Inna Dubchak

List of Publications by Year
in descending order

75 papers	28,656 citations	46918 47 h-index	79541 73 g-index
75 all docs	75 docs citations	75 times ranked	35564 citing authors

#	Article	IF	Citations
1	Initial sequencing and comparative analysis of the mouse genome. Nature, 2002, 420, 520-562.	13.7	6,319
2	The *Chlamydomonas* Genome Reveals the Evolution of Key Animal and Plant Functions. Science, 2007, 318, 245-250.	6.0	2,354
3	VISTA: computational tools for comparative genomics. Nucleic Acids Research, 2004, 32, W273-W279.	6.5	2,033
4	Genome sequence of the Brown Norway rat yields insights into mammalian evolution. Nature, 2004, 428, 493-521.	13.7	1,943
5	The amphioxus genome and the evolution of the chordate karyotype. Nature, 2008, 453, 1064-1071.	13.7	1,496
6	MycoCosm portal: gearing up for 1000 fungal genomes. Nucleic Acids Research, 2014, 42, D699-D704.	6.5	1,187
7	In vivo enhancer analysis of human conserved non-coding sequences. Nature, 2006, 444, 499-502.	13.7	1,072
8	KBase: The United States Department of Energy Systems Biology Knowledgebase. Nature Biotechnology, 2018, 36, 566-569.	9.4	955
9	VISTA Enhancer Browser--a database of tissue-specific human enhancers. Nucleic Acids Research, 2007, 35, D88-D92.	6.5	950
10	The genome of Eucalyptus grandis. Nature, 2014, 510, 356-362.	13.7	725
11	The Genome of the Western Clawed Frog *Xenopus tropicalis*. Science, 2010, 328, 633-636.	6.0	708
12	Green Evolution and Dynamic Adaptations Revealed by Genomes of the Marine Picoeukaryotes *Micromonas*. Science, 2009, 324, 268-272.	6.0	591
13	The genome portal of the Department of Energy Joint Genome Institute: 2014 updates. Nucleic Acids Research, 2014, 42, D26-D31.	6.5	590
14	The tiny eukaryote Ostreococcus provides genomic insights into the paradox of plankton speciation. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 7705-7710.	3.3	563
15	Comparative genome sequencing of Drosophila pseudoobscura: Chromosomal, gene, and cis-element evolution. Genome Research, 2005, 15, 1-18.	2.4	453
16	The Genome Portal of the Department of Energy Joint Genome Institute. Nucleic Acids Research, 2012, 40, D26-D32.	6.5	439
17	RegPrecise 3.0 â€" A resource for genome-scale exploration of transcriptional regulation in bacteria. BMC Genomics, 2013, 14, 745.	1.2	408
18	AVID: A Global Alignment Program. Genome Research, 2003, 13, 97-102.	2.4	405

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19	`<tt>rVista</tt>` for Comparative Sequence-Based Discovery of Functional Transcription Factor Binding Sites. Genome Research, 2002, 12, 832-839.	2.4	384
20	Glocal alignment: finding rearrangements during alignment. Bioinformatics, 2003, 19, i54-i62.	1.8	333
21	IMG/M: a data management and analysis system for metagenomes. Nucleic Acids Research, 2007, 36, D534-D538.	6.5	309
22	Combinatorial Regulation of Endothelial Gene Expression by Ets and Forkhead Transcription Factors. Cell, 2008, 135, 1053-1064.	13.5	306
23	The DNA sequence and biology of human chromosome 19. Nature, 2004, 428, 529-535.	13.7	298
24	Integrative Annotation of 21,037 Human Genes Validated by Full-Length cDNA Clones. PLoS Biology, 2004, 2, e162.	2.6	290
25	Rice SNP-seek database update: new SNPs, indels, and queries. Nucleic Acids Research, 2017, 45, D1075-D1081.	6.5	290
26	Recognition of a protein fold in the context of the SCOP classification. Proteins: Structure, Function and Bioinformatics, 1999, 35, 401-407.	1.5	218
27	Cross-Species Sequence Comparisons: A Review of Methods and Available Resources. Genome Research, 2003, 13, 1-12.	2.4	210
28	Strategies and Tools for Whole-Genome Alignments. Genome Research, 2003, 13, 73-80.	2.4	190
29	The integrated microbial genomes (IMG) system in 2007: data content and analysis tool extensions. Nucleic Acids Research, 2007, 36, D528-D533.	6.5	179
30	RegPrecise: a database of curated genomic inferences of transcriptional regulatory interactions in prokaryotes. Nucleic Acids Research, 2010, 38, D111-D118.	6.5	172
31	Reconstruction of regulatory and metabolic pathways in metal-reducing delta-proteobacteria. Genome Biology, 2004, 5, R90.	13.9	162
32	Visualizing genomes: techniques and challenges. Nature Methods, 2010, 7, S5-S15.	9.0	146
33	RegPredict: an integrated system for regulon inference in prokaryotes by comparative genomics approach. Nucleic Acids Research, 2010, 38, W299-W307.	6.5	130
34	Characterization of Evolutionary Rates and Constraints in Three Mammalian Genomes. Genome Research, 2004, 14, 539-548.	2.4	125
35	Trends in Prokaryotic Evolution Revealed by Comparison of Closely Related Bacterial and Archaeal Genomes. Journal of Bacteriology, 2009, 191, 65-73.	1.0	121
36	Comparative Genomics of Regulation of Fatty Acid and Branched-Chain Amino Acid Utilization in Proteobacteria. Journal of Bacteriology, 2009, 191, 52-64.	1.0	115

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37	Gene expression patterns define key transcriptional events in cell-cycle regulation by cAMP and protein kinase A. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 8561-8566.	3.3	111
38	Alignathon: a competitive assessment of whole-genome alignment methods. Genome Research, 2014, 24, 2077-2089.	2.4	102
39	The splicing regulatory element, UGCAUG, is phylogenetically and spatially conserved in introns that flank tissue-specific alternative exons. Nucleic Acids Research, 2005, 33, 714-724.	6.5	92
40	Automated Whole-Genome Multiple Alignment of Rat, Mouse, and Human. Genome Research, 2004, 14, 685-692.	2.4	79
41	A correlation with exon expression approach to identify cis-regulatory elements for tissue-specific alternative splicing. Nucleic Acids Research, 2007, 35, 4845-4857.	6.5	75
42	RegTransBase â€" a database of regulatory sequences and interactions based on literature: a resource for investigating transcriptional regulation in prokaryotes. BMC Genomics, 2013, 14, 213.	1.2	69
43	Comparative genomics approaches to study organism similarities and differences. Journal of Biomedical Informatics, 2002, 35, 142-150.	2.5	68
44	Prediction of protein folding class from amino acid composition. Proteins: Structure, Function and Bioinformatics, 1993, 16, 79-91.	1.5	66
45	Multiple whole-genome alignments without a reference organism. Genome Research, 2009, 19, 682-689.	2.4	63
46	Comparative genomic reconstruction of transcriptional networks controlling central metabolism in the Shewanella genus. BMC Genomics, 2011, 12, S3.	1.2	59
47	A cis-Regulatory Signature in Ascidians and Flies, Independent of Transcription Factor Binding Sites. Current Biology, 2010, 20, 792-802.	1.8	58
48	VISTA Family of Computational Tools for Comparative Analysis of DNA Sequences and Whole Genomes. , 2006, 338, 69-90.		53
49	ATGC: a database of orthologous genes from closely related prokaryotic genomes and a research platform for microevolution of prokaryotes. Nucleic Acids Research, 2009, 37, D448-D454.	6.5	49
50	Comparative Genomics of the Dormancy Regulons in Mycobacteria. Journal of Bacteriology, 2011, 193, 3446-3452.	1.0	48
51	SNP-Seek II: A resource for allele mining and analysis of big genomic data in Oryza sativa. Current Plant Biology, 2016, 7-8, 16-25.	2.3	48
52	Phylo-VISTA: interactive visualization of multiple DNA sequence alignments. Bioinformatics, 2004, 20, 636-643.	1.8	46
53	Variation in conserved non-coding sequences on chromosome 5q and susceptibility to asthma and atopy. Respiratory Research, 2005, 6, 145.	1.4	43
54	Extensive parallelism in protein evolution. Biology Direct, 2007, 2, 20.	1.9	32

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55	Differential domain evolution and complex RNA processing in a family of paralogous EPB41 (protein) Tj ETQq1 1 0.784314 rgBT /Over	1.3	31
56	Multiple whole genome alignments and novel biomedical applications at the VISTA portal. Nucleic Acids Research, 2007, 35, W669-W674.	6.5	30
57	Conserved genomic collinearity as a source of broadly applicable, fast evolving, markers to resolve species complexes: A case study using the lichen-forming genus Peltigera section Polydactylon. Molecular Phylogenetics and Evolution, 2017, 117, 10-29.	1.2	30
58	GenomeVISTAâ€"an integrated software package for whole-genome alignment and visualization. Bioinformatics, 2014, 30, 2654-2655.	1.8	27
59	RegPrecise web services interface: programmatic access to the transcriptional regulatory interactions in bacteria reconstructed by comparative genomics. Nucleic Acids Research, 2012, 40, W604-W608.	6.5	24
60	Whole-Genome rVISTA: a tool to determine enrichment of transcription factor binding sites in gene promoters from transcriptomic data. Bioinformatics, 2013, 29, 2059-2061.	1.8	22
61	Conservation patterns in different functional sequence categories of divergent Drosophila species. Genomics, 2006, 88, 431-442.	1.3	18
62	Functionally conserved enhancers with divergent sequences in distant vertebrates. BMC Genomics, 2015, 16, 882.	1.2	18
63	Comparative Analysis and Visualization of Genomic Sequences Using VISTA Browser and Associated Computational Tools. Methods in Molecular Biology, 2007, 395, 3-16.	0.4	17
64	New Family of Tungstate-Responsive Transcriptional Regulators in Sulfate-Reducing Bacteria. Journal of Bacteriology, 2013, 195, 4466-4475.	1.0	16
65	Multi-species sequence comparison: the next frontier in genome annotation. Genome Biology, 2003, 4, 122.	13.9	15
66	Transcription Factor Family-Based Reconstruction of Singleton Regulons and Study of the Crp/Fnr, ArsR, and GntR Families in Desulfovibrionales Genomes. Journal of Bacteriology, 2013, 195, 29-38.	1.0	15
67	VISTA Region Viewer (RViewer)â€"a computational system for prioritizing genomic intervals for biomedical studies. Bioinformatics, 2011, 27, 2595-2597.	1.8	11
68	Ïƒ54-dependent regulome in Desulfovibrio vulgaris Hildenborough. BMC Genomics, 2015, 16, 919.	1.2	11
69	The computational challenges of applying comparative-based computational methods to whole genomes. Briefings in Bioinformatics, 2002, 3, 18-22.	3.2	10
70	Obtaining Comparative Genomic Data with the VISTA Family of Computational Tools. Current Protocols in Bioinformatics, 2009, 26, Unit 10.6.	25.8	10
71	Short sequence motifs, overrepresented in mammalian conserved non-coding sequences. BMC Genomics, 2007, 8, 378.	1.2	7
72	An Integrative Computational Approach for Prioritization of Genomic Variants. PLoS ONE, 2014, 9, e114903.	1.1	7

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73	Tandem termination signal in plant mRNAs. Gene, 2011, 481, 1-6.	1.0	4
74	Strategic Integration of Multiple Bioinformatics Resources for System Level Analysis of Biological Networks. Methods in Molecular Biology, 2017, 1613, 85-99.	0.4	3
75	Genome Portal, Joint Genome Institute. , 2013, , 1-10.		0