Inanc Birol

List of Publications by Year in descending order

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INANC RIPOL

#	Article	IF	CITATIONS
1	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	27.8	10,282
2	Circos: An information aesthetic for comparative genomics. Genome Research, 2009, 19, 1639-1645.	5.5	9,003
3	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	27.8	7,168
4	Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209.	27.8	5,055
5	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	27.0	4,139
6	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	27.8	4,075
7	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	27.8	3,483
8	Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature, 2015, 517, 576-582.	27.8	3,209
9	ABySS: A parallel assembler for short read sequence data. Genome Research, 2009, 19, 1117-1123.	5.5	3,134
10	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	27.8	2,839
11	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	27.8	1,778
12	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	28.9	1,742
13	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. Nature Genetics, 2010, 42, 181-185.	21.4	1,504
14	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	27.8	1,428
15	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428
16	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	28.9	1,242
17	The genetic landscape of high-risk neuroblastoma. Nature Genetics, 2013, 45, 279-284.	21.4	990
18	De novo assembly and analysis of RNA-seq data. Nature Methods, 2010, 7, 909-912.	19.0	886

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19	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56.	27.8	761
20	Whole-Genome Sequencing and Social-Network Analysis of a Tuberculosis Outbreak. New England Journal of Medicine, 2011, 364, 730-739.	27.0	665
21	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. Cancer Cell, 2014, 26, 319-330.	16.8	665
22	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	16.8	642
23	Genetic Alterations Activating Kinase and Cytokine Receptor Signaling in High-Risk Acute Lymphoblastic Leukemia. Cancer Cell, 2012, 22, 153-166.	16.8	621
24	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. GigaScience, 2013, 2, 10.	6.4	582
25	ABySS 2.0: resource-efficient assembly of large genomes using a Bloom filter. Genome Research, 2017, 27, 768-777.	5.5	526
26	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	5.5	443
27	<i>De novo</i> transcriptome assembly with ABySS. Bioinformatics, 2009, 25, 2872-2877.	4.1	371
28	Assembling the 20 Gb white spruce (<i>Picea glauca</i>) genome from whole-genome shotgun sequencing data. Bioinformatics, 2013, 29, 1492-1497.	4.1	356
29	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. Blood, 2013, 122, 1256-1265.	1.4	349
30	Concurrent <i>CIC</i> mutations, <i>IDH</i> mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. Journal of Pathology, 2012, 226, 7-16.	4.5	272
31	Divergent clonal selection dominates medulloblastoma at recurrence. Nature, 2016, 529, 351-357.	27.8	266
32	Draft genome of the mountain pine beetle, Dendroctonus ponderosae Hopkins, a major forest pest. Genome Biology, 2013, 14, R27.	9.6	260
33	mrsFAST: a cache-oblivious algorithm for short-read mapping. Nature Methods, 2010, 7, 576-577.	19.0	248
34	Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont <i>Grosmannia clavigera</i> , a lodgepole pine pathogen. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2504-2509.	7.1	218
35	The CHORUS experiment to search for νμ →νÏ,, oscillation. Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment, 1997, 401, 7-44.	1.6	209
36	Reduced adenosine-to-inosine miR-455-5p editing promotes melanoma growth and metastasis. Nature Cell Biology, 2015, 17, 311-321.	10.3	205

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37	Improved white spruce (<i>Picea glauca</i>) genome assemblies and annotation of large gene families of conifer terpenoid and phenolic defense metabolism. Plant Journal, 2015, 83, 189-212.	5.7	200
38	LINKS: Scalable, alignment-free scaffolding of draft genomes with long reads. GigaScience, 2015, 4, 35.	6.4	196
39	Hive plotsrational approach to visualizing networks. Briefings in Bioinformatics, 2012, 13, 627-644.	6.5	187
40	Insights into Conifer Giga-Genomes. Plant Physiology, 2014, 166, 1724-1732.	4.8	164
41	Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. Genome Research, 2008, 18, 1906-1917.	5.5	163
42	ARCS: scaffolding genome drafts with linked reads. Bioinformatics, 2018, 34, 725-731.	4.1	161
43	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. Genome Biology, 2010, 11, R82.	9.6	159
44	Metabolic Control Analysis under Uncertainty: Framework Development and Case Studies. Biophysical Journal, 2004, 87, 3750-3763.	0.5	153
45	NanoSim: nanopore sequence read simulator based on statistical characterization. GigaScience, 2017, 6, 1-6.	6.4	149
46	De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. Genome Biology, 2009, 10, R94.	9.6	130
47	Recurrent targets of aberrant somatic hypermutation in lymphoma. Oncotarget, 2012, 3, 1308-1319.	1.8	127
48	Large-scale profiling of microRNAs for The Cancer Genome Atlas. Nucleic Acids Research, 2016, 44, e3-e3.	14.5	125
49	Sealer: a scalable gap-closing application for finishing draft genomes. BMC Bioinformatics, 2015, 16, 230.	2.6	122
50	Locus co-occupancy, nucleosome positioning, and H3K4me1 regulate the functionality of FOXA2-, HNF4A-, and PDX1-bound loci in islets and liver. Genome Research, 2010, 20, 1037-1051.	5.5	109
51	SNP discovery in black cottonwood (<i>Populus trichocarpa</i>) by population transcriptome resequencing. Molecular Ecology Resources, 2011, 11, 81-92.	4.8	104
52	Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. Bioinformatics, 2010, 26, 1277-1283.	4.1	98
53	Tigmint: correcting assembly errors using linked reads from large molecules. BMC Bioinformatics, 2018, 19, 393.	2.6	97
54	Whole Genome Duplication and Enrichment of Metal Cation Transporters Revealed by De Novo Genome Sequencing of Extremely Halotolerant Black Yeast Hortaea werneckii. PLoS ONE, 2013, 8, e71328.	2.5	96

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55	BioBloom tools: fast, accurate and memory-efficient host species sequence screening using bloom filters. Bioinformatics, 2014, 30, 3402-3404.	4.1	95
56	Transcriptome and full-length cDNA resources for the mountain pine beetle, Dendroctonus ponderosae Hopkins, a major insect pest of pine forests. Insect Biochemistry and Molecular Biology, 2012, 42, 525-536.	2.7	93
57	The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. Nature Communications, 2017, 8, 1433.	12.8	86
58	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. Genome Research, 2010, 20, 791-803.	5.5	84
59	ARKS: chromosome-scale scaffolding of human genome drafts with linked read kmers. BMC Bioinformatics, 2018, 19, 234.	2.6	81
60	The genome and transcriptome of the pine saprophyte Ophiostoma piceae, and a comparison with the bark beetle-associated pine pathogen Grosmannia clavigera. BMC Genomics, 2013, 14, 373.	2.8	72
61	ntEdit: scalable genome sequence polishing. Bioinformatics, 2019, 35, 4430-4432.	4.1	67
62	ntHash: recursive nucleotide hashing. Bioinformatics, 2016, 32, 3492-3494.	4.1	61
63	Complete genomic landscape of a recurring sporadic parathyroid carcinoma. Journal of Pathology, 2013, 230, 249-260.	4.5	57
64	ABySS-Explorer: Visualizing Genome Sequence Assemblies. IEEE Transactions on Visualization and Computer Graphics, 2009, 15, 881-888.	4.4	53
65	ntCard: a streaming algorithm for cardinality estimation in genomics data. Bioinformatics, 2017, 33, 1324-1330.	4.1	53
66	Complete Mitochondrial Genome of a Gymnosperm, Sitka Spruce (Picea sitchensis), Indicates a Complex Physical Structure. Genome Biology and Evolution, 2020, 12, 1174-1179.	2.5	49
67	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. Nature Communications, 2021, 12, 2474.	12.8	49
68	AMPlify: attentive deep learning model for discovery of novel antimicrobial peptides effective against WHO priority pathogens. BMC Genomics, 2022, 23, 77.	2.8	48
69	JAGuaR: Junction Alignments to Genome for RNA-Seq Reads. PLoS ONE, 2014, 9, e102398.	2.5	47
70	A highâ€resolution reference genetic map positioning 8.8ÂK genes for the conifer white spruce: structural genomics implications and correspondence with physical distance. Plant Journal, 2017, 90, 189-203.	5.7	47
71	Evolution of gene structure in the conifer Picea glauca: a comparative analysis of the impact of intron size. BMC Plant Biology, 2014, 14, 95.	3.6	46
72	Organellar Genomes of White Spruce (<i>Picea glauca</i>): Assembly and Annotation. Genome Biology and Evolution, 2016, 8, 29-41.	2.5	46

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73	The Genome of the Beluga Whale (Delphinapterus leucas). Genes, 2017, 8, 378.	2.4	39
74	A search for νμ→νÏ,, oscillation. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 1998, 424, 202-212.	4.1	38
75	Updated genome assembly and annotation of Paenibacillus larvae, the agent of American foulbrood disease of honey bees. BMC Genomics, 2011, 12, 450.	2.8	35
76	The Genome of the North American Brown Bear or Grizzly: Ursus arctos ssp. horribilis. Genes, 2018, 9, 598.	2.4	34
77	Base excision repair deficiency signatures implicate germline and somatic <i>MUTYH</i> aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. Journal of Physical Education and Sports Management, 2019, 5, a003681.	1.2	33
78	RNA-Bloom enables reference-free and reference-guided sequence assembly for single-cell transcriptomes. Genome Research, 2020, 30, 1191-1200.	5.5	33
79	Agent-based control of autocatalytic replicators in networks of reactors. Computers and Chemical Engineering, 2005, 29, 807-815.	3.8	32
80	A novel approach to wildlife transcriptomics provides evidence of diseaseâ€mediated differential expression and changes to the microbiome of amphibian populations. Molecular Ecology, 2018, 27, 1413-1427.	3.9	32
81	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X Genomics' GemCode Sequencing Data. PLoS ONE, 2016, 11, e0163059.	2.5	31
82	The miR-185/PAK6 axis predicts therapy response and regulates survival of drug-resistant leukemic stem cells in CML. Blood, 2020, 136, 596-609.	1.4	30
83	LongStitch: high-quality genome assembly correction and scaffolding using long reads. BMC Bioinformatics, 2021, 22, 534.	2.6	30
84	A Clinically Validated Diagnostic Second-Generation Sequencing Assay for Detection of Hereditary BRCA1 and BRCA2 Mutations. Journal of Molecular Diagnostics, 2013, 15, 796-809.	2.8	29
85	Genome sequences of six Phytophthora species threatening forest ecosystems. Genomics Data, 2016, 10, 85-88.	1.3	29
86	Innovations and challenges in detecting long read overlaps: an evaluation of the state-of-the-art. Bioinformatics, 2017, 33, 1261-1270.	4.1	28
87	Genome-wide sequencing as a first-tier screening test for short tandem repeat expansions. Genome Medicine, 2021, 13, 126.	8.2	27
88	De novo Transcriptome Assemblies of Rana (Lithobates) catesbeiana and Xenopus laevis Tadpole Livers for Comparative Genomics without Reference Genomes. PLoS ONE, 2015, 10, e0130720.	2.5	27
89	Calculation of Molecular Weight Distributions in Non-Linear Free-Radical Polymerization Using the Numerical Fractionation Technique. Macromolecular Theory and Simulations, 2002, 11, 533.	1.4	25
90	The Genome of the Northern Sea Otter (Enhydra lutris kenyoni). Genes, 2017, 8, 379.	2.4	24

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91	Genome-Enhanced Detection and Identification (GEDI) of plant pathogens. PeerJ, 2018, 6, e4392.	2.0	24
92	Genome Sequence of Mycoplasma capricolum subsp. capripneumoniae Strain M1601. Journal of Bacteriology, 2011, 193, 6098-6099.	2.2	23
93	Recurrent tumor-specific regulation of alternative polyadenylation of cancer-related genes. BMC Genomics, 2018, 19, 536.	2.8	22
94	Straglr: discovering and genotyping tandem repeat expansions using whole genome long-read sequences. Genome Biology, 2021, 22, 224.	8.8	22
95	ntJoin: Fast and lightweight assembly-guided scaffolding using minimizer graphs. Bioinformatics, 2020, 36, 3885-3887.	4.1	21
96	Trans-NanoSim characterizes and simulates nanopore RNA-sequencing data. GigaScience, 2020, 9, .	6.4	20
97	Assembling genomes using short-read sequencing technology. Genome Biology, 2010, 11, 202.	9.6	19
98	Konnector v2.0: pseudo-long reads from paired-end sequencing data. BMC Medical Genomics, 2015, 8, S1.	1,5	19
99	HLA predictions from the bronchoalveolar lavage fluid and blood samples of eight COVID-19 patients at the pandemic onset. Bioinformatics, 2021, 36, 5271-5273.	4.1	19
100	Kollector: transcript-informed, targeted <i>de novo</i> assembly of gene loci. Bioinformatics, 2017, 33, 1782-1788.	4.1	18
101	Antimicrobial peptides from Rana [Lithobates] catesbeiana: Gene structure and bioinformatic identification of novel forms from tadpoles. Scientific Reports, 2019, 9, 1529.	3.3	18
102	Spruce gigaâ€genomes: structurally similar yet distinctive with differentially expanding gene families and rapidly evolving genes. Plant Journal, 2022, 111, 1469-1485.	5.7	17
103	Effect of environment partitioning on the survival and coexistence of autocatalytic replicators. Physical Review E, 2002, 66, 051916.	2.1	16
104	Optimal pooling for genome re-sequencing with ultra-high-throughput short-read technologies. Bioinformatics, 2008, 24, i32-i40.	4.1	16
105	De novo assembly of the ringed seal (Pusa hispida) blubber transcriptome: A tool that enables identification of molecular health indicators associated with PCB exposure. Aquatic Toxicology, 2017, 185, 48-57.	4.0	16
106	Static and Dynamic Behavior of Autocatalytic Replicators in Reactor Networks. Industrial & Engineering Chemistry Research, 2004, 43, 3972-3993.	3.7	15
107	Templateâ€Directed Synthesis of Bivalent, Broadâ€5pectrum Hosts for Neuromuscular Blocking Agents**. Angewandte Chemie - International Edition, 2022, 61, .	13.8	15
108	Competition between Robust and Nonrobust Autocatalytic Replicators. Industrial & Engineering Chemistry Research, 2002, 41, 3630-3641.	3.7	14

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109	KLEAT: CLEAVAGE SITE ANALYSIS OF TRANSCRIPTOMES. , 2014, , .		14
110	Statics and dynamics of multiple cubic autocatalytic reactions. Physica D: Nonlinear Phenomena, 2000, 144, 279-297.	2.8	13
111	Measuring Complexity in Reactor Networks with Cubic Autocatalytic Reactions. Industrial & Engineering Chemistry Research, 2005, 44, 2781-2791.	3.7	13
112	Dissect: detection and characterization of novel structural alterations in transcribed sequences. Bioinformatics, 2012, 28, i179-i187.	4.1	13
113	HLA alleles measured from COVID-19 patient transcriptomes reveal associations with disease prognosis in a New York cohort. PeerJ, 2021, 9, e12368.	2.0	13
114	Feedback Control of a Continuous-Flow Stirred Tank Reactor with Competing Autocatalators. Industrial & Engineering Chemistry Research, 2003, 42, 3765-3785.	3.7	12
115	LaneRuler: Automated Lane Tracking for DNA Electrophoresis Gel Images. IEEE Transactions on Automation Science and Engineering, 2010, 7, 706-708.	5.2	12
116	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. BMC Genomics, 2013, 14, 550.	2.8	12
117	Human variation database: an open-source database template for genomic discovery. Bioinformatics, 2011, 27, 1155-1156.	4.1	11
118	TAP: a targeted clinical genomics pipeline for detecting transcript variants using RNA-seq data. BMC Medical Genomics, 2018, 11, 79.	1.5	11
119	Results on the coherent interaction of high energy electrons and photons in oriented single crystals. Nuclear Instruments & Methods in Physics Research B, 2005, 234, 128-137.	1.4	10
120	DIDA: Distributed Indexing Dispatched Alignment. PLoS ONE, 2015, 10, e0126409.	2.5	10
121	ORCA: a comprehensive bioinformatics container environment for education and research. Bioinformatics, 2019, 35, 4448-4450.	4.1	10
122	Mining Amphibian and Insect Transcriptomes for Antimicrobial Peptide Sequences with rAMPage. Antibiotics, 2022, 11, 952.	3.7	10
123	Coherent bremsstrahlung, coherent pair production, birefringence, and polarimetry in the 20–170ÂGeV energy range using aligned crystals. Physical Review Special Topics: Accelerators and Beams, 2008, 11, .	1.8	9
124	Approximately conserved quantity in the Hénon-Heiles problem. Physical Review E, 1995, 52, 4750-4753.	2.1	8
125	Konnector: Connecting paired-end reads using a bloom filter de Bruijn graph. , 2014, , .		8
126	Replicated Landscape Genomics Identifies Evidence of Local Adaptation to Urbanization in Wood Frogs. Journal of Heredity, 2019, 110, 707-719.	2.4	8

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127	Mismatch-tolerant, alignment-free sequence classification using multiple spaced seeds and multiindex Bloom filters. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 16961-16968.	7.1	8
128	Kleat: cleavage site analysis of transcriptomes. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 347-58.	0.7	8
129	Complete Chloroplast Genome Sequence of a White Spruce (Picea glauca, Genotype WS77111) from Eastern Canada. Microbiology Resource Announcements, 2019, 8, .	0.6	7
130	Fusion-Bloom: fusion detection in assembled transcriptomes. Bioinformatics, 2020, 36, 2256-2257.	4.1	7
131	Spaced Seed Data Structures forDe NovoAssembly. International Journal of Genomics, 2015, 2015, 1-8.	1.6	6
132	ntEdit+Sealer: Efficient Targeted Error Resolution and Automated Finishing of Longâ€Read Genome Assemblies. Current Protocols, 2022, 2, e442.	2.9	6
133	Physlr: Next-Generation Physical Maps. Dna, 2022, 2, 116-130.	1.3	5
134	The Genome of the Steller Sea Lion (Eumetopias jubatus). Genes, 2019, 10, 486.	2.4	4
135	Complete Chloroplast Genome Sequence of an Engelmann Spruce (<i>Picea engelmannii</i> , Genotype) Tj ET	Qq1_1_0.78	34314 rgBT ((
136	Complete Chloroplast Genome Sequence of a Black Spruce (Picea mariana) from Eastern Canada. Microbiology Resource Announcements, 2020, 9, .	0.6	4
137	The genome of the forest insect pest <i>Pissodes strobi</i> reveals genome expansion and evidence of a <i>Wolbachia</i> endosymbiont. G3: Genes, Genomes, Genetics, 2022, 12, .	1.8	4
138	Linked-read sequencing for detecting short tandem repeat expansions. Scientific Reports, 2022, 12, .	3.3	4
139	Complete Genome Sequence of Mycobacterium chimaera SJ42, a Nonoutbreak Strain from an Immunocompromised Patient with Pulmonary Disease. Genome Announcements, 2017, 5, .	0.8	3
140	ChopStitch: exon annotation and splice graph construction using transcriptome assembly and whole genome sequencing data. Bioinformatics, 2018, 34, 1697-1704.	4.1	3
141	Abstract 926: Whole genome and transcriptome sequencing defines the spectrum of somatic changes in high-risk neuroblastoma. Cancer Research, 2011, 71, 926-926.	0.9	3
142	Simulating a dynamical system in the presence of a 1/f noise. International Journal of Engineering Science, 1998, 36, 265-271.	5.0	2
143	The trigger and DAQ systems of the Na59 experiment. IEEE Transactions on Nuclear Science, 2004, 51, 1482-1487.	2.0	2
144	Software aspects of the Na59 experiment. IEEE Transactions on Nuclear Science, 2004, 51, 1449-1455.	2.0	2

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145	Identifying cancer mutation targets across thousands of samples: MuteProc, a high throughput mutation analysis pipeline. BMC Bioinformatics, 2013, 14, 167.	2.6	2
146	GraphNER: Using Corpus Level Similarities and Graph Propagation for Named Entity Recognition. , 2018, , .		2
147	GapPredict – A Language Model for Resolving Gaps in Draft Genome Assemblies. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 2802-2808.	3.0	2
148	A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. Frontiers in Genetics, 2021, 12, 665888.	2.3	2
149	Identification of New microRNA Biomarkers and Candidate Target Genes in Primitive CML Cells Using Global Comparative RNA analyses. Blood, 2014, 124, 3133-3133.	1.4	2
150	Signs and approximate magnitudes of Lyapunov exponents in continuous time dynamical systems. Journal of Mathematical Physics, 1997, 38, 4594-4605.	1.1	1
151	Investigating the fermentation dynamics structure of recombinant yeast YPB-G. Computers and Chemical Engineering, 2003, 27, 45-54.	3.8	1
152	Spaced seed data structures. , 2014, , .		1
153	Differential Hive Plots: Seeing Networks Change. Leonardo, 2017, 50, 504-504.	0.3	1
154	Genomic and Cytogenetic Characterization of a Balanced Translocation Disrupting <i>NUP98</i> . Cytogenetic and Genome Research, 2017, 152, 117-121.	1.1	1
155	ntPack: A Software Package for Big Data in Genomics. , 2018, , .		1
156	Identification of Genes Frequently Mutated In FL and DLBCL with Transcriptome, Genome and Exome Sequencing. Blood, 2010, 116, 804-804.	1.4	1
157	RResolver: efficient short-read repeat resolution within ABySS. BMC Bioinformatics, 2022, 23, .	2.6	1
158	Determining Zero Lyapunov Exponents in Continuous Time Dynamical Systems. International Journal of Modern Physics A, 1997, 12, 131-135.	1.5	0
159	Some Algebraic Properties of Continuous Time Dynamical Systems. International Journal of Modern Physics A, 1997, 12, 137-142.	1.5	0
160	AGENT-BASED CONTROL OF DISCRETE SPATIALLY DISTRIBUTED SYSTEMS. IFAC Postprint Volumes IPPV / International Federation of Automatic Control, 2005, 38, 549-554.	0.4	0
161	Genomic analysis of a rare human tumor. BMC Bioinformatics, 2010, 11, .	2.6	0
162	Personalized oncogenomics. Genome Biology, 2010, 11, I5.	9.6	0

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163	Endothelial-hematopoietic transition: from the dorsal aorta to the dish. Experimental Hematology, 2013, 41, S26.	0.4	0
164	Comparative RNA-seq analyses identify new microRNA biomarkers and candidate target genes in patients' drug-resistant CD34+ CML stem/progenitor cells. Experimental Hematology, 2015, 43, S63.	0.4	0
165	Interactive SARS-CoV-2 mutation timemaps. F1000Research, 2021, 10, 68.	1.6	0
166	Interactive SARS-CoV-2 mutation timemaps. F1000Research, 2021, 10, 68.	1.6	0
167	UniqTag: Content-Derived Unique and Stable Identifiers for Gene Annotation. PLoS ONE, 2015, 10, e0128026.	2.5	0
168	Global Transcriptome Profiling Identifies a Key Mir-185-PAK6 Axis That Promotes Survival of Leukemic Stem Cells and Drug-Insensitive Blasts in BCR-ABL+ Human Leukemia. Blood, 2018, 132, 931-931.	1.4	0
169	Sequencing and Assembling the Nuclear and Organelle Genomes of North American Spruces. Compendium of Plant Genomes, 2020, , 1-8.	0.5	0
170	Templateâ€Directed Synthesis of Bivalent, Broadâ€Spectrum Hosts for Neuromuscular Blocking Agents**. Angewandte Chemie, 2022, 134, .	2.0	0
171	RNA-Scoop: interactive visualization of transcripts in single-cell transcriptomes. NAR Genomics and Bioinformatics, 2021, 3, lqab105.	3.2	0