

Inanc Birol

List of Publications by Year in descending order

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171
papers

75,977
citations

22153
59
h-index

6996
154
g-index

196
all docs

196
docs citations

196
times ranked

100974
citing authors

#	ARTICLE	IF	CITATIONS
1	Templateâ€Directed Synthesis of Bivalent, Broadâ€Spectrum Hosts for Neuromuscular Blocking Agents**. Angewandte Chemie - International Edition, 2022, 61, .	13.8	15
2	Templateâ€Directed Synthesis of Bivalent, Broadâ€Spectrum Hosts for Neuromuscular Blocking Agents**. Angewandte Chemie, 2022, 134, .	2.0	0
3	AMPLify: attentive deep learning model for discovery of novel antimicrobial peptides effective against WHO priority pathogens. BMC Genomics, 2022, 23, 77.	2.8	48
4	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
5	ntEdit+Sealer: Efficient Targeted Error Resolution and Automated Finishing of Longâ€Read Genome Assemblies. Current Protocols, 2022, 2, e442.	2.9	6
6	Physlr: Next-Generation Physical Maps. Dna, 2022, 2, 116-130.	1.3	5
7	Linked-read sequencing for detecting short tandem repeat expansions. Scientific Reports, 2022, 12, .	3.3	4
8	RResolver: efficient short-read repeat resolution within ABySS. BMC Bioinformatics, 2022, 23, .	2.6	1
9	Mining Amphibian and Insect Transcriptomes for Antimicrobial Peptide Sequences with rAMPage. Antibiotics, 2022, 11, 952.	3.7	10
10	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
11	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
12	GapPredict â€“ 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
13	Interactive SARS-CoV-2 mutation timemaps. F1000Research, 2021, 10, 68.	1.6	0
14	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. Nature Communications, 2021, 12, 2474.	12.8	49
15	A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. Frontiers in Genetics, 2021, 12, 665888.	2.3	2
16	Interactive SARS-CoV-2 mutation timemaps. F1000Research, 2021, 10, 68.	1.6	0
17	Straglr: discovering and genotyping tandem repeat expansions using whole genome long-read sequences. Genome Biology, 2021, 22, 224.	8.8	22
18	Genome-wide sequencing as a first-tier screening test for short tandem repeat expansions. Genome Medicine, 2021, 13, 126.	8.2	27

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19	HLA alleles measured from COVID-19 patient transcriptomes reveal associations with disease prognosis in a New York cohort. <i>PeerJ</i> , 2021, 9, e12368.	2.0	13
20	LongStitch: high-quality genome assembly correction and scaffolding using long reads. <i>BMC Bioinformatics</i> , 2021, 22, 534.	2.6	30
21	RNA-Scoop: interactive visualization of transcripts in single-cell transcriptomes. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab105.	3.2	0
22	Fusion-Bloom: fusion detection in assembled transcriptomes. <i>Bioinformatics</i> , 2020, 36, 2256-2257.	4.1	7
23	Complete Chloroplast Genome Sequence of a Black Spruce (<i>Picea mariana</i>) from Eastern Canada. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.6	4
24	RNA-Bloom enables reference-free and reference-guided sequence assembly for single-cell transcriptomes. <i>Genome Research</i> , 2020, 30, 1191-1200.	5.5	33
25	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.	2.5	49
26	Trans-NanoSim characterizes and simulates nanopore RNA-sequencing data. <i>GigaScience</i> , 2020, 9, .	6.4	20
27	Mismatch-tolerant, alignment-free sequence classification using multiple spaced seeds and multiindex Bloom filters. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 16961-16968.	7.1	8
28	ntJoin: Fast and lightweight assembly-guided scaffolding using minimizer graphs. <i>Bioinformatics</i> , 2020, 36, 3885-3887.	4.1	21
29	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.	1.4	30
30	Sequencing and Assembling the Nuclear and Organelle Genomes of North American Spruces. <i>Compendium of Plant Genomes</i> , 2020, , 1-8.	0.5	0
31	The Genome of the Steller Sea Lion (<i>Eumetopias jubatus</i>). <i>Genes</i> , 2019, 10, 486.	2.4	4
32	Complete Chloroplast Genome Sequence of an Engelmann Spruce (<i>Picea engelmannii</i> , Genotype) Tj ETQq0.0.0 rgBT /Overlock 1	0.6	4
33	Replicated Landscape Genomics Identifies Evidence of Local Adaptation to Urbanization in Wood Frogs. <i>Journal of Heredity</i> , 2019, 110, 707-719.	2.4	8
34	Complete Chloroplast Genome Sequence of a White Spruce (<i>Picea glauca</i> , Genotype WS77111) from Eastern Canada. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	7
35	ntEdit: scalable genome sequence polishing. <i>Bioinformatics</i> , 2019, 35, 4430-4432.	4.1	67
36	ORCA: a comprehensive bioinformatics container environment for education and research. <i>Bioinformatics</i> , 2019, 35, 4448-4450.	4.1	10

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37	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.	1.2	33
38	Antimicrobial peptides from <i>Rana [Lithobates] catesbeiana</i> : Gene structure and bioinformatic identification of novel forms from tadpoles. <i>Scientific Reports</i> , 2019, 9, 1529.	3.3	18
39	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.	3.9	32
40	ChopStitch: exon annotation and splice graph construction using transcriptome assembly and whole genome sequencing data. <i>Bioinformatics</i> , 2018, 34, 1697-1704.	4.1	3
41	ARCS: scaffolding genome drafts with linked reads. <i>Bioinformatics</i> , 2018, 34, 725-731.	4.1	161
42	Tigmint: correcting assembly errors using linked reads from large molecules. <i>BMC Bioinformatics</i> , 2018, 19, 393.	2.6	97
43	ntPack: A Software Package for Big Data in Genomics. , 2018, , .		1
44	The Genome of the North American Brown Bear or Grizzly: <i>Ursus arctos</i> ssp. <i>horribilis</i> . <i>Genes</i> , 2018, 9, 598.	2.4	34
45	TAP: a targeted clinical genomics pipeline for detecting transcript variants using RNA-seq data. <i>BMC Medical Genomics</i> , 2018, 11, 79.	1.5	11
46	GraphNER: Using Corpus Level Similarities and Graph Propagation for Named Entity Recognition. , 2018, , .		2
47	Recurrent tumor-specific regulation of alternative polyadenylation of cancer-related genes. <i>BMC Genomics</i> , 2018, 19, 536.	2.8	22
48	ARKS: chromosome-scale scaffolding of human genome drafts with linked read kmers. <i>BMC Bioinformatics</i> , 2018, 19, 234.	2.6	81
49	Genome-Enhanced Detection and Identification (GEDi) of plant pathogens. <i>PeerJ</i> , 2018, 6, e4392.	2.0	24
50	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.	1.4	0
51	Innovations and challenges in detecting long read overlaps: an evaluation of the state-of-the-art. <i>Bioinformatics</i> , 2017, 33, 1261-1270.	4.1	28
52	Differential Hive Plots: Seeing Networks Change. <i>Leonardo</i> , 2017, 50, 504-504.	0.3	1
53	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.	5.7	47
54	De novo assembly of the ringed seal (<i>Pusa hispida</i>) blubber transcriptome: A tool that enables identification of molecular health indicators associated with PCB exposure. <i>Aquatic Toxicology</i> , 2017, 185, 48-57.	4.0	16

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55	NanoSim: nanopore sequence read simulator based on statistical characterization. GigaScience, 2017, 6, 1-6.	6.4	149
56	Kollector: transcript-informed, targeted <i>de novo</i> assembly of gene loci. Bioinformatics, 2017, 33, 1782-1788.	4.1	18
57	ABYSS 2.0: resource-efficient assembly of large genomes using a Bloom filter. Genome Research, 2017, 27, 768-777.	5.5	526
58	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. Cell, 2017, 171, 540-556.e25.	28.9	1,742
59	Genomic and Cytogenetic Characterization of a Balanced Translocation Disrupting <i>NUP98</i> . Cytogenetic and Genome Research, 2017, 152, 117-121.	1.1	1
60	Complete Genome Sequence of <i>Mycobacterium chimaera</i> SJ42, a Nonoutbreak Strain from an Immunocompromised Patient with Pulmonary Disease. Genome Announcements, 2017, 5, .	0.8	3
61	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. Cancer Cell, 2017, 32, 204-220.e15.	16.8	642
62	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. Cancer Cell, 2017, 32, 185-203.e13.	16.8	1,428
63	The North American bullfrog draft genome provides insight into hormonal regulation of long noncoding RNA. Nature Communications, 2017, 8, 1433.	12.8	86
64	The Genome of the Beluga Whale (<i>Delphinapterus leucas</i>). Genes, 2017, 8, 378.	2.4	39
65	The Genome of the Northern Sea Otter (<i>Enhydra lutris kenyoni</i>). Genes, 2017, 8, 379.	2.4	24
66	ntCard: a streaming algorithm for cardinality estimation in genomics data. Bioinformatics, 2017, 33, 1324-1330.	4.1	53
67	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X Genomics™ GemCode Sequencing Data. PLoS ONE, 2016, 11, e0163059.	2.5	31
68	Genome sequences of six Phytophthora species threatening forest ecosystems. Genomics Data, 2016, 10, 85-88.	1.3	29
69	ntHash: recursive nucleotide hashing. Bioinformatics, 2016, 32, 3492-3494.	4.1	61
70	Divergent clonal selection dominates medulloblastoma at recurrence. Nature, 2016, 529, 351-357.	27.8	266
71	Large-scale profiling of microRNAs for The Cancer Genome Atlas. Nucleic Acids Research, 2016, 44, e3-e3.	14.5	125
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	Konnector v2.0: pseudo-long reads from paired-end sequencing data. BMC Medical Genomics, 2015, 8, S1.	1.5	19
74	Comparative RNA-seq analyses identify new microRNA biomarkers and candidate target genes in patientsâ€™ drug-resistant CD34+ CML stem/progenitor cells. Experimental Hematology, 2015, 43, S63.	0.4	0
75	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
76	DIDA: Distributed Indexing Dispatched Alignment. PLoS ONE, 2015, 10, e0126409.	2.5	10
77	Spaced Seed Data Structures for De Novo Assembly. International Journal of Genomics, 2015, 2015, 1-8.	1.6	6
78	Reduced adenosine-to-inosine miR-455-5p editing promotes melanoma growth and metastasis. Nature Cell Biology, 2015, 17, 311-321.	10.3	205
79	Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature, 2015, 517, 576-582.	27.8	3,209
80	LINKS: Scalable, alignment-free scaffolding of draft genomes with long reads. GigaScience, 2015, 4, 35.	6.4	196
81	Sealer: a scalable gap-closing application for finishing draft genomes. BMC Bioinformatics, 2015, 16, 230.	2.6	122
82	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. PLoS ONE, 2015, 10, e0130720.	2.5	27
83	UniqTag: Content-Derived Unique and Stable Identifiers for Gene Annotation. PLoS ONE, 2015, 10, e0128026.	2.5	0
84	Kleat: cleavage site analysis of transcriptomes. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2015, , 347-58.	0.7	8
85	JAGuar: Junction Alignments to Genome for RNA-Seq Reads. PLoS ONE, 2014, 9, e102398.	2.5	47
86	Konnector: Connecting paired-end reads using a bloom filter de Bruijn graph. , 2014, , .		8
87	Spaced seed data structures. , 2014, , .		1
88	BioBloom tools: fast, accurate and memory-efficient host species sequence screening using bloom filters. Bioinformatics, 2014, 30, 3402-3404.	4.1	95
89	Insights into Conifer Giga-Genomes. Plant Physiology, 2014, 166, 1724-1732.	4.8	164
90	Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209.	27.8	5,055

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91	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	16.8	665
92	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	28.9	1,242
93	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.	3.6	46
94	KLEAT: CLEAVAGE SITE ANALYSIS OF TRANSCRIPTOMES. , 2014, , .		14
95	Identification of New microRNA Biomarkers and Candidate Target Genes in Primitive CML Cells Using Global Comparative RNA analyses. <i>Blood</i> , 2014, 124, 3133-3133.	1.4	2
96	Draft genome of the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major forest pest. <i>Genome Biology</i> , 2013, 14, R27.	9.6	260
97	Identifying cancer mutation targets across thousands of samples: MuteProc, a high throughput mutation analysis pipeline. <i>BMC Bioinformatics</i> , 2013, 14, 167.	2.6	2
98	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.	2.8	72
99	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.	2.8	29
100	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	6.4	582
101	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. <i>BMC Genomics</i> , 2013, 14, 550.	2.8	12
102	Endothelial-hematopoietic transition: from the dorsal aorta to the dish. <i>Experimental Hematology</i> , 2013, 41, S26.	0.4	0
103	Complete genomic landscape of a recurring sporadic parathyroid carcinoma. <i>Journal of Pathology</i> , 2013, 230, 249-260.	4.5	57
104	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	27.8	4,075
105	Genomic and Epigenomic Landscapes of Adult De Novo Acute Myeloid Leukemia. <i>New England Journal of Medicine</i> , 2013, 368, 2059-2074.	27.0	4,139
106	The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , 2013, 45, 279-284.	21.4	990
107	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013, 499, 43-49.	27.8	2,839
108	Assembling the 20 Gb white spruce (<i>Picea glauca</i>) genome from whole-genome shotgun sequencing data. <i>Bioinformatics</i> , 2013, 29, 1492-1497.	4.1	356

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109	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. Blood, 2013, 122, 1256-1265.	1.4	349
110	Whole Genome Duplication and Enrichment of Metal Cation Transporters Revealed by De Novo Genome Sequencing of Extremely Halotolerant Black Yeast <i>Hortaea werneckii</i> . PLoS ONE, 2013, 8, e71328.	2.5	96
111	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. Nature, 2012, 488, 49-56.	27.8	761
112	Dissect: detection and characterization of novel structural alterations in transcribed sequences. Bioinformatics, 2012, 28, i179-i187.	4.1	13
113	Genetic Alterations Activating Kinase and Cytokine Receptor Signaling in High-Risk Acute Lymphoblastic Leukemia. Cancer Cell, 2012, 22, 153-166.	16.8	621
114	Hive plots--rational approach to visualizing networks. Briefings in Bioinformatics, 2012, 13, 627-644.	6.5	187
115	Transcriptome and full-length cDNA resources for the mountain pine beetle, <i>Dendroctonus ponderosae</i> Hopkins, a major insect pest of pine forests. Insect Biochemistry and Molecular Biology, 2012, 42, 525-536.	2.7	93
116	Comprehensive molecular characterization of human colon and rectal cancer. Nature, 2012, 487, 330-337.	27.8	7,168
117	Comprehensive molecular portraits of human breast tumours. Nature, 2012, 490, 61-70.	27.8	10,282
118	Comprehensive genomic characterization of squamous cell lung cancers. Nature, 2012, 489, 519-525.	27.8	3,483
119	Recurrent targets of aberrant somatic hypermutation in lymphoma. Oncotarget, 2012, 3, 1308-1319.	1.8	127
120	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
121	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. Nature, 2012, 486, 395-399.	27.8	1,778
122	Whole-Genome Sequencing and Social-Network Analysis of a Tuberculosis Outbreak. New England Journal of Medicine, 2011, 364, 730-739.	27.0	665
123	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. Nature, 2011, 476, 298-303.	27.8	1,428
124	SNP discovery in black cottonwood (<i>Populus trichocarpa</i>) by population transcriptome resequencing. Molecular Ecology Resources, 2011, 11, 81-92.	4.8	104
125	Updated genome assembly and annotation of <i>Paenibacillus</i> larvae, the agent of American foulbrood disease of honey bees. BMC Genomics, 2011, 12, 450.	2.8	35
126	Assemblathon 1: A competitive assessment of de novo short read assembly methods. Genome Research, 2011, 21, 2224-2241.	5.5	443

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127	Human variation database: an open-source database template for genomic discovery. <i>Bioinformatics</i> , 2011, 27, 1155-1156.	4.1	11
128	Genome Sequence of <i>Mycoplasma capricolum</i> subsp. <i>capripneumoniae</i> Strain M1601. <i>Journal of Bacteriology</i> , 2011, 193, 6098-6099.	2.2	23
129	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.	7.1	218
130	Abstract 926: Whole genome and transcriptome sequencing defines the spectrum of somatic changes in high-risk neuroblastoma. <i>Cancer Research</i> , 2011, 71, 926-926.	0.9	3
131	Genomic analysis of a rare human tumor. <i>BMC Bioinformatics</i> , 2010, 11, .	2.6	0
132	Somatic mutations altering EZH2 (Tyr641) in follicular and diffuse large B-cell lymphomas of germinal-center origin. <i>Nature Genetics</i> , 2010, 42, 181-185.	21.4	1,504
133	De novo assembly and analysis of RNA-seq data. <i>Nature Methods</i> , 2010, 7, 909-912.	19.0	886
134	mrsFAST: a cache-oblivious algorithm for short-read mapping. <i>Nature Methods</i> , 2010, 7, 576-577.	19.0	248
135	Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. <i>Bioinformatics</i> , 2010, 26, 1277-1283.	4.1	98
136	LaneRuler: Automated Lane Tracking for DNA Electrophoresis Gel Images. <i>IEEE Transactions on Automation Science and Engineering</i> , 2010, 7, 706-708.	5.2	12
137	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. <i>Genome Research</i> , 2010, 20, 791-803.	5.5	84
138	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.	5.5	109
139	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. <i>Genome Biology</i> , 2010, 11, R82.	9.6	159
140	Personalized oncogenomics. <i>Genome Biology</i> , 2010, 11, I5.	9.6	0
141	Assembling genomes using short-read sequencing technology. <i>Genome Biology</i> , 2010, 11, 202.	9.6	19
142	Identification of Genes Frequently Mutated In FL and DLBCL with Transcriptome, Genome and Exome Sequencing. <i>Blood</i> , 2010, 116, 804-804.	1.4	1
143	ABYSS: A parallel assembler for short read sequence data. <i>Genome Research</i> , 2009, 19, 1117-1123.	5.5	3,134
144	De novo transcriptome assembly with ABYSS. <i>Bioinformatics</i> , 2009, 25, 2872-2877.	4.1	371

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145	De novo genome sequence assembly of a filamentous fungus using Sanger, 454 and Illumina sequence data. <i>Genome Biology</i> , 2009, 10, R94.	9.6	130
146	ABYSS-Explorer: Visualizing Genome Sequence Assemblies. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2009, 15, 881-888.	4.4	53
147	Circos: An information aesthetic for comparative genomics. <i>Genome Research</i> , 2009, 19, 1639-1645.	5.5	9,003
148	Optimal pooling for genome re-sequencing with ultra-high-throughput short-read technologies. <i>Bioinformatics</i> , 2008, 24, i32-i40.	4.1	16
149	Genome-wide relationship between histone H3 lysine 4 mono- and tri-methylation and transcription factor binding. <i>Genome Research</i> , 2008, 18, 1906-1917.	5.5	163
150	Coherent bremsstrahlung, coherent pair production, birefringence, and polarimetry in the 20â€“170ÂGeV energy range using aligned crystals. <i>Physical Review Special Topics: Accelerators and Beams</i> , 2008, 11, .	1.8	9
151	AGENT-BASED CONTROL OF DISCRETE SPATIALLY DISTRIBUTED SYSTEMS. <i>IFAC Postprint Volumes IPPV / International Federation of Automatic Control</i> , 2005, 38, 549-554.	0.4	0
152	Results on the coherent interaction of high energy electrons and photons in oriented single crystals. <i>Nuclear Instruments & Methods in Physics Research B</i> , 2005, 234, 128-137.	1.4	10
153	Agent-based control of autocatalytic replicators in networks of reactors. <i>Computers and Chemical Engineering</i> , 2005, 29, 807-815.	3.8	32
154	Measuring Complexity in Reactor Networks with Cubic Autocatalytic Reactions. <i>Industrial & Engineering Chemistry Research</i> , 2005, 44, 2781-2791.	3.7	13
155	The trigger and DAQ systems of the Na59 experiment. <i>IEEE Transactions on Nuclear Science</i> , 2004, 51, 1482-1487.	2.0	2
156	Software aspects of the Na59 experiment. <i>IEEE Transactions on Nuclear Science</i> , 2004, 51, 1449-1455.	2.0	2
157	Static and Dynamic Behavior of Autocatalytic Replicators in Reactor Networks. <i>Industrial & Engineering Chemistry Research</i> , 2004, 43, 3972-3993.	3.7	15
158	Metabolic Control Analysis under Uncertainty: Framework Development and Case Studies. <i>Biophysical Journal</i> , 2004, 87, 3750-3763.	0.5	153
159	Investigating the fermentation dynamics structure of recombinant yeast YPB-G. <i>Computers and Chemical Engineering</i> , 2003, 27, 45-54.	3.8	1
160	Feedback Control of a Continuous-Flow Stirred Tank Reactor with Competing Autocatalators. <i>Industrial & Engineering Chemistry Research</i> , 2003, 42, 3765-3785.	3.7	12
161	Effect of environment partitioning on the survival and coexistence of autocatalytic replicators. <i>Physical Review E</i> , 2002, 66, 051916.	2.1	16
162	Competition between Robust and Nonrobust Autocatalytic Replicators. <i>Industrial & Engineering Chemistry Research</i> , 2002, 41, 3630-3641.	3.7	14

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163	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.	1.4	25
164	Statics and dynamics of multiple cubic autocatalytic reactions. <i>Physica D: Nonlinear Phenomena</i> , 2000, 144, 279-297.	2.8	13
165	Simulating a dynamical system in the presence of a $1/f$ noise. <i>International Journal of Engineering Science</i> , 1998, 36, 265-271.	5.0	2
166	A search for $\hat{1}/2\hat{1}/4\hat{1}/2\hat{1}$, oscillation. <i>Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics</i> , 1998, 424, 202-212.	4.1	38
167	Determining Zero Lyapunov Exponents in Continuous Time Dynamical Systems. <i>International Journal of Modern Physics A</i> , 1997, 12, 131-135.	1.5	0
168	Some Algebraic Properties of Continuous Time Dynamical Systems. <i>International Journal of Modern Physics A</i> , 1997, 12, 137-142.	1.5	0
169	Signs and approximate magnitudes of Lyapunov exponents in continuous time dynamical systems. <i>Journal of Mathematical Physics</i> , 1997, 38, 4594-4605.	1.1	1
170	The CHORUS experiment to search for $\hat{1}/2\hat{1}/4\hat{1}/2\hat{1}$, oscillation. <i>Nuclear Instruments and Methods in Physics Research, Section A: Accelerators, Spectrometers, Detectors and Associated Equipment</i> , 1997, 401, 7-44.	1.6	209
171	Approximately conserved quantity in the HÄ©non-Heiles problem. <i>Physical Review E</i> , 1995, 52, 4750-4753.	2.1	8