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Nucleic Acids Research

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Citation Report

#	ARTICLE	IF	CITATIONS
1	Efficient and accurate detection of splice junctions from RNA-seq with Portcullis. <i>GigaScience</i> , 2018, 7, .	3.3	98
2	Haploinsufficiency in the ANKS1B gene encoding AIDA-1 leads to a neurodevelopmental syndrome. <i>Nature Communications</i> , 2019, 10, 3529.	5.8	20
3	Introduction to Biotech Entrepreneurship: From Idea to Business. , 2019, , .		0
4	Computational Biology Solutions to Identify Enhancers-target Gene Pairs. <i>Computational and Structural Biotechnology Journal</i> , 2019, 17, 821-831.	1.9	29
5	Multilayered control of exon acquisition permits the emergence of novel forms of regulatory control. <i>Genome Biology</i> , 2019, 20, 141.	3.8	13
6	Missense mutations in the C-terminal portion of the B4GALNT2-encoded glycosyltransferase underlying the Sd(a ⁺) phenotype. <i>Biochemistry and Biophysics Reports</i> , 2019, 19, 100659.	0.7	19
7	Comparative Analysis of Gene Expression in Virulent and Attenuated Strains of Infectious Bronchitis Virus at Subcodon Resolution. <i>Journal of Virology</i> , 2019, 93, .	1.5	26
8	Brd4 and P300 Confer Transcriptional Competency during Zygotic Genome Activation. <i>Developmental Cell</i> , 2019, 49, 867-881.e8.	3.1	108
9	Germline mutations in the transcription factor IKZF5 cause thrombocytopenia. <i>Blood</i> , 2019, 134, 2070-2081.	0.6	29
10	PolyASite 2.0: a consolidated atlas of polyadenylation sites from 3 ^{â€²} end sequencing. <i>Nucleic Acids Research</i> , 2020, 48, D174-D179.	6.5	110
11	Characterization of the transient fluorescence wave phenomenon that occurs during H2 production in <i>Chlamydomonas reinhardtii</i> . <i>Journal of Experimental Botany</i> , 2019, 70, 6321-6336.	2.4	15
12	Bovine Genome Database: new annotation tools for a new reference genome. <i>Nucleic Acids Research</i> , 2019, 48, D676-D681.	6.5	18
13	Bioinformatics for Marine Products: An Overview of Resources, Bottlenecks, and Perspectives. <i>Marine Drugs</i> , 2019, 17, 576.	2.2	26
14	The ProteomeXchange consortium in 2020: enabling "big data" approaches in proteomics. <i>Nucleic Acids Research</i> , 2020, 48, D1145-D1152.	6.5	491
15	Complex alternative splicing of human Endonuclease V mRNA, but evidence for only a single protein isoform. <i>PLoS ONE</i> , 2019, 14, e0225081.	1.1	3
16	Genotype-Phenotype Association Analysis Reveals New Pathogenic Factors for Osteogenesis Imperfecta Disease. <i>Frontiers in Pharmacology</i> , 2019, 10, 1200.	1.6	11
17	ReMap 2020: a database of regulatory regions from an integrative analysis of Human and Arabidopsis DNA-binding sequencing experiments. <i>Nucleic Acids Research</i> , 2020, 48, D180-D188.	6.5	95
18	NPInter v4.0: an integrated database of ncRNA interactions. <i>Nucleic Acids Research</i> , 2020, 48, D160-D165.	6.5	106

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19	ENdb: a manually curated database of experimentally supported enhancers for human and mouse. <i>Nucleic Acids Research</i> , 2019, 48, D51-D57.	6.5	41
20	Evolutionary Analysis of Bile Acid-Conjugating Enzymes Reveals a Complex Duplication and Reciprocal Loss History. <i>Genome Biology and Evolution</i> , 2019, 11, 3256-3268.	1.1	11
21	PlantRegMap: charting functional regulatory maps in plants. <i>Nucleic Acids Research</i> , 2020, 48, D1104-D1113.	6.5	333
22	Ensembl 2020. <i>Nucleic Acids Research</i> , 2020, 48, D682-D688.	6.5	1,076
23	The English People at War in the Age of Henry VIII, by Steven Gunn. <i>English Historical Review</i> , 2019, . .	0.0	0
24	Double triage to identify poorly annotated genes in maize: The missing link in community curation. <i>PLoS ONE</i> , 2019, 14, e0224086.	1.1	10
25	Low complexity regions in the proteins of prokaryotes perform important functional roles and are highly conserved. <i>Nucleic Acids Research</i> , 2019, 47, 9998-10009.	6.5	44
26	Phenotypic Plasticity of Fibroblasts during Mammary Carcinoma Development. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4438.	1.8	19
27	Overlapping protein-coding genes in human genome and their coincidental expression in tissues. <i>Scientific Reports</i> , 2019, 9, 13377.	1.6	20
28	RNA-seq-based identification of Star upregulation by islet amyloid formation. <i>Protein Engineering, Design and Selection</i> , 2019, 32, 67-76.	1.0	5
29	An Exonic Switch Regulates Differential Accession of microRNAs to the Cd34 Transcript in Atherosclerosis Progression. <i>Genes</i> , 2019, 10, 70.	1.0	6
30	Expression induction of a class of RD26 genes by drought and salinity stresses in maize. <i>Biologia (Poland)</i> , 2019, 74, 1237-1246.	0.8	1
31	Eutherian third-party data gene collections. <i>Gene Reports</i> , 2019, 16, 100414.	0.4	4
32	Zebrafish macroH2A variants have distinct embryo localization and function. <i>Scientific Reports</i> , 2019, 9, 8632.	1.6	5
33	Accelerating Climate Resilient Plant Breeding by Applying Next-Generation Artificial Intelligence. <i>Trends in Biotechnology</i> , 2019, 37, 1217-1235.	4.9	134
34	Non-canonical translation initiation in yeast generates a cryptic pool of mitochondrial proteins. <i>Nucleic Acids Research</i> , 2019, 47, 5777-5791.	6.5	56
35	Human protein-coding genes and gene feature statistics in 2019. <i>BMC Research Notes</i> , 2019, 12, 315.	0.6	106
36	BarkBase: Epigenomic Annotation of Canine Genomes. <i>Genes</i> , 2019, 10, 433.	1.0	25

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37	HOTAIR as a Prognostic Predictor for Diverse Human Cancers: A Meta- and Bioinformatics Analysis. <i>Cancers</i> , 2019, 11, 778.	1.7	18
38	VarMap: a web tool for mapping genomic coordinates to protein sequence and structure and retrieving protein structural annotations. <i>Bioinformatics</i> , 2019, 35, 4854-4856.	1.8	46
39	g:Profiler: a web server for functional enrichment analysis and conversions of gene lists (2019) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 662	6.5	3,302
40	Challenges and promise at the interface of metaproteomics and genomics: an overview of recent progress in metaproteogenomic data analysis. <i>Expert Review of Proteomics</i> , 2019, 16, 375-390.	1.3	86
41	Aberrant expression of alternative splicing variants in multiple sclerosis – A systematic review. <i>Autoimmunity Reviews</i> , 2019, 18, 721-732.	2.5	19
42	The rs1126616 Single Nucleotide Polymorphism of the Osteopontin Gene Is Independently Associated with Cardiovascular Events in a Chronic Kidney Disease Cohort. <i>Journal of Clinical Medicine</i> , 2019, 8, 592.	1.0	6
43	Volatile 1-octen-3-ol increases patulin production by <i>Penicillium expansum</i> on a patulin-suppressing medium. <i>Mycotoxin Research</i> , 2019, 35, 329-340.	1.3	11
44	Use of whole exome sequencing in the NICU: Case of an extremely low birth weight infant with syndromic features. <i>Molecular and Cellular Probes</i> , 2019, 45, 89-93.	0.9	10
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47	DIANA-LncBase v3: indexing experimentally supported miRNA targets on non-coding transcripts. <i>Nucleic Acids Research</i> , 2020, 48, D101-D110.	6.5	137
48	Comparative genomic analysis of eutherian connexin genes. <i>Scientific Reports</i> , 2019, 9, 16938.	1.6	9
49	Comparative analysis of corrected tiger genome provides clues to its neuronal evolution. <i>Scientific Reports</i> , 2019, 9, 18459.	1.6	24
50	SyntDB:Âdefining orthologues of human long noncoding RNAs across primates. <i>Nucleic Acids Research</i> , 2019, 48, D238-D245.	6.5	16
51	BEST: a web server for brain expression Spatio-temporal pattern analysis. <i>BMC Bioinformatics</i> , 2019, 20, 632.	1.2	13
52	Using INTERSPIA to Explore the Dynamics of Protein-Protein Interactions Among Multiple Species. <i>Current Protocols in Bioinformatics</i> , 2019, 68, e88.	25.8	0
53	Knowledge Base Commons (KBCommons) v1.1: a universal framework for multi-omics data integration and biological discoveries. <i>BMC Genomics</i> , 2019, 20, 947.	1.2	16
54	Constitutive Activation of Natural Killer Cells in Primary Biliary Cholangitis. <i>Frontiers in Immunology</i> , 2019, 10, 2633.	2.2	13

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55	Evolutionary Dynamics of Structural Variation at a Key Locus for Color Pattern Diversification in Cichlid Fishes. <i>Genome Biology and Evolution</i> , 2019, 11, 3452-3465.	1.1	15
56	100 Years of evolving geneâ€“disease complexities and scientific debutants. <i>Briefings in Bioinformatics</i> , 2020, 21, 885-905.	3.2	36
57	Comparative Transcriptomics Analyses across Species, Organs, and Developmental Stages Reveal Functionally Constrained lncRNAs. <i>Molecular Biology and Evolution</i> , 2020, 37, 240-259.	3.5	30
58	APAAtlas: decoding alternative polyadenylation across human tissues. <i>Nucleic Acids Research</i> , 2020, 48, D34-D39.	6.5	41
59	The International Genome Sample Resource (IGSR) collection of open human genomic variation resources. <i>Nucleic Acids Research</i> , 2020, 48, D941-D947.	6.5	221
60	Animal-ImputeDB: a comprehensive database with multiple animal reference panels for genotype imputation. <i>Nucleic Acids Research</i> , 2020, 48, D659-D667.	6.5	25
61	Influenza Vaccine Effectiveness in the Inpatient Setting: Evaluation of Potential Bias in the Test-Negative Design by Use of Alternate Control Groups. <i>American Journal of Epidemiology</i> , 2020, 189, 250-260.	1.6	7
62	Individual Responsibilities in Partial Compliance: Skilled Health Worker Emigration from Under-Served Regions. <i>Public Health Ethics</i> , 2020, 13, 89-98.	0.4	0
63	Metatranscriptomics yields new genomic resources and sensitive detection of infections for diverse blood parasites. <i>Molecular Ecology Resources</i> , 2020, 20, 14-28.	2.2	25
64	VarSite: Disease variants and protein structure. <i>Protein Science</i> , 2020, 29, 111-119.	3.1	77
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66	Enhancers Facilitate the Birth of De Novo Genes and Gene Integration into Regulatory Networks. <i>Molecular Biology and Evolution</i> , 2020, 37, 1165-1178.	3.5	41
67	Genome-Scale Model-Based Identification of Metabolite Indicators for Early Detection of Kidney Toxicity. <i>Toxicological Sciences</i> , 2020, 173, 293-312.	1.4	5
68	RNAInter in 2020: RNA interactome repository with increased coverage and annotation. <i>Nucleic Acids Research</i> , 2020, 48, D189-D197.	6.5	173
69	Ensembl Genomes 2020â€“enabling non-vertebrate genomic research. <i>Nucleic Acids Research</i> , 2020, 48, D689-D695.	6.5	416
70	Nodal paralogues underlie distinct mechanisms for visceral leftâ€“right asymmetry in reptiles and mammals. <i>Nature Ecology and Evolution</i> , 2020, 4, 261-269.	3.4	20
71	Integrating Biology With Rat Genomic Tools. , 2020, , 811-825.		0
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73	Factorial study of the RNA-seq computational workflow identifies biases as technical gene signatures. <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa043.	1.5	4
74	Combined use of feature engineering and machine-learning to predict essential genes in <i>Drosophila melanogaster</i> . <i>NAR Genomics and Bioinformatics</i> , 2020, 2, lqaa051.	1.5	10
75	Aberration of the modulatory functions of intronic microRNA hsa-miR-933 on its host gene ATF2 results in type II diabetes mellitus and neurodegenerative disease development. <i>Human Genomics</i> , 2020, 14, 34.	1.4	6
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78	A Collinearity-Incorporating Homology Inference Strategy for Connecting Emerging Assemblies in the Triticeae Tribe as a Pilot Practice in the Plant Pangenomic Era. <i>Molecular Plant</i> , 2020, 13, 1694-1708.	3.9	126
79	A possible universal role for mRNA secondary structure in bacterial translation revealed using a synthetic operon. <i>Nature Communications</i> , 2020, 11, 4827.	5.8	11
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82	Validation of a Combined Transcriptome and T Cell Receptor Alpha/Beta (TRA/TRB) Repertoire Assay at the Single Cell Level for Paucicellular Samples. <i>Frontiers in Immunology</i> , 2020, 11, 1999.	2.2	3
83	Functional signatures of evolutionarily young CTCF binding sites. <i>BMC Biology</i> , 2020, 18, 132.	1.7	9
84	Transcriptional characterization of conjunctival melanoma identifies the cellular tumor microenvironment and prognostic gene signatures. <i>Scientific Reports</i> , 2020, 10, 17022.	1.6	28
85	Culture of rabbit caecum organoids by reconstituting the intestinal stem cell niche in vitro with pharmacological inhibitors or L-WRN conditioned medium. <i>Stem Cell Research</i> , 2020, 48, 101980.	0.3	11
86	DrLLPS: a data resource of liquid-liquid phase separation in eukaryotes. <i>Nucleic Acids Research</i> , 2020, 48, D288-D295.	6.5	112
87	Reconstruction of the Carbohydrate 6-O Sulfotransferase Gene Family Evolution in Vertebrates Reveals Novel Member, CHST16, Lost in Amniotes. <i>Genome Biology and Evolution</i> , 2020, 12, 993-1012.	1.1	4
88	Natural variation in meiotic recombination rate shapes introgression patterns in intraspecific hybrids between wild and domesticated barley. <i>New Phytologist</i> , 2020, 228, 1852-1863.	3.5	26
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91	Mechanistic Similarities between 3D Human Bronchial Epithelium and Mice Lung, Exposed to Copper Oxide Nanoparticles, Support Non-Animal Methods for Hazard Assessment. <i>Small</i> , 2020, 16, e2000527.	5.2	11
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98	Novel Genomic Regions Associated with Intramuscular Fatty Acid Composition in Rabbits. <i>Animals</i> , 2020, 10, 2090.	1.0	12
99	Longitudinal Multi-omics Analyses Identify Responses of Megakaryocytes, Erythroid Cells, and Plasmablasts as Hallmarks of Severe COVID-19. <i>Immunity</i> , 2020, 53, 1296-1314.e9.	6.6	278
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108	Evolutionary History of the Risk of SNPs for Diffuse-Type Gastric Cancer in the Japanese Population. <i>Genes</i> , 2020, 11, 775.	1.0	2

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110	Comprehensive Analysis of LincRNAs in Classical and Basal-Like Subtypes of Pancreatic Cancer. <i>Cancers</i> , 2020, 12, 2077.	1.7	6
111	Identifying the key regulators that promote cell-cycle activity in the hearts of early neonatal pigs after myocardial injury. <i>PLoS ONE</i> , 2020, 15, e0232963.	1.1	14
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115	Conservation analysis of core cell cycle regulators and their transcriptional behavior during limb regeneration in <i>Ambystoma mexicanum</i> . <i>Mechanisms of Development</i> , 2020, 164, 103651.	1.7	6
116	Gene expression and functional deficits underlie TREM2-knockout microglia responses in human models of Alzheimer's disease. <i>Nature Communications</i> , 2020, 11, 5370.	5.8	160
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127	Comprehensive analysis of structural variants in breast cancer genomes using single-molecule sequencing. <i>Genome Research</i> , 2020, 30, 1258-1273.	2.4	72
128	Candidate risk genes for bipolar disorder are highly conserved during evolution and highly interconnected. <i>Bipolar Disorders</i> , 2021, 23, 400-408.	1.1	8
129	Review on the Computational Genome Annotation of Sequences Obtained by Next-Generation Sequencing. <i>Biology</i> , 2020, 9, 295.	1.3	45
130	B chromosomes of multiple species have intense evolutionary dynamics and accumulated genes related to important biological processes. <i>BMC Genomics</i> , 2020, 21, 656.	1.2	22
131	Exploring Non-coding RNAs in RNAcentral. <i>Current Protocols in Bioinformatics</i> , 2020, 71, e104.	25.8	6
132	Protein Databases Related to Liquid-Liquid Phase Separation. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6796.	1.8	27
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142	Role of the Transcription Factor Yin Yang 1 and Its Selectively Identified Target Survivin in High-Grade B-Cells Non-Hodgkin Lymphomas: Potential Diagnostic and Therapeutic Targets. <i>International Journal of Molecular Sciences</i> , 2020, 21, 6446.	1.8	7
143	Genetic architecture of complex traits and disease risk predictors. <i>Scientific Reports</i> , 2020, 10, 12055.	1.6	14
144	Novel Transformer Networks for Improved Sequence Labeling in genomics. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 97-106.	1.9	15

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145	Expression of acid-labile subunit (ALS) in developing and adult zebrafish and its role in dorso-ventral patterning during development. <i>General and Comparative Endocrinology</i> , 2020, 299, 113591.	0.8	7
146	Investigation of Genetic Variations of IL6 and IL6R as Potential Prognostic and Pharmacogenetics Biomarkers: Implications for COVID-19 and Neuroinflammatory Disorders. <i>Life</i> , 2020, 10, 351.	1.1	24
147	Microenvironment Remodeling and Subsequent Clinical Implications in Diffuse Large B-Cell Histologic Variant of Richter Syndrome. <i>Frontiers in Immunology</i> , 2020, 11, 594841.	2.2	11
148	Benchmarking Orthogroup Inference Accuracy: Revisiting Orthobench. <i>Genome Biology and Evolution</i> , 2020, 12, 2258-2266.	1.1	23
149	Gene expression responses to Zika virus infection in peripheral blood mononuclear cells from pregnant and non-pregnant women. <i>MicrobiologyOpen</i> , 2020, 9, e1134.	1.2	5
150	Computational methods for detecting cancer hotspots. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3567-3576.	1.9	12
151	Transcriptome and translome changes in germinated pollen under heat stress uncover roles of transporter genes involved in pollen tube growth. <i>Plant, Cell and Environment</i> , 2021, 44, 2167-2184.	2.8	25
152	Corneal tissue induces transcription of metallothioneins in monocyte-derived human macrophages. <i>Molecular Immunology</i> , 2020, 128, 188-194.	1.0	5
153	Multicenter Comparison of Molecular Tumor Boards in The Netherlands: Definition, Composition, Methods, and Targeted Therapy Recommendations. <i>Oncologist</i> , 2021, 26, e1347-e1358.	1.9	28
154	Disruptive natural selection by male reproductive potential prevents underexpression of protein-coding genes on the human Y chromosome as a self-domestication syndrome. <i>BMC Genetics</i> , 2020, 21, 89.	2.7	8
155	wg-blimp: an end-to-end analysis pipeline for whole genome bisulfite sequencing data. <i>BMC Bioinformatics</i> , 2020, 21, 169.	1.2	26
156	High confidence copy number variants identified in Holstein dairy cattle from whole genome sequence and genotype array data. <i>Scientific Reports</i> , 2020, 10, 8044.	1.6	16
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