

Inanc Birol

List of Publications by Year in descending order

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171
papers

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25423

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docs citations

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times ranked

110161
citing authors

#	ARTICLE	IF	CITATIONS
1	Template-Directed Synthesis of Bivalent, Broad-Spectrum Hosts for Neuromuscular Blocking Agents**. <i>Angewandte Chemie - International Edition</i> , 2022, 61, .	7.2	15
2	Template-Directed Synthesis of Bivalent, Broad-Spectrum Hosts for Neuromuscular Blocking Agents**. <i>Angewandte Chemie</i> , 2022, 134, .	1.6	0
3	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
4	The genome of the forest insect pest <i>Pissodes strobi</i> reveals genome expansion and evidence of a <i>Wolbachia</i> endosymbiont. <i>G3: Genes, Genomes, Genetics</i> , 2022, 12, .	0.8	4
5	ntEdit+Sealer: Efficient Targeted Error Resolution and Automated Finishing of Long-Read Genome Assemblies. <i>Current Protocols</i> , 2022, 2, e442.	1.3	6
6	Physlr: Next-Generation Physical Maps. <i>Dna</i> , 2022, 2, 116-130.	0.4	5
7	Linked-read sequencing for detecting short tandem repeat expansions. <i>Scientific Reports</i> , 2022, 12, .	1.6	4
8	RResolver: efficient short-read repeat resolution within ABySS. <i>BMC Bioinformatics</i> , 2022, 23, .	1.2	1
9	Mining Amphibian and Insect Transcriptomes for Antimicrobial Peptide Sequences with rAMPage. <i>Antibiotics</i> , 2022, 11, 952.	1.5	10
10	Spruce gigagenomes: structurally similar yet distinctive with differentially expanding gene families and rapidly evolving genes. <i>Plant Journal</i> , 2022, 111, 1469-1485.	2.8	17
11	HLA predictions from the bronchoalveolar lavage fluid and blood samples of eight COVID-19 patients at the pandemic onset. <i>Bioinformatics</i> , 2021, 36, 5271-5273.	1.8	19
12	GapPredict – A Language Model for Resolving Gaps in Draft Genome Assemblies. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2021, 18, 2802-2808.	1.9	2
13	Interactive SARS-CoV-2 mutation timemaps. <i>F1000Research</i> , 2021, 10, 68.	0.8	0
14	A clinical transcriptome approach to patient stratification and therapy selection in acute myeloid leukemia. <i>Nature Communications</i> , 2021, 12, 2474.	5.8	49
15	A Scalable Strand-Specific Protocol Enabling Full-Length Total RNA Sequencing From Single Cells. <i>Frontiers in Genetics</i> , 2021, 12, 665888.	1.1	2
16	Interactive SARS-CoV-2 mutation timemaps. <i>F1000Research</i> , 2021, 10, 68.	0.8	0
17	Stragl: discovering and genotyping tandem repeat expansions using whole genome long-read sequences. <i>Genome Biology</i> , 2021, 22, 224.	3.8	22
18	Genome-wide sequencing as a first-tier screening test for short tandem repeat expansions. <i>Genome Medicine</i> , 2021, 13, 126.	3.6	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.	0.9	13
20	LongStitch: high-quality genome assembly correction and scaffolding using long reads. <i>BMC Bioinformatics</i> , 2021, 22, 534.	1.2	30
21	RNA-Scoop: interactive visualization of transcripts in single-cell transcriptomes. <i>NAR Genomics and Bioinformatics</i> , 2021, 3, lqab105.	1.5	0
22	Fusion-Bloom: fusion detection in assembled transcriptomes. <i>Bioinformatics</i> , 2020, 36, 2256-2257.	1.8	7
23	Complete Chloroplast Genome Sequence of a Black Spruce (<i>Picea mariana</i>) from Eastern Canada. <i>Microbiology Resource Announcements</i> , 2020, 9, .	0.3	4
24	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
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.	1.1	49
26	Trans-NanoSim characterizes and simulates nanopore RNA-sequencing data. <i>GigaScience</i> , 2020, 9, .	3.3	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.	3.3	8
28	ntJoin: Fast and lightweight assembly-guided scaffolding using minimizer graphs. <i>Bioinformatics</i> , 2020, 36, 3885-3887.	1.8	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.	0.6	30
30	Sequencing and Assembling the Nuclear and Organelle Genomes of North American Spruces. <i>Compendium of Plant Genomes</i> , 2020, , 1-8.	0.3	0
31	The Genome of the Steller Sea Lion (<i>Eumetopias jubatus</i>). <i>Genes</i> , 2019, 10, 486.	1.0	4
32	Complete Chloroplast Genome Sequence of an Engelmann Spruce (<i>Picea engelmannii</i> , Genotype) Tj ETQq0,0,0 rgBT /Overlock 1	0.3	4
33	Replicated Landscape Genomics Identifies Evidence of Local Adaptation to Urbanization in Wood Frogs. <i>Journal of Heredity</i> , 2019, 110, 707-719.	1.0	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, .	0.3	7
35	ntEdit: scalable genome sequence polishing. <i>Bioinformatics</i> , 2019, 35, 4430-4432.	1.8	67
36	ORCA: a comprehensive bioinformatics container environment for education and research. <i>Bioinformatics</i> , 2019, 35, 4448-4450.	1.8	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.	0.5	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.	1.6	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.	2.0	32
40	ChopStitch: exon annotation and splice graph construction using transcriptome assembly and whole genome sequencing data. <i>Bioinformatics</i> , 2018, 34, 1697-1704.	1.8	3
41	ARCS: scaffolding genome drafts with linked reads. <i>Bioinformatics</i> , 2018, 34, 725-731.	1.8	161
42	Tigmint: correcting assembly errors using linked reads from large molecules. <i>BMC Bioinformatics</i> , 2018, 19, 393.	1.2	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.	1.0	34
45	TAP: a targeted clinical genomics pipeline for detecting transcript variants using RNA-seq data. <i>BMC Medical Genomics</i> , 2018, 11, 79.	0.7	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.	1.2	22
48	ARKS: chromosome-scale scaffolding of human genome drafts with linked read kmers. <i>BMC Bioinformatics</i> , 2018, 19, 234.	1.2	81
49	Genome-Enhanced Detection and Identification (GEDI) of plant pathogens. <i>PeerJ</i> , 2018, 6, e4392.	0.9	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.	0.6	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.	1.8	28
52	Differential Hive Plots: Seeing Networks Change. <i>Leonardo</i> , 2017, 50, 504-504.	0.2	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.	2.8	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.	1.9	16

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55	NanoSim: nanopore sequence read simulator based on statistical characterization. <i>GigaScience</i> , 2017, 6, 1-6.	3.3	149
56	Kollector: transcript-informed, targeted <i>de novo</i> assembly of gene loci. <i>Bioinformatics</i> , 2017, 33, 1782-1788.	1.8	18
57	ABYSS 2.0: resource-efficient assembly of large genomes using a Bloom filter. <i>Genome Research</i> , 2017, 27, 768-777.	2.4	526
58	Comprehensive Molecular Characterization of Muscle-Invasive Bladder Cancer. <i>Cell</i> , 2017, 171, 540-556.e25.	13.5	1,742
59	Genomic and Cytogenetic Characterization of a Balanced Translocation Disrupting <i>NUP98</i> . <i>Cytogenetic and Genome Research</i> , 2017, 152, 117-121.	0.6	1
60	Complete Genome Sequence of <i>Mycobacterium chimaera</i> SJ42, a Nonoutbreak Strain from an Immunocompromised Patient with Pulmonary Disease. <i>Genome Announcements</i> , 2017, 5, .	0.8	3
61	Integrative Analysis Identifies Four Molecular and Clinical Subsets in Uveal Melanoma. <i>Cancer Cell</i> , 2017, 32, 204-220.e15.	7.7	642
62	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	7.7	1,428
63	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
64	The Genome of the Beluga Whale (<i>Delphinapterus leucas</i>). <i>Genes</i> , 2017, 8, 378.	1.0	39
65	The Genome of the Northern Sea Otter (<i>Enhydra lutris kenyoni</i>). <i>Genes</i> , 2017, 8, 379.	1.0	24
66	ntCard: a streaming algorithm for cardinality estimation in genomics data. <i>Bioinformatics</i> , 2017, 33, 1324-1330.	1.8	53
67	Assembly of the Complete Sitka Spruce Chloroplast Genome Using 10X Genomics™ GemCode Sequencing Data. <i>PLoS ONE</i> , 2016, 11, e0163059.	1.1	31
68	Genome sequences of six <i>Phytophthora</i> species threatening forest ecosystems. <i>Genomics Data</i> , 2016, 10, 85-88.	1.3	29
69	ntHash: recursive nucleotide hashing. <i>Bioinformatics</i> , 2016, 32, 3492-3494.	1.8	61
70	Divergent clonal selection dominates medulloblastoma at recurrence. <i>Nature</i> , 2016, 529, 351-357.	13.7	266
71	Large-scale profiling of microRNAs for The Cancer Genome Atlas. <i>Nucleic Acids Research</i> , 2016, 44, e3-e3.	6.5	125
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	Konnector v2.0: pseudo-long reads from paired-end sequencing data. BMC Medical Genomics, 2015, 8, S1.	0.7	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.	0.2	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.	2.8	200
76	DIDA: Distributed Indexing Dispatched Alignment. PLoS ONE, 2015, 10, e0126409.	1.1	10
77	Spaced Seed Data Structures for De Novo Assembly. International Journal of Genomics, 2015, 2015, 1-8.	0.8	6
78	Reduced adenosine-to-inosine miR-455-5p editing promotes melanoma growth and metastasis. Nature Cell Biology, 2015, 17, 311-321.	4.6	205
79	Comprehensive genomic characterization of head and neck squamous cell carcinomas. Nature, 2015, 517, 576-582.	13.7	3,209
80	LINKS: Scalable, alignment-free scaffolding of draft genomes with long reads. GigaScience, 2015, 4, 35.	3.3	196
81	Sealer: a scalable gap-closing application for finishing draft genomes. BMC Bioinformatics, 2015, 16, 230.	1.2	122
82	De novo Transcriptome Assemblies of <i>Rana (Lithobates) catesbeiana</i> and <i>Xenopus laevis</i> Tadpole Livers for Comparative Genomics without Reference Genomes. PLoS ONE, 2015, 10, e0130720.	1.1	27
83	UniqTag: Content-Derived Unique and Stable Identifiers for Gene Annotation. PLoS ONE, 2015, 10, e0128026.	1.1	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.	1.1	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.	1.8	95
89	Insights into Conifer Giga-Genomes. Plant Physiology, 2014, 166, 1724-1732.	2.3	164
90	Comprehensive molecular characterization of gastric adenocarcinoma. Nature, 2014, 513, 202-209.	13.7	5,055

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91	The Somatic Genomic Landscape of Chromophobe Renal Cell Carcinoma. <i>Cancer Cell</i> , 2014, 26, 319-330.	7.7	665
92	Multiplatform Analysis of 12 Cancer Types Reveals Molecular Classification within and across Tissues of Origin. <i>Cell</i> , 2014, 158, 929-944.	13.5	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.	1.6	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.	0.6	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.	13.9	260
97	Identifying cancer mutation targets across thousands of samples: MuteProc, a high throughput mutation analysis pipeline. <i>BMC Bioinformatics</i> , 2013, 14, 167.	1.2	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.	1.2	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.	1.2	29
100	Assemblathon 2: evaluating de novo methods of genome assembly in three vertebrate species. <i>GigaScience</i> , 2013, 2, 10.	3.3	582
101	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. <i>BMC Genomics</i> , 2013, 14, 550.	1.2	12
102	Endothelial-hematopoietic transition: from the dorsal aorta to the dish. <i>Experimental Hematology</i> , 2013, 41, S26.	0.2	0
103	Complete genomic landscape of a recurring sporadic parathyroid carcinoma. <i>Journal of Pathology</i> , 2013, 230, 249-260.	2.1	57
104	Integrated genomic characterization of endometrial carcinoma. <i>Nature</i> , 2013, 497, 67-73.	13.7	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.	13.9	4,139
106	The genetic landscape of high-risk neuroblastoma. <i>Nature Genetics</i> , 2013, 45, 279-284.	9.4	990
107	Comprehensive molecular characterization of clear cell renal cell carcinoma. <i>Nature</i> , 2013, 499, 43-49.	13.7	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.	1.8	356

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109	Mutational and structural analysis of diffuse large B-cell lymphoma using whole-genome sequencing. <i>Blood</i> , 2013, 122, 1256-1265.	0.6	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> . <i>PLoS ONE</i> , 2013, 8, e71328.	1.1	96
111	Subgroup-specific structural variation across 1,000 medulloblastoma genomes. <i>Nature</i> , 2012, 488, 49-56.	13.7	761
112	Dissect: detection and characterization of novel structural alterations in transcribed sequences. <i>Bioinformatics</i> , 2012, 28, i179-i187.	1.8	13
113	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
114	Hive plots--rational approach to visualizing networks. <i>Briefings in Bioinformatics</i> , 2012, 13, 627-644.	3.2	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. <i>Insect Biochemistry and Molecular Biology</i> , 2012, 42, 525-536.	1.2	93
116	Comprehensive molecular characterization of human colon and rectal cancer. <i>Nature</i> , 2012, 487, 330-337.	13.7	7,168
117	Comprehensive molecular portraits of human breast tumours. <i>Nature</i> , 2012, 490, 61-70.	13.7	10,282
118	Comprehensive genomic characterization of squamous cell lung cancers. <i>Nature</i> , 2012, 489, 519-525.	13.7	3,483
119	Recurrent targets of aberrant somatic hypermutation in lymphoma. <i>Oncotarget</i> , 2012, 3, 1308-1319.	0.8	127
120	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
121	The clonal and mutational evolution spectrum of primary triple-negative breast cancers. <i>Nature</i> , 2012, 486, 395-399.	13.7	1,778
122	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
123	Frequent mutation of histone-modifying genes in non-Hodgkin lymphoma. <i>Nature</i> , 2011, 476, 298-303.	13.7	1,428
124	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
125	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
126	Assemblathon 1: A competitive assessment of de novo short read assembly methods. <i>Genome Research</i> , 2011, 21, 2224-2241.	2.4	443

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127	Human variation database: an open-source database template for genomic discovery. <i>Bioinformatics</i> , 2011, 27, 1155-1156.	1.8	11
128	Genome Sequence of <i>Mycoplasma capricolum</i> subsp. <i>capripneumoniae</i> Strain M1601. <i>Journal of Bacteriology</i> , 2011, 193, 6098-6099.	1.0	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.	3.3	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.	0.4	3
131	Genomic analysis of a rare human tumor. <i>BMC Bioinformatics</i> , 2010, 11, .	1.2	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.	9.4	1,504
133	De novo assembly and analysis of RNA-seq data. <i>Nature Methods</i> , 2010, 7, 909-912.	9.0	886
134	mrsFAST: a cache-oblivious algorithm for short-read mapping. <i>Nature Methods</i> , 2010, 7, 576-577.	9.0	248
135	Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. <i>Bioinformatics</i> , 2010, 26, 1277-1283.	1.8	98
136	LaneRuler: Automated Lane Tracking for DNA Electrophoresis Gel Images. <i>IEEE Transactions on Automation Science and Engineering</i> , 2010, 7, 706-708.	3.4	12
137	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. <i>Genome Research</i> , 2010, 20, 791-803.	2.4	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.	2.4	109
139	Evolution of an adenocarcinoma in response to selection by targeted kinase inhibitors. <i>Genome Biology</i> , 2010, 11, R82.	13.9	159
140	Personalized oncogenomics. <i>Genome Biology</i> , 2010, 11, I5.	13.9	0
141	Assembling genomes using short-read sequencing technology. <i>Genome Biology</i> , 2010, 11, 202.	13.9	19
142	Identification of Genes Frequently Mutated In FL and DLBCL with Transcriptome, Genome and Exome Sequencing. <i>Blood</i> , 2010, 116, 804-804.	0.6	1
143	ABYSS: A parallel assembler for short read sequence data. <i>Genome Research</i> , 2009, 19, 1117-1123.	2.4	3,134
144	De novo transcriptome assembly with ABYSS. <i>Bioinformatics</i> , 2009, 25, 2872-2877.	1.8	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.	13.9	130
146	ABYSS-Explorer: Visualizing Genome Sequence Assemblies. <i>IEEE Transactions on Visualization and Computer Graphics</i> , 2009, 15, 881-888.	2.9	53
147	Circos: An information aesthetic for comparative genomics. <i>Genome Research</i> , 2009, 19, 1639-1645.	2.4	9,003
148	Optimal pooling for genome re-sequencing with ultra-high-throughput short-read technologies. <i>Bioinformatics</i> , 2008, 24, i32-i40.	1.8	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.	2.4	163
150	Coherent bremsstrahlung, coherent pair production, birefringence, and polarimetry in the 20–170 GeV 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.	0.6	10
153	Agent-based control of autocatalytic replicators in networks of reactors. <i>Computers and Chemical Engineering</i> , 2005, 29, 807-815.	2.0	32
154	Measuring Complexity in Reactor Networks with Cubic Autocatalytic Reactions. <i>Industrial & Engineering Chemistry Research</i> , 2005, 44, 2781-2791.	1.8	13
155	The trigger and DAQ systems of the Na59 experiment. <i>IEEE Transactions on Nuclear Science</i> , 2004, 51, 1482-1487.	1.2	2
156	Software aspects of the Na59 experiment. <i>IEEE Transactions on Nuclear Science</i> , 2004, 51, 1449-1455.	1.2	2
157	Static and Dynamic Behavior of Autocatalytic Replicators in Reactor Networks. <i>Industrial & Engineering Chemistry Research</i> , 2004, 43, 3972-3993.	1.8	15
158	Metabolic Control Analysis under Uncertainty: Framework Development and Case Studies. <i>Biophysical Journal</i> , 2004, 87, 3750-3763.	0.2	153
159	Investigating the fermentation dynamics structure of recombinant yeast YPB-G. <i>Computers and Chemical Engineering</i> , 2003, 27, 45-54.	2.0	1
160	Feedback Control of a Continuous-Flow Stirred Tank Reactor with Competing Autocatalators. <i>Industrial & Engineering Chemistry Research</i> , 2003, 42, 3765-3785.	1.8	12
161	Effect of environment partitioning on the survival and coexistence of autocatalytic replicators. <i>Physical Review E</i> , 2002, 66, 051916.	0.8	16
162	Competition between Robust and Nonrobust Autocatalytic Replicators. <i>Industrial & Engineering Chemistry Research</i> , 2002, 41, 3630-3641.	1.8	14

