

Inna Dubchak

List of Publications by Year in descending order

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75
papers

28,656
citations

47006

47
h-index

79698

73
g-index

75
all docs

75
docs citations

75
times ranked

35564
citing authors

#	ARTICLE	IF	CITATIONS
1	KBase: The United States Department of Energy Systems Biology Knowledgebase. <i>Nature Biotechnology</i> , 2018, 36, 566-569.	17.5	955
2	Strategic Integration of Multiple Bioinformatics Resources for System Level Analysis of Biological Networks. <i>Methods in Molecular Biology</i> , 2017, 1613, 85-99.	0.9	3
3	Conserved genomic collinearity as a source of broadly applicable, fast evolving, markers to resolve species complexes: A case study using the lichen-forming genus <i>Peltigera</i> section <i>Polydactylon</i> . <i>Molecular Phylogenetics and Evolution</i> , 2017, 117, 10-29.	2.7	30
4	Rice SNP-seek database update: new SNPs, indels, and queries. <i>Nucleic Acids Research</i> , 2017, 45, D1075-D1081.	14.5	290
5	SNP-Seek II: A resource for allele mining and analysis of big genomic data in <i>Oryza sativa</i> . <i>Current Plant Biology</i> , 2016, 7-8, 16-25.	4.7	48
6	Ĥf54-dependent regulome in <i>Desulfovibrio vulgaris</i> Hildenborough. <i>BMC Genomics</i> , 2015, 16, 919.	2.8	11
7	Functionally conserved enhancers with divergent sequences in distant vertebrates. <i>BMC Genomics</i> , 2015, 16, 882.	2.8	18
8	MycoCosm portal: gearing up for 1000 fungal genomes. <i>Nucleic Acids Research</i> , 2014, 42, D699-D704.	14.5	1,187
9	Alignathon: a competitive assessment of whole-genome alignment methods. <i>Genome Research</i> , 2014, 24, 2077-2089.	5.5	102
10	The genome portal of the Department of Energy Joint Genome Institute: 2014 updates. <i>Nucleic Acids Research</i> , 2014, 42, D26-D31.	14.5	590
11	GenomeVISTA“an integrated software package for whole-genome alignment and visualization. <i>Bioinformatics</i> , 2014, 30, 2654-2655.	4.1	27
12	The genome of <i>Eucalyptus grandis</i> . <i>Nature</i> , 2014, 510, 356-362.	27.8	725
13	An Integrative Computational Approach for Prioritization of Genomic Variants. <i>PLoS ONE</i> , 2014, 9, e114903.	2.5	7
14	RegTransBase “ a database of regulatory sequences and interactions based on literature: a resource for investigating transcriptional regulation in prokaryotes. <i>BMC Genomics</i> , 2013, 14, 213.	2.8	69
15	Whole-Genome rVISTA: a tool to determine enrichment of transcription factor binding sites in gene promoters from transcriptomic data. <i>Bioinformatics</i> , 2013, 29, 2059-2061.	4.1	22
16	New Family of Tungstate-Responsive Transcriptional Regulators in Sulfate-Reducing Bacteria. <i>Journal of Bacteriology</i> , 2013, 195, 4466-4475.	2.2	16
17	Transcription Factor Family-Based Reconstruction of Singleton Regulons and Study of the Crp/Fnr, ArsR, and GntR Families in <i>Desulfovibrionales</i> Genomes. <i>Journal of Bacteriology</i> , 2013, 195, 29-38.	2.2	15
18	RegPrecise 3.0 “ A resource for genome-scale exploration of transcriptional regulation in bacteria. <i>BMC Genomics</i> , 2013, 14, 745.	2.8	408

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19	Genome Portal, Joint Genome Institute. , 2013, , 1-10.		0
20	RegPrecise web services interface: programmatic access to the transcriptional regulatory interactions in bacteria reconstructed by comparative genomics. <i>Nucleic Acids Research</i> , 2012, 40, W604-W608.	14.5	24
21	The Genome Portal of the Department of Energy Joint Genome Institute. <i>Nucleic Acids Research</i> , 2012, 40, D26-D32.	14.5	439
22	Comparative genomic reconstruction of transcriptional networks controlling central metabolism in the <i>Shewanella</i> genus. <i>BMC Genomics</i> , 2011, 12, S3.	2.8	59
23	Tandem termination signal in plant mRNAs. <i>Gene</i> , 2011, 481, 1-6.	2.2	4
24	Comparative Genomics of the Dormancy Regulons in Mycobacteria. <i>Journal of Bacteriology</i> , 2011, 193, 3446-3452.	2.2	48
25	VISTA Region Viewer (RViewer)â€”a computational system for prioritizing genomic intervals for biomedical studies. <i>Bioinformatics</i> , 2011, 27, 2595-2597.	4.1	11
26	A cis-Regulatory Signature in Ascidians and Flies, Independent of Transcription Factor Binding Sites. <i>Current Biology</i> , 2010, 20, 792-802.	3.9	58
27	Visualizing genomes: techniques and challenges. <i>Nature Methods</i> , 2010, 7, S5-S15.	19.0	146
28	RegPrecise: a database of curated genomic inferences of transcriptional regulatory interactions in prokaryotes. <i>Nucleic Acids Research</i> , 2010, 38, D111-D118.	14.5	172
29	The Genome of the Western Clawed Frog <i>Xenopus tropicalis</i> . <i>Science</i> , 2010, 328, 633-636.	12.6	708
30	RegPredict: an integrated system for regulon inference in prokaryotes by comparative genomics approach. <i>Nucleic Acids Research</i> , 2010, 38, W299-W307.	14.5	130
31	Obtaining Comparative Genomic Data with the VISTA Family of Computational Tools. <i>Current Protocols in Bioinformatics</i> , 2009, 26, Unit 10.6.	25.8	10
32	Trends in Prokaryotic Evolution Revealed by Comparison of Closely Related Bacterial and Archaeal Genomes. <i>Journal of Bacteriology</i> , 2009, 191, 65-73.	2.2	121
33	ATGC: a database of orthologous genes from closely related prokaryotic genomes and a research platform for microevolution of prokaryotes. <i>Nucleic Acids Research</i> , 2009, 37, D448-D454.	14.5	49
34	Multiple whole-genome alignments without a reference organism. <i>Genome Research</i> , 2009, 19, 682-689.	5.5	63
35	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes <i>Micromonas</i> . <i>Science</i> , 2009, 324, 268-272.	12.6	591
36	Comparative Genomics of Regulation of Fatty Acid and Branched-Chain Amino Acid Utilization in Proteobacteria. <i>Journal of Bacteriology</i> , 2009, 191, 52-64.	2.2	115

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37	The amphioxus genome and the evolution of the chordate karyotype. <i>Nature</i> , 2008, 453, 1064-1071.	27.8	1,496
38	Combinatorial Regulation of Endothelial Gene Expression by Ets and Forkhead Transcription Factors. <i>Cell</i> , 2008, 135, 1053-1064.	28.9	306
39	The tiny eukaryote <i>Ostreococcus</i> provides genomic insights into the paradox of plankton speciation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7705-7710.	7.1	563
40	VISTA Enhancer Browser—a database of tissue-specific human enhancers. <i>Nucleic Acids Research</i> , 2007, 35, D88-D92.	14.5	950
41	The integrated microbial genomes (IMG) system in 2007: data content and analysis tool extensions. <i>Nucleic Acids Research</i> , 2007, 36, D528-D533.	14.5	179
42	IMG/M: a data management and analysis system for metagenomes. <i>Nucleic Acids Research</i> , 2007, 36, D534-D538.	14.5	309
43	Multiple whole genome alignments and novel biomedical applications at the VISTA portal. <i>Nucleic Acids Research</i> , 2007, 35, W669-W674.	14.5	30
44	A correlation with exon expression approach to identify cis-regulatory elements for tissue-specific alternative splicing. <i>Nucleic Acids Research</i> , 2007, 35, 4845-4857.	14.5	75
45	Extensive parallelism in protein evolution. <i>Biology Direct</i> , 2007, 2, 20.	4.6	32
46	Short sequence motifs, overrepresented in mammalian conserved non-coding sequences. <i>BMC Genomics</i> , 2007, 8, 378.	2.8	7
47	The <i>Chlamydomonas</i> Genome Reveals the Evolution of Key Animal and Plant Functions. <i>Science</i> , 2007, 318, 245-250.	12.6	2,354
48	Comparative Analysis and Visualization of Genomic Sequences Using VISTA Browser and Associated Computational Tools. <i>Methods in Molecular Biology</i> , 2007, 395, 3-16.	0.9	17
49	Conservation patterns in different functional sequence categories of divergent <i>Drosophila</i> species. <i>Genomics</i> , 2006, 88, 431-442.	2.9	18
50	In vivo enhancer analysis of human conserved non-coding sequences. <i>Nature</i> , 2006, 444, 499-502.	27.8	1,072
51	VISTA Family of Computational Tools for Comparative Analysis of DNA Sequences and Whole Genomes. <i>Nucleic Acids Research</i> , 2006, 338, 69-90.		53
52	The splicing regulatory element, UGCAUG, is phylogenetically and spatially conserved in introns that flank tissue-specific alternative exons. <i>Nucleic Acids Research</i> , 2005, 33, 714-724.	14.5	92
53	Comparative genome sequencing of <i>Drosophila pseudoobscura</i> : Chromosomal, gene, and cis-element evolution. <i>Genome Research</i> , 2005, 15, 1-18.	5.5	453
54	Gene expression patterns define key transcriptional events in cell-cycle regulation by cAMP and protein kinase A. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 8561-8566.	7.1	111

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55	Variation in conserved non-coding sequences on chromosome 5q and susceptibility to asthma and atopy. <i>Respiratory Research</i> , 2005, 6, 145.	3.6	43
56	Automated Whole-Genome Multiple Alignment of Rat, Mouse, and Human. <i>Genome Research</i> , 2004, 14, 685-692.	5.5	79
57	Characterization of Evolutionary Rates and Constraints in Three Mammalian Genomes. <i>Genome Research</i> , 2004, 14, 539-548.	5.5	125
58	Phylo-VISTA: interactive visualization of multiple DNA sequence alignments. <i>Bioinformatics</i> , 2004, 20, 636-643.	4.1	46
59	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. <i>PLoS Biology</i> , 2004, 2, e162.	5.6	290
60	The DNA sequence and biology of human chromosome 19. <i>Nature</i> , 2004, 428, 529-535.	27.8	298
61	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. <i>Nature</i> , 2004, 428, 493-521.	27.8	1,943
62	Reconstruction of regulatory and metabolic pathways in metal-reducing delta-proteobacteria. <i>Genome Biology</i> , 2004, 5, R90.	9.6	162
63	Differential domain evolution and complex RNA processing in a family of paralogous EPB41 (protein) Tj ETQq1 1 0.784314 rgBT /Over 2.9 31	2.9	31
64	VISTA: computational tools for comparative genomics. <i>Nucleic Acids Research</i> , 2004, 32, W273-W279.	14.5	2,033
65	Multi-species sequence comparison: the next frontier in genome annotation. <i>Genome Biology</i> , 2003, 4, 122.	9.6	15
66	Strategies and Tools for Whole-Genome Alignments. <i>Genome Research</i> , 2003, 13, 73-80.	5.5	190
67	Glocal alignment: finding rearrangements during alignment. <i>Bioinformatics</i> , 2003, 19, i54-i62.	4.1	333
68	Cross-Species Sequence Comparisons: A Review of Methods and Available Resources. <i>Genome Research</i> , 2003, 13, 1-12.	5.5	210
69	AVID: A Global Alignment Program. <i>Genome Research</i> , 2003, 13, 97-102.	5.5	405
70	<tt>rVista</tt> for Comparative Sequence-Based Discovery of Functional Transcription Factor Binding Sites. <i>Genome Research</i> , 2002, 12, 832-839.	5.5	384
71	The computational challenges of applying comparative-based computational methods to whole genomes. <i>Briefings in Bioinformatics</i> , 2002, 3, 18-22.	6.5	10
72	Comparative genomics approaches to study organism similarities and differences. <i>Journal of Biomedical Informatics</i> , 2002, 35, 142-150.	4.3	68

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73	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	27.8	6,319
74	Recognition of a protein fold in the context of the SCOP classification. Proteins: Structure, Function and Bioinformatics, 1999, 35, 401-407.	2.6	218
75	Prediction of protein folding class from amino acid composition. Proteins: Structure, Function and Bioinformatics, 1993, 16, 79-91.	2.6	66