Zta acts through distal regulatory elements to directly control cellular gene expression. Nucleic Acids Research, 2015, 43, 3563-3577.	6.5	37
446	A multiprotein occupancy map of the mRNP on the 3â€² end of histone mRNAs. Rna, 2015, 21, 1943-1965.	1.6	18
447	Significant expansion of the REST/NRSF cistrome in human versus mouse embryonic stem cells: potential implications for neural development. Nucleic Acids Research, 2015, 43, 5730-5743.	6.5	35
448	Bioinformatics pipeline for functional identification and characterization of proteins. Proceedings of SPIE, 2015, , .	0.8	0
449	Data for in-depth characterisation of the lamb meat proteome from longissimus lumborum. Data in Brief, 2015, 3, 143-148.	0.5	7
450	Analysis of the tryptic search space in UniProt databases. Proteomics, 2015, 15, 48-57.	1.3	13
451	Human germ cell formation in xenotransplants of induced pluripotent stem cells carrying X chromosome aneuploidies. Scientific Reports, 2014, 4, 6432.	1.6	24
452	Integrating Proteomics Profiling Data Sets: A Network Perspective. Methods in Molecular Biology, 2015, 1243, 237-253.	0.4	5
453	Rich annotation of DNA sequencing variants by leveraging the Ensembl Variant Effect Predictor with plugins. Briefings in Bioinformatics, 2015, 16, 255-264.	3.2	41
454	Comparative genome analysis of <scp><i>P</i></scp><i>seudomonas knackmussii</i>â€...<scp>B</scp>13, the first bacterium known to degrade chloroaromatic compounds. Environmental Microbiology, 2015, 17, 91-104.	1.8	52
455	Integrative data analysis indicates an intrinsic disordered domain character of Argonaute-binding motifs. Bioinformatics, 2015, 31, 332-339.	1.8	9

#	ARTICLE	IF	CITATIONS
456	Assessing copy number from exome sequencing and exome array CGH based on CNV spectrum in a large clinical cohort. Genetics in Medicine, 2015, 17, 623-629.	1.1	106
457	Genome Diversity of Spore-Forming <i>Firmicutes</i>. , 0, , 1-18.		6
458	Bioinformatics Analysis of the Human Surfaceome Reveals New Targets for a Variety of Tumor Types. International Journal of Genomics, 2016, 2016, 1-7.	0.8	13
459	Horizontal Gene Transfers from Bacteria toEntamoebaComplex: A Strategy for Dating Events along Species Divergence. Journal of Parasitology Research, 2016, 2016, 1-10.	0.5	5
460	Comparative Analysis of Type IV Pilin in Desulfuromonadales. Frontiers in Microbiology, 2016, 7, 2080.	1.5	14
461	The Verrucomicrobia LexA-Binding Motif: Insights into the Evolutionary Dynamics of the SOS Response. Frontiers in Molecular Biosciences, 2016, 3, 33.	1.6	9
462	Patterns of Transposable Element Expression and Insertion in Cancer. Frontiers in Molecular Biosciences, 2016, 3, 76.	1.6	21
463	Mash: fast genome and metagenome distance estimation using MinHash. Genome Biology, 2016, 17, 132.	3.8	2,099
464	Long Noncoding RNA Identification: Comparing Machine Learning Based Tools for Long Noncoding Transcripts Discrimination. BioMed Research International, 2016, 2016, 1-14.	0.9	1,176
465	A Novel KERA Mutation in a Case of Autosomal Recessive Cornea Plana With Primary Angle-Closure Glaucoma. Journal of Glaucoma, 2016, 25, e106-e109.	0.8	9
466	GGIP: Structure and sequence-based GPCR-GPCR interaction pair predictor. Proteins: Structure, Function and Bioinformatics, 2016, 84, 1224-1233.	1.5	13
467	Computational genomics tools for dissecting tumourâ€"immune cell interactions. Nature Reviews Genetics, 2016, 17, 441-458.	7.7	233
468	CSCdb: a cancer stem cells portal for markers, related genes and functional information. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw023.	1.4	21
469	From data repositories to submission portals: rethinking the role of domain-specific databases in CollecTF. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw055.	1.4	20
470	Maize pan-transcriptome provides novel insights into genome complexity and quantitative trait variation. Scientific Reports, 2016, 6, 18936.	1.6	68
471	Crysalis: an integrated server for computational analysis and design of protein crystallization. Scientific Reports, 2016, 6, 21383.	1.6	35
472	Protein secondary structure prediction using a small training set (compact model) combined with a Complex-valued neural network approach. BMC Bioinformatics, 2016, 17, 362.	1.2	29
473	High-Quality Draft Genome Sequence of an Endophytic Pseudomonas viridiflava Strain with Herbicidal Properties against Its Host, the Weed <i>Lepidium draba</i> L. Genome Announcements, 2016, 4, .	0.8	12

#	ARTICLE	IF	CITATIONS
474	Gene overlapping and size constraints in the viral world. Biology Direct, 2016, 11, 26.	1.9	69
475	Evidence for a non-overlapping subcellular localization of the family I isoforms of soluble inorganic pyrophosphatase in Arabidopsis thaliana. Plant Science, 2016, 253, 229-242.	1.7	12
476	Genome analysis of<i>Hibiscus syriacus</i>provides insights of polyploidization and indeterminate flowering in woody plants. DNA Research, 2017, 24, dsw049.	1.5	38
477	MIB2variants altering NOTCH signalling result in left ventricle hypertrabeculation/non-compaction and are associated with MÃ©nÃ©trier-like gastropathy. Human Molecular Genetics, 2016, 26, ddw365.	1.4	7
478	Comparing genome versus proteome-based identification of clinical bacterial isolates. Briefings in Bioinformatics, 2018, 19, bbw122.	3.2	7
479	A comprehensive next generation sequencing-based virome assessment in brain tissue suggests no major virus - tumor association. Acta Neuropathologica Communications, 2016, 4, 71.	2.4	57
480	Alternative exon usage creates novel transcript variants of tumor suppressor SHREW-1 gene with differential tissue expression profile. Biology Open, 2016, 5, 1607-1619.	0.6	1
481	PHF20 Readers Link Methylation of Histone H3K4 and p53 with H4K16 Acetylation. Cell Reports, 2016, 17, 1158-1170.	2.9	44
482	Complete genome sequence and transcriptomic analysis of a novel marine strain Bacillus weihaiensis reveals the mechanism of brown algae degradation. Scientific Reports, 2016, 6, 38248.	1.6	39
483	Omics in Chlamydomonas for Biofuel Production. Sub-Cellular Biochemistry, 2016, 86, 447-469.	1.0	12
484	Cytokininâ€induced promotion of root meristem size in the fern <i>Azolla</i> supports a shootâ€like origin of euphyllophyte roots. New Phytologist, 2016, 209, 705-720.	3.5	59
485	Genetic Improvement of Industrially Important Fungal Strains. , 2016, , 61-72.		0
486	Conformational flexibility of DENV NS2B/NS3pro: from the inhibitor effect to the serotype influence. Journal of Computer-Aided Molecular Design, 2016, 30, 251-270.	1.3	8
487	Characterization of a Novel Orthomyxo-like Virus Causing Mass Die-Offs of Tilapia. MBio, 2016, 7, e00431-16.	1.8	181
488	Condensin I and II behaviour in interphase nuclei and cells undergoing premature chromosome condensation. Chromosome Research, 2016, 24, 243-269.	1.0	26
489	Expression profiles of long noncoding RNAs in cutaneous squamous cell carcinoma. Epigenomics, 2016, 8, 501-518.	1.0	26
490	Complete genome sequence of Enterococcus faecalis LD33, a bacteriocin-producing strain. Journal of Biotechnology, 2016, 227, 79-80.	1.9	6
491	5SRNAdb: an information resource for 5S ribosomal RNAs. Nucleic Acids Research, 2016, 44, D180-D183.	6.5	42

#	ARTICLE	IF	CITATIONS
492	Cassava (Manihot esculenta) transcriptome analysis in response to infection by the fungus Colletotrichum gloeosporioides using an oligonucleotide-DNA microarray. Journal of Plant Research, 2016, 129, 711-726.	1.2	28
493	Improved definition of the mouse transcriptome via targeted RNA sequencing. Genome Research, 2016, 26, 705-716.	2.4	33
494	Genomic charting of ribosomally synthesized natural product chemical space facilitates targeted mining. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E6343-E6351.	3.3	127
495	Sharing and community curation of mass spectrometry data with Global Natural Products Social Molecular Networking. Nature Biotechnology, 2016, 34, 828-837.	9.4	2,802
496	Identification and Correction of Erroneous Protein Sequences in Public Databases. Methods in Molecular Biology, 2016, 1415, 179-192.	0.4	1
497	Nextâ€generation sequencing identifies novel <i><scp>CACNA</scp>1A</i> gene mutations in episodic ataxia type 2. Molecular Genetics & Genomic Medicine, 2016, 4, 211-222.	0.6	27
498	Identification of microbial populations driving biopolymer degradation in acidic peatlands by metatranscriptomic analysis. Molecular Ecology, 2016, 25, 4818-4835.	2.0	60
499	Towards precision medicine. Nature Reviews Genetics, 2016, 17, 507-522.	7.7	651
500	Targeted next generation sequencing identifies novel NOTCH3 gene mutations in CADASIL diagnostics patients. Human Genomics, 2016, 10, 38.	1.4	21
501	The physiology and habitat of the last universal common ancestor. Nature Microbiology, 2016, 1, 16116.	5.9	739
502	Uncovering oral Neisseria tropism and persistence using metagenomic sequencing. Nature Microbiology, 2016, 1, 16070.	5.9	68
503	CRISPRdigger: detecting CRISPRs with better direct repeat annotations. Scientific Reports, 2016, 6, 32942.	1.6	19
504	Natural Selection in the Great Apes. Molecular Biology and Evolution, 2016, 33, 3268-3283.	3.5	70
505	Patients with genetically heterogeneous synchronous colorectal cancer carry rare damaging germline mutations in immune-related genes. Nature Communications, 2016, 7, 12072.	5.8	49
506	Circular RNA profiling reveals an abundant circHIPK3 that regulates cell growth by sponging multiple miRNAs. Nature Communications, 2016, 7, 11215.	5.8	1,729
507	Integrating Epigenomics into the Understanding of Biomedical Insight. Bioinformatics and Biology Insights, 2016, 10, BBI.S38427.	1.0	22
508	Abundance and Temperature Dependency of Protein-Protein Interaction Revealed by Interface Structure Analysis and Stability Evolution. Scientific Reports, 2016, 6, 26737.	1.6	13
509	Most of the tight positional conservation of transcription factor binding sites near the transcription start site reflects their co-localization within regulatory modules. BMC Bioinformatics, 2016, 17, 479.	1.2	1

#	Article	IF	Citations
510	Evaluating the effect of database inflation in proteogenomic search on sensitive and reliable peptide identification. BMC Genomics, 2016, 17, 1031.	1.2	34
511	Assessment of transfer methods for comparative genomics of regulatory networks in bacteria. BMC Bioinformatics, 2016, 17, 277.	1.2	8
512	ArthropodaCyc: a CycADS powered collection of BioCyc databases to analyse and compare metabolism of arthropods. Database: the Journal of Biological Databases and Curation, 2016, 2016, baw081.	1.4	22
513	Type VI secretion systems of human gut Bacteroidales segregate into three genetic architectures, two of which are contained on mobile genetic elements. BMC Genomics, 2016, 17, 58.	1.2	121
514	PGA: an R/Bioconductor package for identification of novel peptides using a customized database derived from RNA-Seq. BMC Bioinformatics, 2016, 17, 244.	1.2	48
515	Cells with surface expression of CD133highCD71low are enriched for tripotent colony-forming progenitor cells in the adult murine pancreas. Stem Cell Research, 2016, 16, 40-53.	0.3	25
516	Genomic characterization and assessment of the virulence and antibiotic resistance of the novel species Paenibacillus sp. strain VT-400, a potentially pathogenic bacterium in the oral cavity of patients with hematological malignancies. Gut Pathogens, 2016, 8, 6.	1.6	20
517	Metatranscriptomic analysis of diverse microbial communities reveals core metabolic pathways and microbiome-specific functionality. Microbiome, 2016, 4, 2.	4.9	118
518	Complete genome sequence of a psychotrophic Pseudarthrobacter sulfonivorans strain Ar51 (CGMCC) Tj ETQq0 0 0 rgBT /Overlock 10 2016, 231, 81-82.	1.9	27
519	Topology based identification and comprehensive classification of four-transmembrane helix containing proteins (4TMs) in the human genome. BMC Genomics, 2016, 17, 268.	1.2	10
520	Optimizing sgRNA position markedly improves the efficiency of CRISPR/dCas9-mediated transcriptional repression. Nucleic Acids Research, 2016, 44, e141-e141.	6.5	118
521	Chlamydial seasonal dynamics and isolation of â€˜<scp><i>C</i></scp><i>andidatus</i>â€…<scp>N</scp>eptunochlamydia vexilliferaeâ€™ from a <scp>T</scp>yrrhenian coastal lake. Environmental Microbiology, 2016, 18, 2405-2417.	1.8	21
522	Evaluation of the impact of <scp>RNA</scp> preservation methods ofÂspiders for <i>de novo</i> transcriptome assembly. Molecular Ecology Resources, 2016, 16, 662-672.	2.2	36
523	Microbial community dynamics during the early stages of plant polymer breakdown in paddy soil. Environmental Microbiology, 2016, 18, 2825-2842.	1.8	72
524	Identification of genes containing expanded purine repeats in the human genome and their apparent protective role against cancer. Journal of Biomolecular Structure and Dynamics, 2016, 34, 689-704.	2.0	6
525	Computational identification of piRNA targets on mouse mRNAs. Bioinformatics, 2016, 32, 1170-1177.	1.8	22
526	Computational approaches to predict bacteriophageâ€"host relationships. FEMS Microbiology Reviews, 2016, 40, 258-272.	3.9	394
527	Complete genome sequence of deoxynivalenol-degrading bacterium Devosia sp. strain A16. Journal of Biotechnology, 2016, 218, 21-22.	1.9	13

#	Article	IF	Citations
528	The Transporter Classification Database (TCDB): recent advances. Nucleic Acids Research, 2016, 44, D372-D379.	6.5	711
529	Large-scale machine learning for metagenomics sequence classification. Bioinformatics, 2016, 32, 1023-1032.	1.8	65
530	High-resolution phylogenetic microbial community profiling. ISME Journal, 2016, 10, 2020-2032.	4.4	232
531	Structural Insights into <i>Mycobacterium tuberculosis</i> Rv2671 Protein as a Dihydrofolate Reductase Functional Analogue Contributing to <i>para</i>-Aminosalicylic Acid Resistance. Biochemistry, 2016, 55, 1107-1119.	1.2	22
532	Complete genome sequence of a psychotrophic Arthrobacter strain A3 (CGMCC 1.8987), a novel long-chain hydrocarbons producer. Journal of Biotechnology, 2016, 222, 23-24.	1.9	6
533	HLA class II sequence variants influence tuberculosis risk in populations of European ancestry. Nature Genetics, 2016, 48, 318-322.	9.4	123
534	Nonribosomal Peptide and Polyketide Biosynthesis. Methods in Molecular Biology, 2016, , .	0.4	3
535	RNA sequencing validation of the Complexity INdex inÂSARComas prognostic signature. European Journal of Cancer, 2016, 57, 104-111.	1.3	66
536	NONCODEv4: Annotation of Noncoding RNAs with Emphasis on Long Noncoding RNAs. Methods in Molecular Biology, 2016, 1402, 243-254.	0.4	28
537	PlantPReS: A database for plant proteome response to stress. Journal of Proteomics, 2016, 143, 69-72.	1.2	37
538	MitoCarta2.0: an updated inventory of mammalian mitochondrial proteins. Nucleic Acids Research, 2016, 44, D1251-D1257.	6.5	1,170
539	Isolation and Complete Genome Sequence of Algibacter alginolytica sp. nov., a Novel Seaweed-Degrading Bacteroidetes Bacterium with Diverse Putative Polysaccharide Utilization Loci. Applied and Environmental Microbiology, 2016, 82, 2975-2987.	1.4	87
541	Complete genome sequence of an aromatic compound degrader Arthrobacter sp. YC-RL1. Journal of Biotechnology, 2016, 219, 34-35.	1.9	24
542	Unraveling the mechanisms of extreme radioresistance in prokaryotes: Lessons from nature. Mutation Research - Reviews in Mutation Research, 2016, 767, 92-107.	2.4	42
543	KEGG as a reference resource for gene and protein annotation. Nucleic Acids Research, 2016, 44, D457-D462.	6.5	5,435
544	Database resources of the National Center for Biotechnology Information. Nucleic Acids Research, 2016, 44, D7-D19.	6.5	1,417
545	Complete genome sequence of Enterococcus durans KLDS6.0930, a strain with probiotic properties. Journal of Biotechnology, 2016, 217, 49-50.	1.9	13
546	deepBase v2.0: identification, expression, evolution and function of small RNAs, LncRNAs and circular RNAs from deep-sequencing data. Nucleic Acids Research, 2016, 44, D196-D202.	6.5	203

#	Article	IF	Citations
547	Pushing the annotation of cellular activities to a higher resolution: Predicting functions at the isoform level. Methods, 2016, 93, 110-118.	1.9	9
548	Global diversity and biogeography of deep-sea pelagic prokaryotes. ISME Journal, 2016, 10, 596-608.	4.4	191
549	Advances in long noncoding RNAs: identification, structure prediction and function annotation. Briefings in Functional Genomics, 2016, 15, 38-46.	1.3	111
550	Preventing E-cadherin aberrant N-glycosylation at Asn-554 improves its critical function in gastric cancer. Oncogene, 2016, 35, 1619-1631.	2.6	103
551	Transcriptome of larvae representing the Rhipicephalus sanguineus complex. Molecular and Cellular Probes, 2017, 31, 85-90.	0.9	10
552	Mechanism of Deletion Removing All Dystrophin Exons in a Canine Model for DMD Implicates Concerted Evolution of X Chromosome Pseudogenes. Molecular Therapy - Methods and Clinical Development, 2017, 4, 62-71.	1.8	6
553	Characterization of globulin storage proteins of a low prolamin cereal species in relation to celiac disease. Scientific Reports, 2017, 7, 39876.	1.6	18
554	Comparative Analysis of Mitochondrial N-Termini from Mouse, Human, and Yeast. Molecular and Cellular Proteomics, 2017, 16, 512-523.	2.5	71
555	Dynamic changes in the transcriptome of Populus hopeiensis in response to abscisic acid. Scientific Reports, 2017, 7, 42708.	1.6	11
556	Genome Sequence of Delftia acidovorans HK171, a Nematicidal Bacterium Isolated from Tomato Roots. Genome Announcements, 2017, 5, .	0.8	1
557	Inhibition of Debaryomyces nepalensis xylose reductase by lignocellulose derived by-products. Biochemical Engineering Journal, 2017, 121, 73-82.	1.8	11
558	Identification and bacterial characteristics of Xenorhabdus hominickii ANU101 from an entomopathogenic nematode, Steinernema monticolum. Journal of Invertebrate Pathology, 2017, 144, 74-87.	1.5	24
559	A subcellular map of the human proteome. Science, 2017, 356, .	6.0	2,079
560	Identification of sequence variants influencing immunoglobulin levels. Nature Genetics, 2017, 49, 1182-1191.	9.4	90
561	Peripheral blood AKAP7 expression as an early marker for lymphocyte-mediated post-stroke blood brain barrier disruption. Scientific Reports, 2017, 7, 1172.	1.6	33
562	Genomic Signature of Kin Selection in an Ant with Obligately Sterile Workers. Molecular Biology and Evolution, 2017, 34, 1780-1787.	3.5	47
563	APRICOT: an integrated computational pipeline for the sequence-based identification and characterization of RNA-binding proteins. Nucleic Acids Research, 2017, 45, e96-e96.	6.5	22
564	proBAMconvert: A Conversion Tool for proBAM/proBed. Journal of Proteome Research, 2017, 16, 2639-2644.	1.8	8

#	Article	IF	Citations
565	Plant Argonaute Proteins. Methods in Molecular Biology, 2017, , .	0.4	1
566	Identification and Analysis of WG/GW ARGONAUTE-Binding Domains. Methods in Molecular Biology, 2017, 1640, 241-256.	0.4	0
567	Downstream targets of GWAS-detected genes for breast, lung, and prostate and colon cancer converge to G1/S transition pathway. Human Molecular Genetics, 2017, 26, 1465-1471.	1.4	4
568	Low glucose concentrations within typical industrial operating conditions have minimal effect on the transcriptome of recombinant CHO cells. Biotechnology Progress, 2017, 33, 771-785.	1.3	7
569	Energy Balance Modulation Impacts Epigenetic Reprogramming, ERÎ± and ERÎ² Expression, and Mammary Tumor Development in MMTV-neu Transgenic Mice. Cancer Research, 2017, 77, 2500-2511.	0.4	28
570	A Generic Method for Accelerating LSH-Based Similarity Join Processing. IEEE Transactions on Knowledge and Data Engineering, 2017, 29, 712-726.	4.0	16
571	Isolation and complete genome sequence of Halorientalis hydrocarbonoclasticus sp. nov., a hydrocarbon-degrading haloarchaeon. Extremophiles, 2017, 21, 1081-1090.	0.9	23
572	FANTOM5 CAGE profiles of human and mouse samples. Scientific Data, 2017, 4, 170112.	2.4	195
573	A Hierarchical Algorithm for Extreme Clustering. , 2017, , .		45
574	Caloric restriction delays age-related methylation drift. Nature Communications, 2017, 8, 539.	5.8	204
575	EnSVMB: Metagenomics Fragments Classification using Ensemble SVM and BLAST. Scientific Reports, 2017, 7, 9440.	1.6	13
576	N-myc regulates growth and fiber cell differentiation in lens development. Developmental Biology, 2017, 429, 105-117.	0.9	37
577	Metabolic potential and <i>in situ</i> activity of marine Marinimicrobia bacteria in an anoxic water column. Environmental Microbiology, 2017, 19, 4392-4416.	1.8	40
578	Random walk with restart: A powerful network propagation algorithm in Bioinformatics field. , 2017, , .		9
579	An integrative strategy to identify the entire protein coding potential of prokaryotic genomes by proteogenomics. Genome Research, 2017, 27, 2083-2095.	2.4	112
580	Accessing the genomic information of unculturable oceanic picoeukaryotes by combining multiple single cells. Scientific Reports, 2017, 7, 41498.	1.6	47
581	Deguelin exerts potent nematocidal activity via the mitochondrial respiratory chain. FASEB Journal, 2017, 31, 4515-4532.	0.2	25
582	Complete genome sequence of Stenotrophomonas sp. KCTC 12332, a biotechnological potential bacterium. Journal of Biotechnology, 2017, 256, 27-30.	1.9	4

#	ARTICLE	IF	CITATIONS
583	Complete genome sequence of a phthalic acid esters degrading Mycobacterium sp. YC-RL4. Brazilian Journal of Microbiology, 2017, 48, 607-609.	0.8	9
584	mTFkb: a knowledgebase for fundamental annotation of mouse transcription factors. Scientific Reports, 2017, 7, 3022.	1.6	21
585	Araport11: a complete reannotation of the <i>Arabidopsis thaliana</i> reference genome. Plant Journal, 2017, 89, 789-804.	2.8	925
586	Assessment of cancer and virus antigens for cross-reactivity in human tissues. Bioinformatics, 2017, 33, 104-111.	1.8	17
587	RNA-sequencing of a mouse-model of spinal muscular atrophy reveals tissue-wide changes in splicing of U12-dependent introns. Nucleic Acids Research, 2017, 45, 395-416.	6.5	87
588	Distinguishing long non-coding RNAs from mRNAs using a two-layer structured classifier. , 2017, , .		3
589	Towards enhanced and interpretable clustering/classification in integrative genomics. Nucleic Acids Research, 2017, 45, e169-e169.	6.5	1
590	Expitope 2.0: a tool to assess immunotherapeutic antigens for their potential cross-reactivity against naturally expressed proteins in human tissues. BMC Cancer, 2017, 17, 892.	1.1	22
591	The genomic plant warehouse framework: A systematic literature review. , 2017, , .		1
592	MiRNA profiling of gastrointestinal stromal tumors by next-generation sequencing. Oncotarget, 2017, 8, 37225-37238.	0.8	34
593	Centralization, Fragmentation, and Replication in the Genomic Data Commons. , 2017, , 46-73.		9
594	Evolution of mobile genetic element composition in an epidemic methicillin-resistant Staphylococcus aureus: temporal changes correlated with frequent loss and gain events. BMC Genomics, 2017, 18, 684.	1.2	43
595	Comparison of RNAi Sequences in Insect-Resistant Plants to Expressed Sequences of a Beneficial Lady Beetle: A Closer Look at Off-Target Considerations. Insects, 2017, 8, 27.	1.0	6
596	Draft Genome Sequence of Heavy Metal-Resistant Soil Bacterium Serratia marcescens S2I7, Which Has the Ability To Degrade Polyaromatic Hydrocarbons. Genome Announcements, 2017, 5, .	0.8	6
597	Molecular and Structural Characterization of the Tegumental 20.6-kDa Protein in Clonorchis sinensis as a Potential Druggable Target. International Journal of Molecular Sciences, 2017, 18, 557.	1.8	13
598	Exo-miRExplorer: A Comprehensive Resource for Exploring and Comparatively Analyzing Exogenous MicroRNAs. Frontiers in Microbiology, 2017, 8, 126.	1.5	6
599	Short-Term Exposure of Paddy Soil Microbial Communities to Salt Stress Triggers Different Transcriptional Responses of Key Taxonomic Groups. Frontiers in Microbiology, 2017, 8, 400.	1.5	19
600	Unexpected Dominance of Elusive Acidobacteria in Early Industrial Soft Coal Slags. Frontiers in Microbiology, 2017, 8, 1023.	1.5	32

#	Article	IF	Citations
601	DNA methylation levels in candidate genes associated with chronological age in mammals are not conserved in a long-lived seabird. PLoS ONE, 2017, 12, e0189181.	1.1	7
602	Genetic polymorphisms of cytochrome P450-1A2 (CYP1A2) among Emiratis. PLoS ONE, 2017, 12, e0183424.	1.1	16
603	New reference genome sequences of hot pepper reveal the massive evolution of plant disease-resistance genes by retroduplication. Genome Biology, 2017, 18, 210.	3.8	255
604	Longitudinal genomic surveillance of multidrug-resistant Escherichia coli carriage in a long-term care facility in the United Kingdom. Genome Medicine, 2017, 9, 70.	3.6	44
605	Differential analysis between somatic mutation and germline variation profiles reveals cancer-related genes. Genome Medicine, 2017, 9, 79.	3.6	30
606	LCS-TA to identify similar fragments in RNA 3D structures. BMC Bioinformatics, 2017, 18, 456.	1.2	15
607	Structural Chemogenomics Databases to Navigate Proteinâ€"Ligand Interaction Space. , 2017, , 444-471.		1
608	Alga-PrAS (Algal Protein Annotation Suite): A Database of Comprehensive Annotation in Algal Proteomes. Plant and Cell Physiology, 2017, 58, pcw212.	1.5	11
609	Livebearing or egg-laying mammals: 27 decisive nucleotides of FAM168. BioScience Trends, 2017, 11, 169-178.	1.1	1
610	Genome-scale examination of NBS-encoding genes in blueberry. Scientific Reports, 2018, 8, 3429.	1.6	18
611	Recognition of the polycistronic nature of human genes is critical to understanding the genotype-phenotype relationship. Genome Research, 2018, 28, 609-624.	2.4	54
612	Comparative Analysis of Immune Cells Reveals a Conserved Regulatory Lexicon. Cell Systems, 2018, 6, 381-394.e7.	2.9	19
613	Conventional and pioneer modes of glucocorticoid receptor interaction with enhancer chromatin in vivo. Nucleic Acids Research, 2018, 46, 203-214.	6.5	63
614	The genome sequence of the soft-rot fungus <i>Penicillium purpurogenum</i> reveals a high gene dosage for lignocellulolytic enzymes. Mycology, 2018, 9, 59-69.	2.0	12
615	Updates on resources, software tools, and databases for plant proteomics in 2016â€"2017. Electrophoresis, 2018, 39, 1543-1557.	1.3	11
616	A novel prognostic sixâ€CpG signature in glioblastomas. CNS Neuroscience and Therapeutics, 2018, 24, 167-177.	1.9	30
617	Symposium review: Mining metagenomic and metatranscriptomic data for clues about microbial metabolic functions in ruminants. Journal of Dairy Science, 2018, 101, 5605-5618.	1.4	24
618	Prediction of CpG Islands as an Intrinsic Clustering Property Found in Many Eukaryotic DNA Sequences and Its Relation to DNA Methylation. Methods in Molecular Biology, 2018, 1766, 31-47.	0.4	5

#	Article	IF	Citations
619	Cas13d Is a Compact RNA-Targeting Type VI CRISPR Effector Positively Modulated by a WYL-Domain-Containing Accessory Protein. Molecular Cell, 2018, 70, 327-339.e5.	4.5	356
620	Complete genome sequence of Marivivens sp. JLT3646, a potential aromatic compound degrader. Marine Genomics, 2018, 38, 9-11.	0.4	11
621	Critical evaluation of bioinformatics tools for the prediction of protein crystallization propensity. Briefings in Bioinformatics, 2018, 19, 838-852.	3.2	22
622	Novel Role of FBXW7 Circular RNA in Repressing Glioma Tumorigenesis. Journal of the National Cancer Institute, 2018, 110, 304-315.	3.0	813
623	Biomedical applications of genome-scale metabolic network reconstructions of human pathogens. Current Opinion in Biotechnology, 2018, 51, 70-79.	3.3	30
624	Protein Structure Modeling. , 2018, , 113-127.		0
625	Characterization of drug-induced splicing complexity in prostate cancer cell line using long read technology. , 2018, , .		1
626	Review: â€œPyrophosphate and pyrophosphatases in plants, their involvement in stress responses and their possible relationship to secondary metabolismâ€• Plant Science, 2018, 267, 11-19.	1.7	35
627	Genome-wide mapping of estrogen receptor Î± binding sites by ChIP-seq to identify genes related to sexual maturity in hens. Gene, 2018, 642, 32-42.	1.0	7
628	Complete genome sequence of human pathogen Kosakonia cowanii type strain 888-76 T. Brazilian Journal of Microbiology, 2018, 49, 16-17.	0.8	18
629	Proteogenomic Analysis of Epibacterium Mobile BBCC367, a Relevant Marine Bacterium Isolated From the South Pacific Ocean. Frontiers in Microbiology, 2018, 9, 3125.	1.5	4
630	OBSOLETE: Transcriptome and Epigenome Applications for Coronary Heart Disease Research. , 2018, , .		0
631	Evolutionary dynamics of the Wnt gene family: implications for lophotrochozoans. Journal of Oceanology and Limnology, 2018, 36, 1720-1730.	0.6	4
632	A comprehensive fungi-specific 18S rRNA gene sequence primer toolkit suited for diverse research issues and sequencing platforms. BMC Microbiology, 2018, 18, 190.	1.3	84
633	Comparative Genomics and Proteomic Analysis of Assimilatory Sulfate Reduction Pathways in Anaerobic Methanotrophic Archaea. Frontiers in Microbiology, 2018, 9, 2917.	1.5	33
634	The translation of non-canonical open reading frames controls mucosal immunity. Nature, 2018, 564, 434-438.	13.7	159
635	Defense responses of lentil (Lens culinaris) genotypes carrying non-allelic ascochyta blight resistance genes to Ascochyta lentis infection. PLoS ONE, 2018, 13, e0204124.	1.1	25
636	<i>Bacillus subtilis</i> exhibits MnmC-like tRNA modification activities. RNA Biology, 2018, 15, 1167-1173.	1.5	9

#	ARTICLE	IF	CITATIONS
637	Achieving Accurate Sequence and Annotation Data for Caulobacter vibrioides CB13. Current Microbiology, 2018, 75, 1642-1648.	1.0	6
638	Interspecies cross-feeding orchestrates carbon degradation in the rumen ecosystem. Nature Microbiology, 2018, 3, 1274-1284.	5.9	144
639	A genomic infection control study for Staphylococcus aureus in two Ghanaian hospitals. Infection and Drug Resistance, 2018, Volume 11, 1757-1765.	1.1	24
640	ZFLNC: a comprehensive and well-annotated database for zebrafish lncRNA. Database: the Journal of Biological Databases and Curation, 2018, 2018, .	1.4	27
641	FtsZ of Filamentous, Heterocyst-Forming Cyanobacteria Has a Conserved N-Terminal Peptide Required for Normal FtsZ Polymerization and Cell Division. Frontiers in Microbiology, 2018, 9, 2260.	1.5	24
642	Novel halfâ€•life extended antiâ€•MIF nanobodies protect against endotoxic shock. FASEB Journal, 2018, 32, 3411-3422.	0.2	27
643	Multiple model species selection for transcriptomics analysis of non-model organisms. BMC Bioinformatics, 2018, 19, 284.	1.2	8
644	LncADeep: an<i>ab initio</i>lncRNA identification and functional annotation tool based on deep learning. Bioinformatics, 2018, 34, 3825-3834.	1.8	110
645	Proteomic identification of Axc, a novel beta-lactamase with carbapenemase activity in a meropenem-resistant clinical isolate of Achromobacter xylosoxidans. Scientific Reports, 2018, 8, 8181.	1.6	10
646	Transcriptional and Translational Landscape of Equine Torovirus. Journal of Virology, 2018, 92, .	1.5	24
647	Evidence for plant-derived xenomiRs based on a large-scale analysis of public small RNA sequencing data from human samples. PLoS ONE, 2018, 13, e0187519.	1.1	31
648	High resolution annotation of zebrafish transcriptome using long-read sequencing. Genome Research, 2018, 28, 1415-1425.	2.4	69
649	Blazing Signature Filter: a library for fast pairwise similarity comparisons. BMC Bioinformatics, 2018, 19, 221.	1.2	6
650	A Novel Eukaryotic Denitrification Pathway in Foraminifera. Current Biology, 2018, 28, 2536-2543.e5.	1.8	75
651	Estimating the Intra-taxa Diversity, Population Genetic Structure, and Evolutionary Pathways of Cryptococcus neoformans and Cryptococcus gattii. Frontiers in Genetics, 2018, 9, 148.	1.1	30
652	Genome-Wide Analysis of the PYL Gene Family and Identification of PYL Genes That Respond to Abiotic Stress in Brassica napus. Genes, 2018, 9, 156.	1.0	55
653	ACIâ€•1 betaâ€•lactamase is widespread across human gut microbiomes in Negativicutes due to transposons harboured by tailed prophages. Environmental Microbiology, 2018, 20, 2288-2300.	1.8	20
654	Comprehensive analysis of coding-lncRNA gene co-expression network uncovers conserved functional lncRNAs in zebrafish. BMC Genomics, 2018, 19, 112.	1.2	36

#	Article	IF	Citations
655	Silencing of circRNA.2837 Plays a Protective Role in Sciatic Nerve Injury by Sponging the miR-34 Family via Regulating Neuronal Autophagy. Molecular Therapy - Nucleic Acids, 2018, 12, 718-729.	2.3	71
656	Complete genome sequence of Enterococcus durans KLDS6.0933, a potential probiotic strain with high cholesterol removal ability. Gut Pathogens, 2018, 10, 32.	1.6	19
657	Molecular evolution and functional divergence of eukaryotic translation initiation factor 2-alpha kinases. PLoS ONE, 2018, 13, e0194335.	1.1	13
658	Methanogens in the Antarctic Dry Valley permafrost. FEMS Microbiology Ecology, 2018, 94, .	1.3	22
659	A second RNA-binding protein is essential for ethanol tolerance provided by the bacterial OLE ribonucleoprotein complex. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E6319-E6328.	3.3	9
660	Genome Annotation. , 2019, , 195-209.		3
661	Proteinâ€“Protein Interaction Databases. , 2019, , 988-996.		3
662	Integrated genomic epidemiology and phenotypic profiling of Clostridium difficile across intra-hospital and community populations in Colombia. Scientific Reports, 2019, 9, 11293.	1.6	12
663	Approaches to metagenomic classification and assembly. , 2019, , .		1
664	DIFFUSE: predicting isoform functions from sequences and expression profiles via deep learning. Bioinformatics, 2019, 35, i284-i294.	1.8	28
665	Complete Whole-Genome Sequence of Haemophilus haemolyticus NCTC 10839. Microbiology Resource Announcements, 2019, 8, .	0.3	1
666	Genome Sequence of Lipopeptide- and Antioxidant-Producing Strain Bacillus velezensis NWUMFkBS10.5. Microbiology Resource Announcements, 2019, 8, .	0.3	2
667	Meta-Qtest: meta-analysis of quadratic test for rare variants. BMC Medical Genomics, 2019, 12, 102.	0.7	2
668	Comparative genomics identifies potential virulence factors in <i>Clostridium tertium</i> and <i>C. paraputrificum</i>. Virulence, 2019, 10, 657-676.	1.8	13
669	SMYD2 Drives Mesendodermal Differentiation of Human Embryonic Stem Cells Through Mediating the Transcriptional Activation of Key Mesendodermal Genes. Stem Cells, 2019, 37, 1401-1415.	1.4	14
670	Complete Whole-Genome Sequences of Two Raoultella terrigena Strains, NCTC 13097 and NCTC 13098, Isolated from Human Cases. Microbiology Resource Announcements, 2019, 8, .	0.3	2
671	CASP1 variants influence subcellular caspase-1 localization, pyroptosome formation, pro-inflammatory cell death and macrophage deformability. Clinical Immunology, 2019, 208, 108232.	1.4	9
672	A Combined Transcriptomic and Genomic Analysis Identifies a Gene Signature Associated With the Response to Anti-TNF Therapy in Rheumatoid Arthritis. Frontiers in Immunology, 2019, 10, 1459.	2.2	24

#	Article	IF	Citations
673	Enhancement of growth and salt tolerance of tomato seedlings by a natural halotolerant actinobacterium Glutamicibacter halophytocola KLBMP 5180 isolated from a coastal halophyte. Plant and Soil, 2019, 445, 307-322.	1.8	51
674	U2 <scp>AF</scp> ⁶⁵ assemblies drive sequenceâ€specific splice site recognition. EMBO Reports, 2019, 20, e47604.	2.0	21
675	Contrasting patterns of longitudinal population dynamics and antimicrobial resistance mechanisms in two priority bacterial pathogens over 7Âyears in a single center. Genome Biology, 2019, 20, 184.	3.8	22
676	In vivo epigenetic editing of Sema6a promoter reverses transcallosal dysconnectivity caused by C11orf46/Arl14ep risk gene. Nature Communications, 2019, 10, 4112.	5.8	34
677	Identifying blood-specific age-related DNA methylation markers on the Illumina MethylationEPICÂ® BeadChip. Forensic Science International, 2019, 303, 109944.	1.3	22
678	Short communication: Complete genome sequence of Lactobacillus plantarum J26, a probiotic strain with immunomodulatory activity. Journal of Dairy Science, 2019, 102, 10838-10844.	1.4	12
679	An African Salmonella Typhimurium ST313 sublineage with extensive drug-resistance and signatures of host adaptation. Nature Communications, 2019, 10, 4280.	5.8	80
680	Frequent Loss of IRF2 in Cancers Leads to Immune Evasion through Decreased MHC Class I Antigen Presentation and Increased PD-L1 Expression. Journal of Immunology, 2019, 203, 1999-2010.	0.4	63
681	One Health Genomic Surveillance of Escherichia coli Demonstrates Distinct Lineages and Mobile Genetic Elements in Isolates from Humans versus Livestock. MBio, 2019, 10, .	1.8	130
682	In silico prediction reveals the existence of potential bioactive neuropeptides produced by the human gut microbiota. Food Research International, 2019, 119, 221-226.	2.9	8
683	'Candidatus Ornithobacterium hominis': insights gained from draft genomes obtained from nasopharyngeal swabs. Microbial Genomics, 2019, 5, .	1.0	16
684	Whole genome sequence of Vibrio cholerae directly from dried spotted filter paper. PLoS Neglected Tropical Diseases, 2019, 13, e0007330.	1.3	7
685	Detection of Epstein-Barr Virus Infection in Non-Small Cell Lung Cancer. Cancers, 2019, 11, 759.	1.7	36
686	Integrative characterization of G-Quadruplexes in the three-dimensional chromatin structure. Epigenetics, 2019, 14, 894-911.	1.3	61
687	High throughput LC-MS/MS-based proteomic analysis of excretory-secretory products from short-term in vitro culture of Haemonchus contortus. Journal of Proteomics, 2019, 204, 103375.	1.2	44
688	A voting mechanism-based linear epitope prediction system for the host-specific Iridoviridae family. BMC Bioinformatics, 2019, 20, 192.	1.2	1
689	The MACADAM database: a MetAboliC pAthways DAtabase for Microbial taxonomic groups for mining potential metabolic capacities of archaeal and bacterial taxonomic groups. Database: the Journal of Biological Databases and Curation, 2019, 2019, .	1.4	29
690	Conserved Secondary Structures in Viral mRNAs. Viruses, 2019, 11, 401.	1.5	22

#	ARTICLE	IF	CITATIONS
691	Effect of paleopolyploidy and allopolyploidy on gene expression in banana. BMC Genomics, 2019, 20, 244.	1.2	22
692	Genome-wide association study on the body temperature changes of a broiler-type strain Taiwan country chickens under acute heat stress. Journal of Thermal Biology, 2019, 82, 33-42.	1.1	8
693	Origination and evolution of orphan genes and de novo genes in the genome of Caenorhabditis elegans. Science China Life Sciences, 2019, 62, 579-593.	2.3	21
694	Genome-wide discovery of structured noncoding RNAs in bacteria. BMC Microbiology, 2019, 19, 66.	1.3	40
695	Essentials of Bioinformatics, Volume I. , 2019, , .		8
696	Complete genome sequence of a novel aerobic denitrifying strain, Pseudomonas monteilii CY06. Marine Genomics, 2019, 47, 100661.	0.4	2
697	Prediction of Long Non-Coding RNAs Based on Deep Learning. Genes, 2019, 10, 273.	1.0	23
698	Integron-Derived Aminoglycoside-Sensing Riboswitches Control Aminoglycoside Acetyltransferase Resistance Gene Expression. Antimicrobial Agents and Chemotherapy, 2019, 63, .	1.4	11
699	Tools and Methods in Analysis of Complex Sequences. , 2019, , 155-167.		0
700	Prioritizing candidate genes for fertility in dairy cows using gene-based analysis, functional annotation and differential gene expression. BMC Genomics, 2019, 20, 255.	1.2	30
701	The first chromosomeâ€level genome for a marine mammal as a resource to study ecology and evolution. Molecular Ecology Resources, 2019, 19, 944-956.	2.2	27
702	CircHMGCS1 Promotes Hepatoblastoma Cell Proliferation by Regulating the IGF Signaling Pathway and Glutaminolysis. Theranostics, 2019, 9, 900-919.	4.6	60
703	Genetic meta-analysis of diagnosed Alzheimerâ€™s disease identifies new risk loci and implicates Aβ², tau, immunity and lipid processing. Nature Genetics, 2019, 51, 414-430.	9.4	1,962
704	Text-mining in cancer research may help identify effective treatments. Translational Lung Cancer Research, 2019, 8, S460-S463.	1.3	6
705	Transcriptome analysis identifies genes related to the waxy coating on blueberry fruit in two northern-adapted rabbiteye breeding populations. BMC Plant Biology, 2019, 19, 460.	1.6	22
706	Identification of The Canidae Iron Regulatory Hormone Hepcidin. Scientific Reports, 2019, 9, 19400.	1.6	5
707	Common and rare sequence variants influencing tumor biomarkers in blood. Cancer Epidemiology Biomarkers and Prevention, 2019, 29, cebp.1060.2018.	1.1	9
708	SKmDB: an integrated database of next generation sequencing information in skeletal muscle. Bioinformatics, 2019, 35, 847-855.	1.8	2

#	ARTICLE	IF	CITATIONS
709	The genomic organization and expression pattern of the low-affinity Fc gamma receptors (FcÎ³R) in the GÃ¶ttingen minipig. Immunogenetics, 2019, 71, 123-136.	1.2	6
710	Biogeochemical Regimes in Shallow Aquifers Reflect the Metabolic Coupling of the Elements Nitrogen, Sulfur, and Carbon. Applied and Environmental Microbiology, 2019, 85, .	1.4	47
711	The Genome of the Common Marmoset. , 2019, , 313-333.		1
712	Molecular epidemiology and expression of capsular polysaccharides in Staphylococcus aureus clinical isolates in the United States. PLoS ONE, 2019, 14, e0208356.	1.1	33
713	The UNITE database for molecular identification of fungi: handling dark taxa and parallel taxonomic classifications. Nucleic Acids Research, 2019, 47, D259-D264.	6.5	2,072
714	Selecting lipopeptideâ€producing, <i>Fusariumâ€</i>suppressing <i>Bacillus</i> spp.: Metabolomic and genomic probing of <i>Bacillus velezensis</i> NWUMFkBS10.5. MicrobiologyOpen, 2019, 8, e00742.	1.2	31
715	Functionally diverse type V CRISPR-Cas systems. Science, 2019, 363, 88-91.	6.0	342
716	Circ_Lrp6, a Circular RNA Enriched in Vascular Smooth Muscle Cells, Acts as a Sponge Regulating miRNA-145 Function. Circulation Research, 2019, 124, 498-510.	2.0	140
717	Using the sORFs.Org Database. Current Protocols in Bioinformatics, 2019, 65, e68.	25.8	9
718	BetaDL: A protein beta-sheet predictor utilizing a deep learning model and independent set solution. Computers in Biology and Medicine, 2019, 104, 241-249.	3.9	4
719	Resources and tools for the high-throughput, multi-omic study of intestinal microbiota. Briefings in Bioinformatics, 2019, 20, 1032-1056.	3.2	10
720	Provenance-based fault tolerance technique recommendation for cloud-based scientific workflows: a practical approach. Cluster Computing, 2020, 23, 123-148.	3.5	11
721	Differential nucleosome spacing in neurons and glia. Neuroscience Letters, 2020, 714, 134559.	1.0	10
723	An adaptive test for metaâ€analysis of rare variant association studies. Genetic Epidemiology, 2020, 44, 104-116.	0.6	2
724	Genome-wide characterization and analysis of microsatellite sequences in camelid species. Mammal Research, 2020, 65, 359-373.	0.6	6
725	miRNAs Predicted to Regulate Host Anti-viral Gene Pathways in IPNV-Challenged Atlantic Salmon Fry Are Affected by Viral Load, and Associated With the Major IPN Resistance QTL Genotypes in Late Infection. Frontiers in Immunology, 2020, 11, 2113.	2.2	28
726	Comparative eye and liver differentially expressed genes reveal monochromatic vision and cancer resistance in the shortfin mako shark (Isurus oxyrinchus). Genomics, 2020, 112, 4817-4826.	1.3	4
727	Comparative Analysis of ROS Network Genes in Extremophile Eukaryotes. International Journal of Molecular Sciences, 2020, 21, 9131.	1.8	10

#	Article	IF	Citations
728	lncRNA_Mdeep: An Alignment-Free Predictor for Distinguishing Long Non-Coding RNAs from Protein-Coding Transcripts by Multimodal Deep Learning. International Journal of Molecular Sciences, 2020, 21, 5222.	1.8	12
729	Circular RNAs regulate its parental genes transcription in the AD mouse model using two methods of library construction. FASEB Journal, 2020, 34, 10342-10356.	0.2	8
730	A comprehensive rat transcriptome built from large scale RNA-seq-based annotation. Nucleic Acids Research, 2020, 48, 8320-8331.	6.5	19
731	Evolutionary Analysis of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) Reveals Genomic Divergence with Implications for Universal Vaccine Efficacy. Vaccines, 2020, 8, 591.	2.1	3
732	Cytoskeletal and synaptic polarity of LWamide-like+ ganglion neurons in the sea anemone <i>Nematostella vectensis</i>. Journal of Experimental Biology, 2020, 223, .	0.8	7
733	miRTissue ce: extending miRTissue web service with the analysis of ceRNA-ceRNA interactions. BMC Bioinformatics, 2020, 21, 199.	1.2	12
734	Sequence diversity analyses of an improved rhesus macaque genome enhance its biomedical utility. Science, 2020, 370, .	6.0	105
735	Predicting Long non-coding RNAs through feature ensemble learning. BMC Genomics, 2020, 21, 865.	1.2	2
736	Revealing Epigenetic Factors of circRNA Expression by Machine Learning in Various Cellular Contexts. IScience, 2020, 23, 101842.	1.9	8
737	The Role of the Human Growth Hormone Gene Family in Pregnancy. , 0, , .		0
738	The Transfer of the Ferredoxin Gene From the Chloroplast to the Nuclear Genome Is Ancient Within the Paraphyletic Genus Thalassiosira. Frontiers in Microbiology, 2020, 11, 523689.	1.5	4
739	Integrating whole-genome sequencing within the National Antimicrobial Resistance Surveillance Program in the Philippines. Nature Communications, 2020, 11, 2719.	5.8	62
740	Single Particle Imaging with FEL Using Photon Correlations. Topics in Applied Physics, 2020, , 435-455.	0.4	1
741	miR-379 links glucocorticoid treatment with mitochondrial response in Duchenne muscular dystrophy. Scientific Reports, 2020, 10, 9139.	1.6	15
742	GreenCircRNA: a database for plant circRNAs that act as miRNA decoys. Database: the Journal of Biological Databases and Curation, 2020, 2020, .	1.4	23
743	Transcriptomic identification of TMIGD1 and its relationship with the ileal epithelial cell differentiation in Crohnâ€™s disease. American Journal of Physiology - Renal Physiology, 2020, 319, G109-G120.	1.6	9
744	Formate Utilization by the Crenarchaeon Desulfurococcus amylolyticus. Microorganisms, 2020, 8, 454.	1.6	4
745	Refgenie: a reference genome resource manager. GigaScience, 2020, 9, .	3.3	32

#	Article	IF	Citations
746	The Gut Microbiota in Prediabetes and Diabetes: A Population-Based Cross-Sectional Study. Cell Metabolism, 2020, 32, 379-390.e3.	7.2	233
747	Increasing incidence of group B streptococcus neonatal infections in the Netherlands is associated with clonal expansion of CC17 and CC23. Scientific Reports, 2020, 10, 9539.	1.6	25
748	Understanding the proteome encoded by â€œnon-coding RNAsâ€: new insights into human genome. Science China Life Sciences, 2020, 63, 986-995.	2.3	17
749	Complete genome sequence of Sphingomonas sp. Cra20, a drought resistant and plant growth promoting rhizobacteria. Genomics, 2020, 112, 3648-3657.	1.3	41
750	Pitfalls in variant annotation for hereditary cancer diagnostics: The example of IlluminaÂ® VariantStudioÂ®. Genomics, 2021, 113, 748-754.	1.3	0
751	Regulation of ribosomal protein genes: An ordered anarchy. Wiley Interdisciplinary Reviews RNA, 2021, 12, e1632.	3.2	72
752	A Robust and Precise ConvNet for Small Non-Coding RNA Classification (RPC-snRC). IEEE Access, 2021, 9, 19379-19390.	2.6	7
753	Identified the novel resistant biomarkers for taxane-based therapy for triple-negative breast cancer. International Journal of Medical Sciences, 2021, 18, 2521-2531.	1.1	11
754	Interface Prediction for GPCR Oligomerization Between Transmembrane Helices. Methods in Molecular Biology, 2021, 2315, 99-110.	0.4	0
756	Genomic exploration of Bacillus thuringiensis MORWBS1.1 - candidate biocontrol agent, predicts genes for biosynthesis of zwittermicin, 4,5-DOPA dioxygenase extradiol, and quercetin 2,3-dioxygenase. Molecular Plant-Microbe Interactions, 2021, 34, 602-605.	1.4	5
757	ATF3-Induced Mammary Tumors Exhibit Molecular Features of Human Basal-Like Breast Cancer. International Journal of Molecular Sciences, 2021, 22, 2353.	1.8	4
759	Microbiome-based environmental monitoring of a dairy processing facility highlights the challenges associated with low microbial-load samples. Npj Science of Food, 2021, 5, 4.	2.5	18
760	A genome-wide association study for gut metagenome in Chinese adults illuminates complex diseases. Cell Discovery, 2021, 7, 9.	3.1	49
761	Demographic History, Adaptation, and NRAP Convergent Evolution at Amino Acid Residue 100 in the World Northernmost Cattle from Siberia. Molecular Biology and Evolution, 2021, 38, 3093-3110.	3.5	27
762	Genomic Epidemiology of CC30 Methicillin-Resistant Staphylococcus aureus Strains from Argentina Reveals Four Major Clades with Distinctive Genetic Features. MSphere, 2021, 6, .	1.3	11
763	A systematic review of computational methods for predicting long noncoding RNAs. Briefings in Functional Genomics, 2021, 20, 162-173.	1.3	13
764	ATRX Alteration Contributes to Tumor Growth and Immune Escape in Pleomorphic Sarcomas. Cancers, 2021, 13, 2151.	1.7	10
765	Identity and compatibility of reference genome resources. NAR Genomics and Bioinformatics, 2021, 3, lqab036.	1.5	8

#	ARTICLE	IF	CITATIONS
766	Zygotorulaspora dagestanica sp. nov., a novel ascomycetous yeast species associated with the Georgian honeysuckle (Lonicera iberica M. Bieb.). International Journal of Systematic and Evolutionary Microbiology, 2021, 71, .	0.8	3
767	Snipe: highly sensitive pathogen detection from metagenomic sequencing data. Briefings in Bioinformatics, 2021, 22, .	3.2	2
768	Dog10K_Boxer_Tasha_1.0: A Long-Read Assembly of the Dog Reference Genome. Genes, 2021, 12, 847.	1.0	19
769	Genome Sequence Resource of Pseudomonas fulva HARBPS9.1â€"Candidate Biocontrol Agent. Phytopathology, 2021, 111, 896-898.	1.1	3
771	<scp>NOVOWrap</scp>: An automated solution for plastid genome assembly and structure standardization. Molecular Ecology Resources, 2021, 21, 2177-2186.	2.2	22
772	Potential syntrophic relationship between coral-associated Prosthecochloris and its companion sulfate-reducing bacterium unveiled by genomic analysis. Microbial Genomics, 2021, 7, .	1.0	5
773	Multiple roles of H2A.Z in regulating promoter chromatin architecture in human cells. Nature Communications, 2021, 12, 2524.	5.8	22
774	Relationship of the Pine Growth Promoting Pantoea eucalypti FBS135 with Type Strains P. eucalypti LMG 24197T and P. vagans 24199T. Life, 2021, 11, 608.	1.1	3
775	Transcriptomic Analysis of Changes in Gene Expression During Flowering Induction in Sugarcane Under Controlled Photoperiodic Conditions. Frontiers in Plant Science, 2021, 12, 635784.	1.7	13
776	Variance-component-based meta-analysis of geneâ€"environment interactions for rare variants. G3: Genes, Genomes, Genetics, 2021, 11, .	0.8	2
777	Draft genome sequence and potential identification of a biosurfactant from Brevibacterium casei strain LS14 an isolate from fresh water Loktak Lake. 3 Biotech, 2021, 11, 326.	1.1	3
779	Large-scale protein level comparison of Deltaproteobacteria reveals cohesive metabolic groups. ISME Journal, 2022, 16, 307-320.	4.4	71
780	Conversion of dietary inositol into propionate and acetate by commensal Anaerostipes associates with host health. Nature Communications, 2021, 12, 4798.	5.8	76
781	Microbiome Analysis of the Rhizosphere from Wilt Infected Pomegranate Reveals Complex Adaptations in Fusariumâ€"A Preliminary Study. Agriculture (Switzerland), 2021, 11, 831.	1.4	9
782	The genome of the extremophile Artemia provides insight into strategies to cope with extreme environments. BMC Genomics, 2021, 22, 635.	1.2	20
784	New Insights Into Mitochondrial Dysfunction at Disease Susceptibility Loci in the Development of Type 2 Diabetes. Frontiers in Endocrinology, 2021, 12, 694893.	1.5	6
785	Epigenetic clock and methylation studies in vervet monkeys. GeroScience, 2022, 44, 699-717.	2.1	18
786	PHIAF: prediction of phage-host interactions with GAN-based data augmentation and sequence-based feature fusion. Briefings in Bioinformatics, 2022, 23, .	3.2	18

#	ARTICLE	IF	CITATIONS
787	Omics for the Improvement of Abiotic, Biotic, and Agronomic Traits in Major Cereal Crops: Applications, Challenges, and Prospects. Plants, 2021, 10, 1989.	1.6	39
788	The genome of the naturally evolved obesity-prone Ossabaw miniature pig. IScience, 2021, 24, 103081.	1.9	9
789	STAT: a fast, scalable, MinHash-based k-mer tool to assess Sequence Read Archive next-generation sequence submissions. Genome Biology, 2021, 22, 270.	3.8	45
790	Current methods, future directions and considerations of DNA-based taxonomic identification in wildlife forensics. Forensic Science International Animals and Environments, 2021, 1, 100030.	0.3	3
791	A Re-Assessment of Positive Selection on Mitochondrial Genomes of High-Elevation Phrynocephalus Lizards. Journal of Molecular Evolution, 2021, 89, 95-102.	0.8	3
792	Specificity of Detection Is the Key Attribute of Selected Reaction Monitoring. SpringerBriefs in Systems Biology, 2013, , 9-13.	0.1	1
793	De Novo Approach to Classify Protein-Coding and Noncoding Transcripts Based on Sequence Composition. Methods in Molecular Biology, 2014, 1182, 203-207.	0.4	8
794	Computational Prediction of B Cell Epitopes from Antigen Sequences. Methods in Molecular Biology, 2014, 1184, 197-215.	0.4	24
795	Bioinformatics Tools for the Discovery of New Nonribosomal Peptides. Methods in Molecular Biology, 2016, 1401, 209-232.	0.4	8
796	Microarrays as Research Tools and Diagnostic Devices. RNA Technologies, 2015, , 259-280.	0.2	7
797	The physiology of trace elements in biological methane production. Bioresource Technology, 2017, 241, 775-786.	4.8	28
798	Sawfly Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. Genome Biology and Evolution, 2020, 12, 1099-1188.	1.1	17
799	Genome Variation Map: a worldwide collection of genome variations across multiple species. Nucleic Acids Research, 2021, 49, D1186-D1191.	6.5	40
800	Robust high-throughput prokaryote de novo assembly and improvement pipeline for Illumina data. Microbial Genomics, 2016, 2, e000083.	1.0	208
801	Genomic correlates of extraintestinal infection are linked with changes in cell morphology in Campylobacter jejuni. Microbial Genomics, 2019, 5, .	1.0	6
802	Genomic surveillance of Escherichia coli ST131 identifies local expansion and serial replacement of subclones. Microbial Genomics, 2020, 6, .	1.0	33
803	Comprehensive genome analyses of Sellimonas intestinalis, a potential biomarker of homeostasis gut recovery. Microbial Genomics, 2020, 6, .	1.0	28
819	Motor Function Deficits in the Estrogen Receptor Beta Knockout Mouse: Role on Excitatory Neurotransmission and Myelination in the Motor Cortex. Neuroendocrinology, 2021, 111, 27-44.	1.2	10

#	ARTICLE	IF	CITATIONS
821	Oncodomains: A protein domain-centric framework for analyzing rare variants in tumor samples. PLoS Computational Biology, 2017, 13, e1005428.	1.5	25
822	A new domestic cat genome assembly based on long sequence reads empowers feline genomic medicine and identifies a novel gene for dwarfism. PLoS Genetics, 2020, 16, e1008926.	1.5	79
823	Simultaneous RNA-Seq Analysis of a Mixed Transcriptome of Rice and Blast Fungus Interaction. PLoS ONE, 2012, 7, e49423.	1.1	242
824	The Chaperonin-60 Universal Target Is a Barcode for Bacteria That Enables De Novo Assembly of Metagenomic Sequence Data. PLoS ONE, 2012, 7, e49755.	1.1	130
825	A Comparison of the Whole Genome Approach of MeDIP-Seq to the Targeted Approach of the Infinium HumanMethylation450 BeadChipÂ® for Methylome Profiling. PLoS ONE, 2012, 7, e50233.	1.1	83
826	Planarians as a Model to Assess In Vivo the Role of Matrix Metalloproteinase Genes during Homeostasis and Regeneration. PLoS ONE, 2013, 8, e55649.	1.1	38
827	Consequences of Normalizing Transcriptomic and Genomic Libraries of Plant Genomes Using a Duplex-Specific Nuclease and Tetramethylammonium Chloride. PLoS ONE, 2013, 8, e55913.	1.1	37
828	Sequencing and Characterisation of an Extensive Atlantic Salmon (Salmo salar L.) MicroRNA Repertoire. PLoS ONE, 2013, 8, e70136.	1.1	29
829	Increasing the Yield in Targeted Next-Generation Sequencing by Implicating CNV Analysis, Non-Coding Exons and the Overall Variant Load: The Example of Retinal Dystrophies. PLoS ONE, 2013, 8, e78496.	1.1	199
830	CNVannotator: A Comprehensive Annotation Server for Copy Number Variation in the Human Genome. PLoS ONE, 2013, 8, e80170.	1.1	26
831	On the Encoding of Proteins for Disordered Regions Prediction. PLoS ONE, 2013, 8, e82252.	1.1	8
832	Sebnif: An Integrated Bioinformatics Pipeline for the Identification of Novel Large Intergenic Noncoding RNAs (lincRNAs) - Application in Human Skeletal Muscle Cells. PLoS ONE, 2014, 9, e84500.	1.1	21
833	Bioinformatics Analysis of Bacterial Annexins â€" Putative Ancestral Relatives of Eukaryotic Annexins. PLoS ONE, 2014, 9, e85428.	1.1	14
834	The Vertebrate RCAN Gene Family: Novel Insights into Evolution, Structure and Regulation. PLoS ONE, 2014, 9, e85539.	1.1	19
835	The Draft Genome Sequence of European Pear (Pyrus communis L. â€˜Bartlettâ€™). PLoS ONE, 2014, 9, e92644.	1.1	241
836	Finding Sequences for over 270 Orphan Enzymes. PLoS ONE, 2014, 9, e97250.	1.1	16
837	Comparison of Deep-Water Viromes from the Atlantic Ocean and the Mediterranean Sea. PLoS ONE, 2014, 9, e100600.	1.1	42
838	Coherent Somatic Mutation in Autoimmune Disease. PLoS ONE, 2014, 9, e101093.	1.1	24

#	Article	IF	Citations
839	PredPPCrys: Accurate Prediction of Sequence Cloning, Protein Production, Purification and Crystallization Propensity from Protein Sequences Using Multi-Step Heterogeneous Feature Fusion and Selection. PLoS ONE, 2014, 9, e105902.	1.1	27
840	Coordinated Gene Expression of Neuroinflammatory and Cell Signaling Markers in Dorsolateral Prefrontal Cortex during Human Brain Development and Aging. PLoS ONE, 2014, 9, e110972.	1.1	44
841	A Note on an Exon-Based Strategy to Identify Differentially Expressed Genes in RNA-Seq Experiments. PLoS ONE, 2014, 9, e115964.	1.1	12
842	Molecular Bases of Catalysis and ADP-Ribose Preference of Human Mn2+-Dependent ADP-Ribose/CDP-Alcohol Diphosphatase and Conversion by Mutagenesis to a Preferential Cyclic ADP-Ribose Phosphohydrolase. PLoS ONE, 2015, 10, e0118680.	1.1	3
843	Population Genomic Analysis of 962 Whole Genome Sequences of Humans Reveals Natural Selection in Non-Coding Regions. PLoS ONE, 2015, 10, e0121644.	1.1	13
844	Structural Effects of Protein Aging: Terminal Marking by Deamidation in Human Triosephosphate Isomerase. PLoS ONE, 2015, 10, e0123379.	1.1	18
845	Increasing Nucleosome Occupancy Is Correlated with an Increasing Mutation Rate so Long as DNA Repair Machinery Is Intact. PLoS ONE, 2015, 10, e0136574.	1.1	29
846	Re-Annotator: Annotation Pipeline for Microarray Probe Sequences. PLoS ONE, 2015, 10, e0139516.	1.1	94
847	Transcriptomic Analysis of Grapevine (cv. Summer Black) Leaf, Using the Illumina Platform. PLoS ONE, 2016, 11, e0147369.	1.1	20
848	GNAI3: Another Candidate Gene to Screen in Persons with Ocular Albinism. PLoS ONE, 2016, 11, e0162273.	1.1	3
849	Large-scale bioactivity analysis of the small-molecule assayed proteome. PLoS ONE, 2017, 12, e0171413.	1.1	4
850	DNApod: DNA polymorphism annotation database from next-generation sequence read archives. PLoS ONE, 2017, 12, e0172269.	1.1	2
851	Effects of age and nutritional state on the expression of gustatory receptors in the honeybee (Apis) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50	1.1	20
852	Transcription of putative tonoplast transporters in response to glyphosate and paraquat stress in Conyza bonariensis and Conyza canadensis and selection of reference genes for qRT-PCR. PLoS ONE, 2017, 12, e0180794.	1.1	27
853	Bayesian Phylogenetic Analysis of Avipoxviruses from North American Wild Birds Demonstrates New Insights into Host Specificity and Interspecies Transmission. Avian Diseases, 2019, 63, 427.	0.4	8
854	StructAnalyzer - a tool for sequence vs. structure similarity analysis. Acta Biochimica Polonica, 2017, 63, 753-757.	0.3	5
855	M-GWAS for the Gut Microbiome in Chinese Adults Illuminates on Complex Diseases. SSRN Electronic Journal, 0, , .	0.4	4
856	A catalogue of human secreted proteins and its implications. AIMS Biophysics, 2016, 3, 563-570.	0.3	5

#	ARTICLE	IF	CITATIONS
857	Systematic Identification and Definition of Consistently Well-Characterized Protein-Coding Exons Using Next Generation Sequencing Technology. Journal of Genomes and Exomes, 0, 2, 1-18.	0.0	1
858	PFP-RFSM: Protein fold prediction by using random forests and sequence motifs. Journal of Biomedical Science and Engineering, 2013, 06, 1161-1170.	0.2	10
859	Comparative genomics explains the evolutionary success of reef-forming corals. ELife, 2016, 5, .	2.8	169
860	Structural modeling of the flagellum MS ring protein FliF reveals similarities to the type III secretion system and sporulation complex. PeerJ, 2016, 4, e1718.	0.9	30
861	Variant profiling of evolving prokaryotic populations. PeerJ, 2017, 5, e2997.	0.9	16
862	Strain- and plasmid-level deconvolution of a synthetic metagenome by sequencing proximity ligation products. PeerJ, 2014, 2, e415.	0.9	111
863	Potential Autoepitope within the Extracellular Region of Contactin-Associated Protein-like 2 in Mice. British Journal of Medicine and Medical Research, 2014, 4, 416-432.	0.2	1
865	Data integration and evolutionary analysis of long non-coding RNAs in 25 flowering plants. BMC Genomics, 2021, 22, 739.	1.2	7
866	Transcriptome dynamics during metamorphosis of imaginal discs into wings and thoracic dorsum in Apis mellifera castes. BMC Genomics, 2021, 22, 756.	1.2	7
867	Citrobacter amalonaticus Inhibits the Growth of Citrobacter rodentium in the Gut Lumen. MBio, 2021, 12, e0241021.	1.8	9
869	A Reference Rice Genome Sequence in the 10K Genome Era. , 2013, , 1-7.		0
870	Expression profiling of putative type 2 diabetes susceptibility genes in human islets and in rat beta cell lines. Journal of Diabetes Mellitus, 2013, 03, 27-32.	0.1	0
871	Can We Understand Parameter Values in the Human Genome?. Springer Proceedings in Complexity, 2013, , 1071-1076.	0.2	0
872	In Silico Analysis of the CST6 Tumor Suppressor Gene. International Journal of Systems Biology and Biomedical Technologies, 2013, 2, 42-58.	0.2	1
873	An Information Integration Approach for Classifying Coding and Non-Coding Genomic Data. Lecture Notes in Electrical Engineering, 2014, , 1085-1093.	0.3	0
874	Metagenomic Analysis of the Saliva Microbiome with Merlin. Advances in Intelligent Systems and Computing, 2014, , 191-199.	0.5	1
875	GenoScan: Genomic Scanner for Putative miRNA Precursors. Lecture Notes in Computer Science, 2014, , 266-277.	1.0	0
876	Revealing Cell-Type Specific Differences in Protein Occupancy on RNA. Springer Theses, 2015, , 73-88.	0.0	0

#	Article	IF	Citations
878	Taxonomy and Classification of Viruses. , 0, , 1390-1404.		4
883	Genomic Analysis of the Moderately Haloalkaliphilic Bacterium Oceanobacillus kimchii Strain X50T with Improved High-Quality Draft Genome Sequences. Journal of Microbiology and Biotechnology, 2015, 25, 1971-1976.	0.9	1
891	Improving Studentsâ€™ Representational Competence through a Course-Based Undergraduate Research Experience. Models and Modeling in Science Education, 2018, , 177-201.	0.6	3
892	Transcriptome and Epigenome Applications for Coronary Heart Disease Research. , 2018, , 572-581.		0
896	Comparative Analyses of 35 Marine Mammal Genomes Provide Insights into the Evolution of Aquatic Life. SSRN Electronic Journal, 0, , .	0.4	0
898	Application of shotgun metagenomics to smoked salmon experimentally spiked: Comparison between sequencing and microbiological data using different bioinformatic approaches. Italian Journal of Food Safety, 2019, 8, 8462.	0.5	1
904	Role of the BMP6 protein in breast cancer and other types of cancer. Growth Factors, 2021, 39, 1-13.	0.5	5
910	Flexible approaches for teaching computational genomics in a health information management program. Perspectives in Health Information Management / AHIMA, American Health Information Management Association, 2013, 10, 1b.	0.0	2
911	A Previously Undiscovered Circular RNA, circTNFAIP3, and Its Role in Coronavirus Replication. MBio, 2021, 12, e0298421.	1.8	10
913	Comparative analysis of transposable elements provides insights into genome evolution in the genus Camelus. BMC Genomics, 2021, 22, 842.	1.2	4
914	LNCRI: Long Non-Coding RNA Identifier in Multiple Species. IEEE Access, 2021, 9, 167219-167228.	2.6	2
916	Revealing antimicrobial resistance profile of the novel probiotic candidate Faecalibacterium prausnitzii DSM 17677. International Journal of Food Microbiology, 2022, 363, 109501.	2.1	8
917	Deriving Ranges of Optimal Estimated Transcript Expression due to Nonidentifiability. Journal of Computational Biology, 2022, 29, 121-139.	0.8	8
918	Finding novel enzymes by in silico bioprospecting approach. , 2022, , 347-364.		1
919	Isolation and characterization of halophilic isolates from Indian salterns and their screening for production of hydrolytic enzymes. Environmental Challenges, 2022, 6, 100426.	2.0	7
920	Chromosomeâ€level <i>Thlaspi arvense</i> genome provides new tools for translational research and for a newly domesticated cash cover crop of the cooler climates. Plant Biotechnology Journal, 2022, 20, 944-963.	4.1	18
921	A survey on the algorithm and development of multiple sequence alignment. Briefings in Bioinformatics, 2022, 23, .	3.2	8
922	Presence of optrA-mediated linezolid resistance in multiple lineages and plasmids of Enterococcus faecalis revealed by long read sequencing. Microbiology (United Kingdom), 2022, 168, .	0.7	9

#	ARTICLE	IF	CITATIONS
924	Comparative Genomics on Cultivated and Uncultivated Freshwater and Marine â€œ<i>Candidatus</i>Manganitrophaceaeâ€•Species Implies Their Worldwide Reach in Manganese Chemolithoautotrophy. MBio, 2022, 13, e0342121.	1.8	4
925	Chromosome-scale Echinococcus granulosus (genotype G1) genome reveals the Eg95 gene family and conservation of the EG95-vaccine molecule. Communications Biology, 2022, 5, 199.	2.0	7
926	Snake Venomics: Fundamentals, Recent Updates, and a Look to the Next Decade. Toxins, 2022, 14, 247.	1.5	19
927	Sex differences in the genetic regulation of the blood transcriptome response to glucocorticoid receptor activation. Translational Psychiatry, 2021, 11, 632.	2.4	8
928	Evaluating the Genetic Capacity of Mycoplasmas for Coenzyme A Biosynthesis in a Search for New Anti-mycoplasma Targets. Frontiers in Microbiology, 2021, 12, 791756.	1.5	2
929	A peptidoform based proteomic strategy for studying functions of postâ€•translational modifications. Proteomics, 2022, 22, 2100316.	1.3	7
930	The Cellular and Viral circRNAome Induced by Respiratory Syncytial Virus Infection. MBio, 2021, 12, e0307521.	1.8	15
932	Empirical Study of Protein Feature Representation on Deep Belief Networks Trained With Small Data for Secondary Structure Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2023, 20, 955-966.	1.9	1
933	Prediction and Inferred Evolution of Acid Tolerance Genes in the Biotechnologically Important Acidihalobacter Genus. Frontiers in Microbiology, 2022, 13, 848410.	1.5	6
960	A distributed computational search strategy for the identification of diagnostics targets: application to finding aptamer targets for methicillin-resistant staphylococci. Journal of Integrative Bioinformatics, 2014, 11, 242.	1.0	0
961	Comparative transcriptomics reveals circadian and pluripotency networks as two pillars of longevity regulation. Cell Metabolism, 2022, 34, 836-856.e5.	7.2	33
962	Human Papillomavirus Minor Capsid Protein L2 Mediates Intracellular Trafficking into and Passage beyond the Endoplasmic Reticulum. Microbiology Spectrum, 2022, 10, .	1.2	3
964	Sphingomonas psychrotolerans sp. nov., isolated from root surface of Leontopodium leontopodioides in the Tianshan Mountains, Xinjiang, China. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	5
968	Denitrification in foraminifera has an ancient origin and is complemented by associated bacteria. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, .	3.3	9
969	Chloroplastic pentatricopeptide repeat proteins (PPR) in albino plantlets of Agave angustifolia Haw. reveal unexpected behavior. BMC Plant Biology, 2022, 22, .	1.6	3
970	Insights into the Antimicrobial Resistance Profile of a Next Generation Probiotic Akkermansia muciniphila DSM 22959. International Journal of Environmental Research and Public Health, 2022, 19, 9152.	1.2	7
972	Contrasting long-term dynamics of antimicrobial resistance and virulence plasmids in Salmonella Typhimurium from animals. Microbial Genomics, 2022, 8, .	1.0	1
973	Reconstruction of Archaeal Genomes from Short-Read Metagenomes. Methods in Molecular Biology, 2022, , 487-527.	0.4	0

#	ARTICLE	IF	CITATIONS
976	Genome mining of Fusarium reveals structural and functional diversity of pectin lyases: a bioinformatics approach. 3 Biotech, 2022, 12, .	1.1	1
978	Hephaestia mangrovi sp. nov., a novel endophytic bacterium isolated from Aegiceras corniculatum. International Journal of Systematic and Evolutionary Microbiology, 2022, 72, .	0.8	0
979	Thermal proteome profiling reveals Haemonchus orphan protein HCO_011565 as a target of the nematocidal small molecule UMW-868. Frontiers in Pharmacology, 0, 13, .	1.6	9
980	Immunoinformatics Approach to Design Multi-Epitope-Based Vaccine against Machupo Virus Taking Viral Nucleocapsid as a Potential Candidate. Vaccines, 2022, 10, 1732.	2.1	6
982	REBASE: a database for DNA restriction and modification: enzymes, genes and genomes. Nucleic Acids Research, 2023, 51, D629-D630.	6.5	30
983	WochenendeÂâ€”Âmodular and flexible alignment-based shotgun metagenome analysis. BMC Genomics, 2022, 23, .	1.2	3
984	Reference-based read clustering improves the de novo genome assembly of microbial strains. Computational and Structural Biotechnology Journal, 2023, 21, 444-451.	1.9	0
985	Viridiplantae-specific GLXI and GLXII isoforms co-evolved and detoxify glucosone in planta. Plant Physiology, 2023, 191, 1214-1233.	2.3	3
986	Impact of antibiotic perturbation on fecal viral communities in mice. G3: Genes, Genomes, Genetics, 2023, 13, .	0.8	1
987	Proteomic analysis of Sarcoptes scabiei reveals that proteins differentially expressed between eggs and female adult stages are involved predominantly in genetic information processing, metabolism and/or host-parasite interactions. PLoS Neglected Tropical Diseases, 2022, 16, e0010946.	1.3	0
988	Small RNA Targets: Advances in Prediction Tools and High-Throughput Profiling. Biology, 2022, 11, 1798.	1.3	3
989	New insights into the regulation mechanism of red claw crayfish (Cherax quadricarinatus) hepatopancreas under air exposure using transcriptome analysis. Fish and Shellfish Immunology, 2023, 132, 108505.	1.6	1
990	Multiomics Integration at Single-Cell Resolution Using Bayesian Networks: A Case Study in Hepatocellular Carcinoma. OMICS A Journal of Integrative Biology, 2023, 27, 24-33.	1.0	1
991	A genome-wide association study identifies distinct variants associated with pulmonary function among European and African ancestries from the UK Biobank. Communications Biology, 2023, 6, .	2.0	3
992	The redlegged earth mite draft genome provides new insights into pesticide resistance evolution and demography in its invasive Australian range. Journal of Evolutionary Biology, 2023, 36, 381-398.	0.8	5
993	The effects of altered <scp>DNA</scp> damage repair genes on mutational processes and immune cell infiltration in esophageal squamous cell carcinoma. Cancer Medicine, 2023, 12, 10077-10090.	1.3	2
995	Comparative Genomics Identifies Novel Genetic Changes Associated with Oxacillin, Vancomycin and Daptomycin Susceptibility in ST100 Methicillin-Resistant Staphylococcus aureus. Antibiotics, 2023, 12, 372.	1.5	2
996	Functionally Significant Variants in Genes Associated with Abdominal Obesity: A Review. Journal of Personalized Medicine, 2023, 13, 460.	1.1	3

#	Article	IF	Citations
998	A novel circular RNA circRBMS3 regulates proliferation and metastasis of osteosarcoma by targeting miR-424-eIF4B/YRDC axis. Aging, 2023, , 1564-1590.	1.4	2
999	Unveiling the role of emerging metagenomics for the examination of hypersaline environments. Biotechnology and Genetic Engineering Reviews, 0, , 1-39.	2.4	2
1001	Standardization and Interpretation of RNA-sequencing for Transplantation. Transplantation, 2023, 107, 2155-2167.	0.5	3
1002	Comparing genomic variant identification protocols for Candida auris. Microbial Genomics, 2023, 9, .	1.0	2
1004	PHIHNE: predicting Phage-Host Interaction through Heterogeneous Network Embedding. , 2022, , .		0
1009	Using De Novo Metagenome Assembly for Improved Metagenomic Classification. , 2023, , .		0
1013	Bioinformatics and Biostatistics in Precision Medicine. , 2023, , 189-235.		1