

# Inanc Birol

## List of Publications by Year in descending order

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171  
papers

75,977  
citations

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g-index

196  
all docs

196  
docs citations

196  
times ranked

110161  
citing authors

#	ARTICLE	IF	CITATIONS
1	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	13.7	10,282
2	Circos: An information aesthetic for comparative genomics. Genome Research, 2009, 19, 1639-1645.	2.4	9,003
3	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	13.7	7,168
4	Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209.	13.7	5,055
5	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. New England Journal of Medicine, 2013, 368, 2059-2074.	13.9	4,139
6	Integrated genomic characterization of endometrial carcinoma. Nature, 2013, 497, 67-73.	13.7	4,075
7	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	13.7	3,483
8	Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature, 2015, 517, 576-582.	13.7	3,209
9	ABYSS: A parallel assembler for short read sequence data. Genome Research, 2009, 19, 1117-1123.	2.4	3,134
10	Comprehensive molecular characterization of clear cell renal cell carcinoma. Nature, 2013, 499, 43-49.	13.7	2,839
11	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	13.7	1,778
12	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	13.5	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.	9.4	1,504
14	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	13.7	1,428
15	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	7.7	1,428
16	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. Cell, 2014, 158, 929-944.	13.5	1,242
17	The genetic landscape of high-risk neuroblastoma. Nature Genetics, 2013, 45, 279-284.	9.4	990
18	De novo assembly and analysis of RNA-seq data. Nature Methods, 2010, 7, 909-912.	9.0	886

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19	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012, 488, 49-56.	13.7	761
20	Whole-Genome Sequencing and Social-Network Analysis of a Tuberculosis Outbreak. <i>New England Journal of Medicine</i> , 2011, 364, 730-739.	13.9	665
21	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	7.7	665
22	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	7.7	642
23	Genetic Alterations Activating Kinase and Cytokine Receptor Signaling in High-Risk Acute Lymphoblastic Leukemia. <i>Cancer Cell</i> , 2012, 22, 153-166.	7.7	621
24	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	3.3	582
25	ABYSS 2.0: resource-efficient assembly of large genomes using a Bloom filter. <i>Genome Research</i> , 2017, 27, 768-777.	2.4	526
26	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	2.4	443
27	<i>De novo</i> transcriptome assembly with ABySS. <i>Bioinformatics</i> , 2009, 25, 2872-2877.	1.8	371
28	Assembling the 20 Gb white spruce (<i>Picea glauca</i>) genome from whole-genome shotgun sequencing data. <i>Bioinformatics</i> , 2013, 29, 1492-1497.	1.8	356
29	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. <i>Blood</i> , 2013, 122, 1256-1265.	0.6	349
30	Concurrent <i>CIC</i> mutations, <i>IDH</i> mutations, and 1p/19q loss distinguish oligodendrogliomas from other cancers. <i>Journal of Pathology</i> , 2012, 226, 7-16.	2.1	272
31	Divergent clonal selection dominates medulloblastoma at recurrence. <i>Nature</i> , 2016, 529, 351-357.	13.7	266
32	Draft genome of the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major forest pest. <i>Genome Biology</i> , 2013, 14, R27.	13.9	260
33	mrsFAST: a cache-oblivious algorithm for short-read mapping. <i>Nature Methods</i> , 2010, 7, 576-577.	9.0	248
34	Genome and transcriptome analyses of the mountain pine beetle-fungal symbiont <i>Grosmannia clavigera</i>, a lodgepole pine pathogen. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 2504-2509.	3.3	218
35	The CHORUS experiment to search for $\hat{1}/2\hat{1}/4\hat{+}\hat{1}/2\hat{I}$ , oscillation. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 1997, 401, 7-44.	0.7	209
36	Reduced adenosine-to-inosine miR-455-5p editing promotes melanoma growth and metastasis. <i>Nature Cell Biology</i> , 2015, 17, 311-321.	4.6	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. <i>Plant Journal</i> , 2015, 83, 189-212.	2.8	200
38	LINKS: Scalable, alignment-free scaffolding of draft genomes with long reads. <i>GigaScience</i> , 2015, 4, 35.	3.3	196
39	Hive plots--rational approach to visualizing networks. <i>Briefings in Bioinformatics</i> , 2012, 13, 627-644.	3.2	187
40	Insights into Conifer Giga-Genomes. <i>Plant Physiology</i> , 2014, 166, 1724-1732.	2.3	164
41	Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. <i>Genome Research</i> , 2008, 18, 1906-1917.	2.4	163
42	ARCS: scaffolding genome drafts with linked reads. <i>Bioinformatics</i> , 2018, 34, 725-731.	1.8	161
43	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. <i>Genome Biology</i> , 2010, 11, R82.	13.9	159
44	Metabolic Control Analysis under Uncertainty: Framework Development and Case Studies. <i>Biophysical Journal</i> , 2004, 87, 3750-3763.	0.2	153
45	NanoSim: nanopore sequence read simulator based on statistical characterization. <i>GigaScience</i> , 2017, 6, 1-6.	3.3	149
46	De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. <i>Genome Biology</i> , 2009, 10, R94.	13.9	130
47	Recurrent targets of aberrant somatic hypermutation in lymphoma. <i>Oncotarget</i> , 2012, 3, 1308-1319.	0.8	127
48	Large-scale profiling of microRNAs for The Cancer Genome Atlas. <i>Nucleic Acids Research</i> , 2016, 44, e3-e3.	6.5	125
49	Sealer: a scalable gap-closing application for finishing draft genomes. <i>BMC Bioinformatics</i> , 2015, 16, 230.	1.2	122
50	Locus co-occupancy, nucleosome positioning, and H3K4me1 regulate the functionality of FOXA2-, HNF4A-, and PDX1-bound loci in islets and liver. <i>Genome Research</i> , 2010, 20, 1037-1051.	2.4	109
51	SNP discovery in black cottonwood ( <i>Populus trichocarpa</i> ) by population transcriptome resequencing. <i>Molecular Ecology Resources</i> , 2011, 11, 81-92.	2.2	104
52	Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. <i>Bioinformatics</i> , 2010, 26, 1277-1283.	1.8	98
53	Tigmint: correcting assembly errors using linked reads from large molecules. <i>BMC Bioinformatics</i> , 2018, 19, 393.	1.2	97
54	Whole Genome Duplication and Enrichment of Metal Cation Transporters Revealed by De Novo Genome Sequencing of Extremely Halotolerant Black Yeast <i>Hortaea werneckii</i> . <i>PLoS ONE</i> , 2013, 8, e71328.	1.1	96

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55	BioBloom tools: fast, accurate and memory-efficient host species sequence screening using bloom filters. <i>Bioinformatics</i> , 2014, 30, 3402-3404.	1.8	95
56	Transcriptome and full-length cDNA resources for the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major insect pest of pine forests. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 525-536.	1.2	93
57	The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. <i>Nature Communications</i> , 2017, 8, 1433.	5.8	86
58	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. <i>Genome Research</i> , 2010, 20, 791-803.	2.4	84
59	ARKS: chromosome-scale scaffolding of human genome drafts with linked read kmers. <i>BMC Bioinformatics</i> , 2018, 19, 234.	1.2	81
60	The genome and transcriptome of the pine saprophyte <i>Ophiostoma piceae</i> , and a comparison with the bark beetle-associated pine pathogen <i>Grosmannia clavigera</i> . <i>BMC Genomics</i> , 2013, 14, 373.	1.2	72
61	ntEdit: scalable genome sequence polishing. <i>Bioinformatics</i> , 2019, 35, 4430-4432.	1.8	67
62	ntHash: recursive nucleotide hashing. <i>Bioinformatics</i> , 2016, 32, 3492-3494.	1.8	61
63	Complete genomic landscape of a recurring sporadic parathyroid carcinoma. <i>Journal of Pathology</i> , 2013, 230, 249-260.	2.1	57
64	ABYSS-Explorer: Visualizing Genome Sequence Assemblies. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2009, 15, 881-888.	2.9	53
65	ntCard: a streaming algorithm for cardinality estimation in genomics data. <i>Bioinformatics</i> , 2017, 33, 1324-1330.	1.8	53
66	Complete Mitochondrial Genome of a Gymnosperm, Sitka Spruce ( <i>Picea sitchensis</i> ), Indicates a Complex Physical Structure. <i>Genome Biology and Evolution</i> , 2020, 12, 1174-1179.	1.1	49
67	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 2474.	5.8	49
68	AMPLify: attentive deep learning model for discovery of novel antimicrobial peptides effective against WHO priority pathogens. <i>BMC Genomics</i> , 2022, 23, 77.	1.2	48
69	JAGuaR: Junction Alignments to Genome for RNA-Seq Reads. <i>PLoS ONE</i> , 2014, 9, e102398.	1.1	47
70	A high-resolution reference genetic map positioning 8.8K genes for the conifer white spruce: structural genomics implications and correspondence with physical distance. <i>Plant Journal</i> , 2017, 90, 189-203.	2.8	47
71	Evolution of gene structure in the conifer <i>Picea glauca</i> : a comparative analysis of the impact of intron size. <i>BMC Plant Biology</i> , 2014, 14, 95.	1.6	46
72	Organellar Genomes of White Spruce ( <i>Picea glauca</i> ): Assembly and Annotation. <i>Genome Biology and Evolution</i> , 2016, 8, 29-41.	1.1	46

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73	The Genome of the Beluga Whale ( <i>Delphinapterus leucas</i> ). <i>Genes</i> , 2017, 8, 378.	1.0	39
74	A search for $\frac{1}{2}\frac{1}{4}\hat{a}\hat{t}'\frac{1}{2}\hat{l}$ , oscillation. <i>Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics</i> , 1998, 424, 202-212.	1.5	38
75	Updated genome assembly and annotation of <i>Paenibacillus</i> larvae, the agent of American foulbrood disease of honey bees. <i>BMC Genomics</i> , 2011, 12, 450.	1.2	35
76	The Genome of the North American Brown Bear or Grizzly: <i>Ursus arctos</i> ssp. <i>horribilis</i> . <i>Genes</i> , 2018, 9, 598.	1.0	34
77	Base excision repair deficiency signatures implicate germline and somatic <i>MUTYH</i> aberrations in pancreatic ductal adenocarcinoma and breast cancer oncogenesis. <i>Journal of Physical Education and Sports Management</i> , 2019, 5, a003681.	0.5	33
78	RNA-Bloom enables reference-free and reference-guided sequence assembly for single-cell transcriptomes. <i>Genome Research</i> , 2020, 30, 1191-1200.	2.4	33
79	Agent-based control of autocatalytic replicators in networks of reactors. <i>Computers and Chemical Engineering</i> , 2005, 29, 807-815.	2.0	32
80	A novel approach to wildlife transcriptomics provides evidence of disease-mediated differential expression and changes to the microbiome of amphibian populations. <i>Molecular Ecology</i> , 2018, 27, 1413-1427.	2.0	32
81	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X Genomics™ GemCode Sequencing Data. <i>PLoS ONE</i> , 2016, 11, e0163059.	1.1	31
82	The miR-185/PAK6 axis predicts therapy response and regulates survival of drug-resistant leukemic stem cells in CML. <i>Blood</i> , 2020, 136, 596-609.	0.6	30
83	LongStitch: high-quality genome assembly correction and scaffolding using long reads. <i>BMC Bioinformatics</i> , 2021, 22, 534.	1.2	30
84	A Clinically Validated Diagnostic Second-Generation Sequencing Assay for Detection of Hereditary BRCA1 and BRCA2 Mutations. <i>Journal of Molecular Diagnostics</i> , 2013, 15, 796-809.	1.2	29
85	Genome sequences of six <i>Phytophthora</i> species threatening forest ecosystems. <i>Genomics Data</i> , 2016, 10, 85-88.	1.3	29
86	Innovations and challenges in detecting long read overlaps: an evaluation of the state-of-the-art. <i>Bioinformatics</i> , 2017, 33, 1261-1270.	1.8	28
87	Genome-wide sequencing as a first-tier screening test for short tandem repeat expansions. <i>Genome Medicine</i> , 2021, 13, 126.	3.6	27
88	De novo Transcriptome Assemblies of <i>Rana</i> ( <i>Lithobates</i> ) <i>catesbeiana</i> and <i>Xenopus laevis</i> Tadpole Livers for Comparative Genomics without Reference Genomes. <i>PLoS ONE</i> , 2015, 10, e0130720.	1.1	27
89	Calculation of Molecular Weight Distributions in Non-Linear Free-Radical Polymerization Using the Numerical Fractionation Technique. <i>Macromolecular Theory and Simulations</i> , 2002, 11, 533.	0.6	25
90	The Genome of the Northern Sea Otter ( <i>Enhydra lutris kenyoni</i> ). <i>Genes</i> , 2017, 8, 379.	1.0	24

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91	Genome-Enhanced Detection and Identification (GEDI) of plant pathogens. PeerJ, 2018, 6, e4392.	0.9	24
92	Genome Sequence of Mycoplasma capricolum subsp. capripneumoniae Strain M1601. Journal of Bacteriology, 2011, 193, 6098-6099.	1.0	23
93	Recurrent tumor-specific regulation of alternative polyadenylation of cancer-related genes. BMC Genomics, 2018, 19, 536.	1.2	22
94	Straglr: discovering and genotyping tandem repeat expansions using whole genome long-read sequences. Genome Biology, 2021, 22, 224.	3.8	22
95	ntJoin: Fast and lightweight assembly-guided scaffolding using minimizer graphs. Bioinformatics, 2020, 36, 3885-3887.	1.8	21
96	Trans-NanoSim characterizes and simulates nanopore RNA-sequencing data. GigaScience, 2020, 9, .	3.3	20
97	Assembling genomes using short-read sequencing technology. Genome Biology, 2010, 11, 202.	13.9	19
98	Konnector v2.0: pseudo-long reads from paired-end sequencing data. BMC Medical Genomics, 2015, 8, S1.	0.7	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.	1.8	19
100	Kollector: transcript-informed, targeted <i>de novo</i> assembly of gene loci. Bioinformatics, 2017, 33, 1782-1788.	1.8	18
101	Antimicrobial peptides from Rana [Lithobates] catesbeiana: Gene structure and bioinformatic identification of novel forms from tadpoles. Scientific Reports, 2019, 9, 1529.	1.6	18
102	Spruce giga-€ genomes: structurally similar yet distinctive with differentially expanding gene families and rapidly evolving genes. Plant Journal, 2022, 111, 1469-1485.	2.8	17
103	Effect of environment partitioning on the survival and coexistence of autocatalytic replicators. Physical Review E, 2002, 66, 051916.	0.8	16
104	Optimal pooling for genome re-sequencing with ultra-high-throughput short-read technologies. Bioinformatics, 2008, 24, i32-i40.	1.8	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.	1.9	16
106	Static and Dynamic Behavior of Autocatalytic Replicators in Reactor Networks. Industrial & Engineering Chemistry Research, 2004, 43, 3972-3993.	1.8	15
107	Template-€Directed Synthesis of Bivalent, Broad-€Spectrum Hosts for Neuromuscular Blocking Agents**. Angewandte Chemie - International Edition, 2022, 61, .	7.2	15
108	Competition between Robust and Nonrobust Autocatalytic Replicators. Industrial & Engineering Chemistry Research, 2002, 41, 3630-3641.	1.8	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.	1.3	13
111	Measuring Complexity in Reactor Networks with Cubic Autocatalytic Reactions. Industrial & Engineering Chemistry Research, 2005, 44, 2781-2791.	1.8	13
112	Dissect: detection and characterization of novel structural alterations in transcribed sequences. Bioinformatics, 2012, 28, i179-i187.	1.8	13
113	HLA alleles measured from COVID-19 patient transcriptomes reveal associations with disease prognosis in a New York cohort. PeerJ, 2021, 9, e12368.	0.9	13
114	Feedback Control of a Continuous-Flow Stirred Tank Reactor with Competing Autocatalators. Industrial & Engineering Chemistry Research, 2003, 42, 3765-3785.	1.8	12
115	LaneRuler: Automated Lane Tracking for DNA Electrophoresis Gel Images. IEEE Transactions on Automation Science and Engineering, 2010, 7, 706-708.	3.4	12
116	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. BMC Genomics, 2013, 14, 550.	1.2	12
117	Human variation database: an open-source database template for genomic discovery. Bioinformatics, 2011, 27, 1155-1156.	1.8	11
118	TAP: a targeted clinical genomics pipeline for detecting transcript variants using RNA-seq data. BMC Medical Genomics, 2018, 11, 79.	0.7	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.	0.6	10
120	DIDA: Distributed Indexing Dispatched Alignment. PLoS ONE, 2015, 10, e0126409.	1.1	10
121	ORCA: a comprehensive bioinformatics container environment for education and research. Bioinformatics, 2019, 35, 4448-4450.	1.8	10
122	Mining Amphibian and Insect Transcriptomes for Antimicrobial Peptide Sequences with rAMPage. Antibiotics, 2022, 11, 952.	1.5	10
123	Coherent bremsstrahlung, coherent pair production, birefringence, and polarimetry in the 20â€“170ÂGeV energy range using aligned crystals. Physical Review Special Topics: Accelerators and Beams, 2008, 11, .	1.8	9
124	Approximately conserved quantity in the HÃ©non-Heiles problem. Physical Review E, 1995, 52, 4750-4753.	0.8	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.	1.0	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.	3.3	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 ( <i>Picea glauca</i> , Genotype WS77111) from Eastern Canada. Microbiology Resource Announcements, 2019, 8, .	0.3	7
130	Fusion-Bloom: fusion detection in assembled transcriptomes. Bioinformatics, 2020, 36, 2256-2257.	1.8	7
131	Spaced Seed Data Structures for De Novo Assembly. International Journal of Genomics, 2015, 2015, 1-8.	0.8	6
132	ntEdit+Sealer: Efficient Targeted Error Resolution and Automated Finishing of Long-Read Genome Assemblies. Current Protocols, 2022, 2, e442.	1.3	6
133	Physlr: Next-Generation Physical Maps. Dna, 2022, 2, 116-130.	0.4	5
134	The Genome of the Steller Sea Lion ( <i>Eumetopias jubatus</i> ). Genes, 2019, 10, 486.	1.0	4
135	Complete Chloroplast Genome Sequence of an Engelmann Spruce ( <i>Picea engelmannii</i> , Genotype) Tj ETQq1.1.0.784314 rgBT (0.3)	0.3	4
136	Complete Chloroplast Genome Sequence of a Black Spruce ( <i>Picea mariana</i> ) from Eastern Canada. Microbiology Resource Announcements, 2020, 9, .	0.3	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, .	0.8	4
138	Linked-read sequencing for detecting short tandem repeat expansions. Scientific Reports, 2022, 12, .	1.6	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.	1.8	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.	0.4	3
142	Simulating a dynamical system in the presence of a 1/f noise. International Journal of Engineering Science, 1998, 36, 265-271.	2.7	2
143	The trigger and DAQ systems of the Na59 experiment. IEEE Transactions on Nuclear Science, 2004, 51, 1482-1487.	1.2	2
144	Software aspects of the Na59 experiment. IEEE Transactions on Nuclear Science, 2004, 51, 1449-1455.	1.2	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.	1.2	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.	1.9	2
148	A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. Frontiers in Genetics, 2021, 12, 665888.	1.1	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.	0.6	2
150	Signs and approximate magnitudes of Lyapunov exponents in continuous time dynamical systems. Journal of Mathematical Physics, 1997, 38, 4594-4605.	0.5	1
151	Investigating the fermentation dynamics structure of recombinant yeast YPB-G. Computers and Chemical Engineering, 2003, 27, 45-54.	2.0	1
152	Spaced seed data structures. , 2014, , .		1
153	Differential Hive Plots: Seeing Networks Change. Leonardo, 2017, 50, 504-504.	0.2	1
154	Genomic and Cytogenetic Characterization of a Balanced Translocation Disrupting <b><i>NUP98</i></b>. Cytogenetic and Genome Research, 2017, 152, 117-121.	0.6	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.	0.6	1
157	RResolver: efficient short-read repeat resolution within ABySS. BMC Bioinformatics, 2022, 23, .	1.2	1
158	Determining Zero Lyapunov Exponents in Continuous Time Dynamical Systems. International Journal of Modern Physics A, 1997, 12, 131-135.	0.5	0
159	Some Algebraic Properties of Continuous Time Dynamical Systems. International Journal of Modern Physics A, 1997, 12, 137-142.	0.5	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, .	1.2	0
162	Personalized oncogenomics. Genome Biology, 2010, 11, I5.	13.9	0

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163	Endothelial-hematopoietic transition: from the dorsal aorta to the dish. <i>Experimental Hematology</i> , 2013, 41, S26.	0.2	0
164	Comparative RNA-seq analyses identify new microRNA biomarkers and candidate target genes in patients' drug-resistant CD34+ CML stem/progenitor cells. <i>Experimental Hematology</i> , 2015, 43, S63.	0.2	0
165	Interactive SARS-CoV-2 mutation timemaps. <i>F1000Research</i> , 2021, 10, 68.	0.8	0
166	Interactive SARS-CoV-2 mutation timemaps. <i>F1000Research</i> , 2021, 10, 68.	0.8	0
167	UniqTag: Content-Derived Unique and Stable Identifiers for Gene Annotation. <i>PLoS ONE</i> , 2015, 10, e0128026.	1.1	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. <i>Blood</i> , 2018, 132, 931-931.	0.6	0
169	Sequencing and Assembling the Nuclear and Organelle Genomes of North American Spruces. <i>Compendium of Plant Genomes</i> , 2020, , 1-8.	0.3	0
170	Template-Directed Synthesis of Bivalent, Broad-Spectrum Hosts for Neuromuscular Blocking Agents**. <i>Angewandte Chemie</i> , 2022, 134, .	1.6	0
171	RNA-Scoop: interactive visualization of transcripts in single-cell transcriptomes. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab105.	1.5	0