

Isidore Rigoutsos

List of Publications by Year in descending order

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Version: 2024-02-01

167
papers

22,458
citations

22548

61
h-index

14779

131
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173
all docs

173
docs citations

173
times ranked

35901
citing authors

#	ARTICLE	IF	CITATIONS
1	MicroRNA-139 Expression Is Dispensable for the Generation of Influenza-Specific CD8+ T Cell Responses. <i>Journal of Immunology</i> , 2022, 208, 603-617.	0.4	2
2	IsoMiRmap: fast, deterministic and exhaustive mining of isomiRs from short RNA-seq datasets. <i>Bioinformatics</i> , 2021, 37, 1828-1838.	1.8	11
3	The transcriptional trajectories of pluripotency and differentiation comprise genes with antithetical architecture and repetitive-element content. <i>BMC Biology</i> , 2021, 19, 60.	1.7	5
4	Unraveling the role of microRNA/isomiR network in multiple primary melanoma pathogenesis. <i>Cell Death and Disease</i> , 2021, 12, 473.	2.7	13
5	RNase H ² promotes robust piRNA production by generating 2',3'-cyclic phosphate-containing precursors. <i>Nature Communications</i> , 2021, 12, 4498.	5.8	6
6	Megakaryocyte-specific knockout of the Mir-99b/let7e/125a cluster lowers platelet count without altering platelet function. <i>Blood Cells, Molecules, and Diseases</i> , 2021, 92, 102624.	0.6	1
7	Unification of miRNA and isomiR research: the mirGFF3 format and the mirtop API. <i>Bioinformatics</i> , 2020, 36, 698-703.	1.8	33
8	IsomiRs and tRNA-derived fragments are associated with metastasis and patient survival in uveal melanoma. <i>Pigment Cell and Melanoma Research</i> , 2020, 33, 52-62.	1.5	37
9	On the expanding roles of tRNA fragments in modulating cell behavior. <i>Nucleic Acids Research</i> , 2020, 48, 9433-9448.	6.5	107
10	Long-term exposure of human endothelial cells to metformin modulates miRNAs and isomiRs. <i>Scientific Reports</i> , 2020, 10, 21782.	1.6	14
11	Therapeutic potential of FLANC, a novel primate-specific long non-coding RNA in colorectal cancer. <i>Gut</i> , 2020, 69, 1818-1831.	6.1	80
12	Ribosomal RNA fragmentation into short RNAs (rRFs) is modulated in a sex- and population of origin-specific manner. <i>BMC Biology</i> , 2020, 18, 38.	1.7	36
13	Abstract IA31: Novel nuclear and mitochondrial RNAs that are linked to key pathways and depend on sex, population origin, race, tissue, and disease. , 2020, , .		0
14	Abstract CO10: The wiring between genes and short noncoding RNAs in cancer depends on race/ethnicity and sex. , 2020, , .		0
15	Abstract B077: Ribosomal RNAs are fragmented into short RNAs in a manner that depends on a person's sex, population origin, and race: implications for health disparities and personalized medicine. , 2020, , .		0
16	Abstract PO-127: The short non-coding RNAs known as "ribosomal RNA-derived fragments" (rRFs) are linked to race disparities in TNBC. , 2020, , .		0
17	Short RNA regulators: the past, the present, the future, and implications for precision medicine and health disparities. <i>Current Opinion in Biotechnology</i> , 2019, 58, 202-210.	3.3	14
18	Exploration of CCA-added RNAs revealed the expression of mitochondrial non-coding RNAs regulated by CCA-adding enzyme. <i>RNA Biology</i> , 2019, 16, 1817-1825.	1.5	8

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19	TRNA-derived fragments as sex-dependent circulating candidate biomarkers for Parkinson's disease. <i>Parkinsonism and Related Disorders</i> , 2019, 65, 203-209.	1.1	49
20	tRNA Fragments Show Intertwining with mRNAs of Specific Repeat Content and Have Links to Disparities. <i>Cancer Research</i> , 2019, 79, 3034-3049.	0.4	72
21	Small RNA Sequencing across Diverse Biofluids Identifies Optimal Methods for exRNA Isolation. <i>Cell</i> , 2019, 177, 446-462.e16.	13.5	214
22	MINTbase v2.0: a comprehensive database for tRNA-derived fragments that includes nuclear and mitochondrial fragments from all The Cancer Genome Atlas projects. <i>Nucleic Acids Research</i> , 2018, 46, D152-D159.	6.5	155
23	Profiles of miRNA Isoforms and tRNA Fragments in Prostate Cancer. <i>Scientific Reports</i> , 2018, 8, 5314.	1.6	57
24	Accurate Profiling and Quantification of tRNA Fragments from RNA-Seq Data: A Vade Mecum for MINTmap. <i>Methods in Molecular Biology</i> , 2018, 1680, 237-255.	0.4	21
25	Race Disparities in the Contribution of miRNA Isoforms and tRNA-Derived Fragments to Triple-Negative Breast Cancer. <i>Cancer Research</i> , 2018, 78, 1140-1154.	0.4	90
26	Abstract B64: Race and prostate cancer: miRNA isoforms and tRNA fragments could hold some of the answers. , 2018, , .		0
27	Abstract B63: Race and triple-negative breast cancer: Advances in noncoding RNA research together with a systems-biology-level analysis uncover key molecular differences. , 2018, , .		0
28	MINTmap: fast and exhaustive profiling of nuclear and mitochondrial tRNA fragments from short RNA-seq data. <i>Scientific Reports</i> , 2017, 7, 41184.	1.6	123
29	Threshold-seq: a tool for determining the threshold in short RNA-seq datasets. <i>Bioinformatics</i> , 2017, 33, 2034-2036.	1.8	10
30	Knowledge about the presence or absence of miRNA isoforms (isomiRs) can successfully discriminate amongst 32 TCGA cancer types. <i>Nucleic Acids Research</i> , 2017, 45, 2973-2985.	6.5	158
31	An miRNA Expression Signature for the Human Colonic Stem Cell Niche Distinguishes Malignant from Normal Epithelia. <i>Cancer Research</i> , 2017, 77, 3778-3790.	0.4	18
32	N-BLR, a primate-specific non-coding transcript leads to colorectal cancer invasion and migration. <i>Genome Biology</i> , 2017, 18, 98.	3.8	97
33	Integrated Genomic Characterization of Pancreatic Ductal Adenocarcinoma. <i>Cancer Cell</i> , 2017, 32, 185-203.e13.	7.7	1,428
34	Increasing cell density globally enhances the biogenesis of Piwi-interacting RNAs in <i>Bombyx mori</i> germ cells. <i>Scientific Reports</i> , 2017, 7, 4110.	1.6	14
35	The biogenesis pathway of tRNA-derived piRNAs in <i>Bombyx</i> germ cells. <i>Nucleic Acids Research</i> , 2017, 45, 9108-9120.	6.5	34
36	YAMAT-seq: an efficient method for high-throughput sequencing of mature transfer RNAs. <i>Nucleic Acids Research</i> , 2017, 45, gkx005.	6.5	84

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37	Assessment of isomiR Discrimination Using Commercial qPCR Methods. <i>Non-coding RNA</i> , 2017, 3, 18.	1.3	40
38	Abstract P4-08-01: IsomiRs and tRNA fragments are race-dependent regulators in breast cancer. , 2017, , .		0
39	Abstract B43: Transcriptomic Heterogeneity of microRNA Isoforms and tRNA Fragments contributes to Race-based Differences in Breast and Prostate Cancers. , 2017, , .		0
40	Abstract 4423: Deep sequencing of lung cancer samples using different library preparation methods produces discordant short non-coding RNA profiles. , 2017, , .		0
41	Abstract 5438: Knowledge of which miRNA isoforms are expressed in a sample can successfully discriminate amongst the 32 TCGA cancer types. , 2017, , .		0
42	Post-transcriptional Regulation of BRCA2 through Interactions with miR-19a and miR-19b. <i>Frontiers in Genetics</i> , 2016, 7, 143.	1.1	20
43	Aging-associated changes in microRNA expression profile of internal anal sphincter smooth muscle: Role of microRNA-133a. <i>American Journal of Physiology - Renal Physiology</i> , 2016, 311, G964-G973.	1.6	23
44	Integrative Multi-omic Analysis of Human Platelet eQTLs Reveals Alternative Start Site in Mitofusin 2. <i>American Journal of Human Genetics</i> , 2016, 98, 883-897.	2.6	27
45	GPRC5A is a potential oncogene in pancreatic ductal adenocarcinoma cells that is upregulated by gemcitabine with help from HuR. <i>Cell Death and Disease</i> , 2016, 7, e2294-e2294.	2.7	50
46	MINTbase: a framework for the interactive exploration of mitochondrial and nuclear tRNA fragments. <i>Bioinformatics</i> , 2016, 32, 2481-2489.	1.8	89
47	Consequential considerations when mapping tRNA fragments. <i>BMC Bioinformatics</i> , 2016, 17, 123.	1.2	38
48	The mRNA-binding protein HuR promotes hypoxia-induced chemoresistance through posttranscriptional regulation of the proto-oncogene PIM1 in pancreatic cancer cells. <i>Oncogene</i> , 2016, 35, 2529-2541.	2.6	96
49	Multi-focal control of mitochondrial gene expression by oncogenic MYC provides potential therapeutic targets in cancer. <i>Oncotarget</i> , 2016, 7, 72395-72414.	0.8	30
50	Abstract A29: Gender-specific and race-specific regulatory noncoding RNAs are prevalent in healthy and in cancerous tissues. , 2016, , .		0
51	Abstract PR04: The molecular biology of nuclear and mitochondrial regulatory noncoding RNAs differs between white and African American patients with triple-negative breast cancer. , 2016, , .		0
52	Abstract A46: Tissue biology is shaped by noncoding RNAs that depend on gender, population, and race. , 2016, , .		0
53	Abstract 2665: SHOT-RNAs: A novel class of tRNA-derived functional RNAs expressed in hormone-dependent cancers. , 2016, , .		0
54	Abstract 1995: HuR dependent inhibition of PARC enhances PARP inhibitor therapy for DNA repair proficient and deficient pancreatic cancer cells. , 2016, , .		0

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55	Abstract A41: GPRC5A acts as a potent oncogene in pancreatic cancer. <i>Cancer Research</i> , 2016, 76, A41-A41.	0.4	1
56	Post-transcriptional regulation of BRCA1 through its coding sequence by the miR-15/107 group of miRNAs. <i>Frontiers in Genetics</i> , 2015, 6, 242.	1.1	26
57	Reply to Backes and Keller: Identification of novel tissue-specific and primate-specific human microRNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2851-E2851.	3.3	7
58	Beyond the one-locus-one-miRNA paradigm: microRNA isoforms enable deeper insights into breast cancer heterogeneity. <i>Nucleic Acids Research</i> , 2015, 43, 9158-9175.	6.5	134
59	Mitochondrial tRNA-lookalikes in nuclear chromosomes: Could they be functional?. <i>RNA Biology</i> , 2015, 12, 375-380.	1.5	37
60	Sex hormone-dependent tRNA halves enhance cell proliferation in breast and prostate cancers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E3816-25.	3.3	295
61	Analysis of 13 cell types reveals evidence for the expression of numerous novel primate- and tissue-specific microRNAs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1106-15.	3.3	376
62	“Off-Spotter” very fast and exhaustive enumeration of genomic lookalikes for designing CRISPR/Cas guide RNAs. <i>Biology Direct</i> , 2015, 10, 4.	1.9	96
63	Dissecting tRNA-derived fragment complexities using personalized transcriptomes reveals novel fragment classes and unexpected dependencies. <i>Oncotarget</i> , 2015, 6, 24797-24822.	0.8	146
64	Abstract A05: The mRNA-binding protein HuR promotes hypoxia-induced chemoresistance through post-transcriptional regulation of the serine-threonine kinase PIM1. , 2015, , .		0
65	Abstract A71: Post-transcriptional regulation of the proto-oncogene PIM1 by the mRNA stability factor HuR: implications for pancreatic cancer therapeutic response and cell survival. , 2015, , .		0
66	Abstract A78: Profiling of miRNA interactions in pancreatic adenocarcinoma by Argonaute CLIP-seq suggests a highly dynamic repertoire of targets. , 2015, , .		0
67	Abstract A34: Regulation of pancreatic cells by isomiRs. , 2015, , .		0
68	Abstract 2113: Targeting tumor-associated hypoxia to overcome chemoresistance in pancreatic ductal adenocarcinoma (PDA). , 2015, , .		0
69	Abstract 232: Characterization of the human miRNA-ome reveals numerous novel, tissue-specific miRNAs that are implicated in cancer biology. , 2015, , .		0
70	Abstract 3997: Expression profiling of a panel of apoptosis-associated microRNAs in acute myeloid leukemia identifies differentially expressed microRNAs that target epigenetic modifiers. , 2015, , .		0
71	Abstract 231: MicroRNA isoforms come of age: Going beyond the one-locus-one-microRNA paradigm in cancer biology. , 2015, , .		0
72	Expression Profiling of a Panel of Apoptosis Related Micrnas in Patients with Acute Myeloid Leukemia. <i>Blood</i> , 2015, 126, 4971-4971.	0.6	2

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73	Nuclear and mitochondrial tRNA-lookalikes in the human genome. <i>Frontiers in Genetics</i> , 2014, 5, 344.	1.1	36
74	MiR-103a-3p targets the 5' UTR of <i>GPRC5A</i> in pancreatic cells. <i>Rna</i> , 2014, 20, 1431-1439.	1.6	129
75	The human platelet: strong transcriptome correlations among individuals associate weakly with the platelet proteome. <i>Biology Direct</i> , 2014, 9, 3.	1.9	77
76	HuR Posttranscriptionally Regulates WEE1: Implications for the DNA Damage Response in Pancreatic Cancer Cells. <i>Cancer Research</i> , 2014, 74, 1128-1140.	0.4	91
77	Argonaute CLIP-Seq reveals miRNA targetome diversity across tissue types. <i>Scientific Reports</i> , 2014, 4, 5947.	1.6	88
78	The emerging roles of GPRC5A in diseases. <i>Oncoscience</i> , 2014, 1, 765-776.	0.9	61
79	IsomiR expression profiles in human lymphoblastoid cell lines exhibit population and gender dependencies. <i>Oncotarget</i> , 2014, 5, 8790-8802.	0.8	103
80	Characterization of the Short RNA Transcriptome of the Anucleate Platelet. <i>Blood</i> , 2014, 124, 4990-4990.	0.6	0
81	The complex transcriptional landscape of the anucleate human platelet. <i>BMC Genomics</i> , 2013, 14, 1.	1.2	913
82	The microRNAs within the DLK1-DIO3 genomic region: involvement in disease pathogenesis. <i>Cellular and Molecular Life Sciences</i> , 2013, 70, 795-814.	2.4	246
83	HuR is a post-transcriptional regulator of core metabolic enzymes in pancreatic cancer. <i>RNA Biology</i> , 2013, 10, 1312-1323.	1.5	53
84	The miR-17/92 cluster: a comprehensive update on its genomics, genetics, functions and increasingly important and numerous roles in health and disease. <i>Cell Death and Differentiation</i> , 2013, 20, 1603-1614.	5.0	722
85	Abstract 628: A novel chemoresistance mechanism: HuR post-transcriptionally regulates WEE1, the mitotic inhibitor, upon DNA damage in pancreatic adenocarcinoma cells. , 2013, , .		0
86	Towards a Reference Human Platelet Transcriptome: Evaluation Of Inter-Individual Correlations and Its Relationship With a Platelet Proteome. <i>Blood</i> , 2013, 122, 2297-2297.	0.6	0
87	HuR's post-transcriptional regulation of death receptor 5 in pancreatic cancer cells. <i>Cancer Biology and Therapy</i> , 2012, 13, 946-955.	1.5	36
88	Interactive exploration of RNA22 microRNA target predictions. <i>Bioinformatics</i> , 2012, 28, 3322-3323.	1.8	193
89	microRNAs in colon cancer: A roadmap for discovery. <i>FEBS Letters</i> , 2012, 586, 3000-3007.	1.3	30
90	Molecular dynamics simulations of Ago silencing complexes reveal a large repertoire of admissible seed-less targets. <i>Scientific Reports</i> , 2012, 2, 569.	1.6	62

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91	Beyond mRNAs and Mirnas: Unraveling the Full-Spectrum of the Normal Human Platelet Transcriptome Through Next-Generation Sequencing. <i>Blood</i> , 2012, 120, 3298-3298.	0.6	3
92	Abstract A18: HuR, an RNA binding protein, is critical for the DNA damage response in pancreatic cancer cells.. , 2012, , .		0
93	The Complex Transcriptional Landscape of the Human Platelet. <i>Blood</i> , 2012, 120, 390-390.	0.6	1
94	Coding-Independent Regulation of the Tumor Suppressor PTEN by Competing Endogenous mRNAs. <i>Cell</i> , 2011, 147, 344-357.	13.5	926
95	OMiR: Identification of associations between OMIM diseases and microRNAs. <i>Genomics</i> , 2011, 97, 71-76.	1.3	14
96	Evaluation of Methods for De Novo Genome Assembly from High-Throughput Sequencing Reads Reveals Dependencies That Affect the Quality of the Results. <i>PLoS ONE</i> , 2011, 6, e24182.	1.1	29
97	The Evi1, microRNA-143, K-Ras axis in colon cancer. <i>FEBS Letters</i> , 2011, 585, 693-699.	1.3	27
98	Inhibition of the Single Downstream Target BAG1 Activates the Latent Apoptotic Potential of MYC. <i>Molecular and Cellular Biology</i> , 2011, 31, 5037-5045.	1.1	18
99	Short RNAs: How Big Is This Iceberg?. <i>Current Biology</i> , 2010, 20, R110-R113.	1.8	8
100	Decoy for microRNAs. <i>Nature</i> , 2010, 465, 1016-1017.	13.7	44
101	Atypical transcription of microRNA gene fragments. <i>Nucleic Acids Research</i> , 2010, 38, 2775-2787.	6.5	12
102	MicroRNA Target Prediction. <i>Molecular Medicine and Medicinal</i> , 2010, , 237-263.	0.4	4
103	Dynamic changes in the human methylome during differentiation. <i>Genome Research</i> , 2010, 20, 320-331.	2.4	930
104	High-Throughput Sequencing of the Human Platelet Transcriptome. <i>Blood</i> , 2010, 116, 481-481.	0.6	2
105	Anchoring millions of distinct reads on the human genome within seconds. , 2010, , .		1
106	New Tricks for Animal MicroRNAs: Targeting of Amino Acid Coding Regions at Conserved and Nonconserved Sites. <i>Cancer Research</i> , 2009, 69, 3245-3248.	0.4	207
107	Alu and B1 Repeats Have Been Selectively Retained in the Upstream and Intronic Regions of Genes of Specific Functional Classes. <i>PLoS Computational Biology</i> , 2009, 5, e1000610.	1.5	74
108	MicroRNA 125a and its regulation of the p53 tumor suppressor gene. <i>FEBS Letters</i> , 2009, 583, 3725-3730.	1.3	87

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109	Insights into the Regulation of a Common Variant of HMGA2 Associated with Human Height During Embryonic Development. <i>Stem Cell Reviews and Reports</i> , 2009, 5, 328-333.	5.6	15
110	Arginine methylation of Piwi proteins catalysed by dPRMT5 is required for Ago3 and Aub stability. <i>Nature Cell Biology</i> , 2009, 11, 652-658.	4.6	219
111	miR-34a contributes to megakaryocytic differentiation of K562 cells independently of p53. <i>Blood</i> , 2009, 114, 2181-2192.	0.6	142
112	MicroRNA-134 Modulates the Differentiation of Mouse Embryonic Stem Cells, Where It Causes Post-Transcriptional Attenuation of Nanog and LRH1. <i>Stem Cells</i> , 2008, 26, 17-29.	1.4	213
113	MicroRNAs to Nanog, Oct4 and Sox2 coding regions modulate embryonic stem cell differentiation. <i>Nature</i> , 2008, 455, 1124-1128.	13.7	1,288
114	High-resolution metagenomics targets specific functional types in complex microbial communities. <i>Nature Biotechnology</i> , 2008, 26, 1029-1034.	9.4	254
115	BLOSUM62 miscalculations improve search performance. <i>Nature Biotechnology</i> , 2008, 26, 274-275.	9.4	79
116	Human and mouse introns are linked to the same processes and functions through each genome's most frequent non-conserved motifs. <i>Nucleic Acids Research</i> , 2008, 36, 3484-3493.	6.5	30
117	The amphioxus genome illuminates vertebrate origins and cephalochordate biology. <i>Genome Research</i> , 2008, 18, 1100-1111.	2.4	456
118	The Expression of MicroRNA miR-107 Decreases Early in Alzheimer's Disease and May Accelerate Disease Progression through Regulation of β -Site Amyloid Precursor Protein-Cleaving Enzyme 1. <i>Journal of Neuroscience</i> , 2008, 28, 1213-1223.	1.7	745
119	What's in the mix: phylogenetic classification of metagenome sequence samples. <i>Current Opinion in Microbiology</i> , 2007, 10, 499-503.	2.3	100
120	Use of simulated data sets to evaluate the fidelity of metagenomic processing methods. <i>Nature Methods</i> , 2007, 4, 495-500.	9.0	322
121	Accurate phylogenetic classification of variable-length DNA fragments. <i>Nature Methods</i> , 2007, 4, 63-72.	9.0	524
122	Metagenomic and functional analysis of hindgut microbiota of a wood-feeding higher termite. <i>Nature</i> , 2007, 450, 560-565.	13.7	1,181
123	A Pattern-Based Method for the Identification of MicroRNA Binding Sites and Their Corresponding Heteroduplexes. <i>Cell</i> , 2006, 126, 1203-1217.	13.5	1,827
124	Metagenomic analysis of two enhanced biological phosphorus removal (EBPR) sludge communities. <i>Nature Biotechnology</i> , 2006, 24, 1263-1269.	9.4	634
125	A linguistic model for the rational design of antimicrobial peptides. <i>Nature</i> , 2006, 443, 867-869.	13.7	214
126	Data mining and clinical data repositories: Insights from a 667,000 patient data set. <i>Computers in Biology and Medicine</i> , 2006, 36, 1351-1377.	3.9	150

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127	A generic motif discovery algorithm for sequential data. <i>Bioinformatics</i> , 2006, 22, 21-28.	1.8	66
128	Short blocks from the noncoding parts of the human genome have instances within nearly all known genes and relate to biological processes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 6605-6610.	3.3	111
129	Evolution of distinct EGF domains with specific functions. <i>Protein Science</i> , 2005, 14, 1091-1103.	3.1	155
130	Sensitive detection of sequence similarity using combinatorial pattern discovery: A challenging study of two distantly related protein families. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 926-937.	1.5	7
131	A sensitive, support-vector-machine method for the detection of horizontal gene transfers in viral, archaeal and bacterial genomes. <i>Nucleic Acids Research</i> , 2005, 33, 3699-3707.	6.5	59
132	A new computational method for the detection of horizontal gene transfer events. <i>Nucleic Acids Research</i> , 2005, 33, 922-933.	6.5	82
133	Metabolic and transcriptional patterns accompanying glutamine depletion and repletion in mouse hepatoma cells: a model for physiological regulatory networks. <i>Physiological Genomics</i> , 2004, 16, 247-255.	1.0	23
134	Transcriptional organization of the <i>Clostridium acetobutylicum</i> genome. <i>Nucleic Acids Research</i> , 2004, 32, 1973-1981.	6.5	53
135	The web server of IBM's Bioinformatics and Pattern Discovery group: 2004 update. <i>Nucleic Acids Research</i> , 2004, 32, W10-W15.	6.5	2
136	Report on BIODDD04. SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining, 2004, 6, 153-154.	3.2	0
137	Genomic analysis of immunity in a Urochordate and the emergence of the vertebrate immune system: awaiting for Godot. <i>Immunogenetics</i> , 2003, 55, 570-581.	1.2	278
138	Global secondary structure packing angle bias in proteins. <i>Proteins: Structure, Function and Bioinformatics</i> , 2003, 53, 252-261.	1.5	8
139	Structural details (kinks and non- α conformations) in transmembrane helices are intrahelically determined and can be predicted by sequence pattern descriptors. <i>Nucleic Acids Research</i> , 2003, 31, 4625-4631.	6.5	26
140	The web server of IBM's Bioinformatics and Pattern Discovery group. <i>Nucleic Acids Research</i> , 2003, 31, 3645-3650.	6.5	4
141	In Silico Pattern-Based Analysis of the Human Cytomegalovirus Genome. <i>Journal of Virology</i> , 2003, 77, 4326-4344.	1.5	54
142	Reevaluation of human cytomegalovirus coding potential. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13585-13590.	3.3	171
143	Evaluation of annotation strategies using an entire genome sequence. <i>Bioinformatics</i> , 2003, 19, 717-726.	1.8	65
144	Dictionary-driven prokaryotic gene finding. <i>Nucleic Acids Research</i> , 2002, 30, 2710-2725.	6.5	31

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145	Finding patterns in three-dimensional graphs: algorithms and applications to scientific data mining. IEEE Transactions on Knowledge and Data Engineering, 2002, 14, 731-749.	4.0	30
146	Dictionary-driven protein annotation. Nucleic Acids Research, 2002, 30, 3901-3916.	6.5	24
147	The Draft Genome of <i>Ciona intestinalis</i> : Insights into Chordate and Vertebrate Origins. Science, 2002, 298, 2157-2167.	6.0	1,539
148	Non- α -helical elements modulate polytopic membrane protein architecture ¹¹ Edited by G. Von Heijne. Journal of Molecular Biology, 2001, 306, 349-362.	2.0	105
149	In silico structural and functional analysis of the human cytomegalovirus (HHV5) genome 1 Edited by F. Cohen. Journal of Molecular Biology, 2001, 310, 1151-1166.	2.0	41
150	DELPHI: A pattern-based method for detecting sequence similarity. IBM Journal of Research and Development, 2001, 45, 455-473.	3.2	11
151	The Emergence of Pattern Discovery Techniques in Computational Biology. Metabolic Engineering, 2000, 2, 159-177.	3.6	71
152	Knowledge discovery in biological domains (tutorial AM-3). , 2000, , .		1
153	Sequence homology detection through large scale pattern discovery. , 1999, , .		7
154	An Approximation Algorithm for Alignment of Multiple Sequences using Motif Discovery. Journal of Combinatorial Optimization, 1999, 3, 247-275.	0.8	16
155	Dictionary building via unsupervised hierarchical motif discovery in the sequence space of natural proteins. , 1999, 37, 264-277.		45
156	Building dictionaries of 1D and 3D motifs by mining the Unaligned 1D sequences of 17 archaeal and bacterial genomes. Proceedings, 1999, , 223-33.	0.3	5
157	Managing statistical behavior of large data sets in shared-nothing architectures. IEEE Transactions on Parallel and Distributed Systems, 1998, 9, 1073-1087.	4.0	1
158	Motif discovery without alignment or enumeration (extended abstract). , 1998, , .		20
159	Combinatorial pattern discovery in biological sequences: The TEIRESIAS algorithm [published erratum appears in Bioinformatics 1998;14(2):229]. Bioinformatics, 1998, 14, 55-67.	1.8	451
160	Geometric hashing: an overview. IEEE Computational Science and Engineering, 1997, 4, 10-21.	0.6	413
161	A Bayesian Approach to Model Matching with Geometric Hashing. Computer Vision and Image Understanding, 1995, 62, 11-26.	3.0	52
162	Searching in parallel for similar strings [biological sequences]. IEEE Computational Science and Engineering, 1994, 1, 60-75.	0.6	13

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163	Visuo-Tactual Coarseness Estimation Tasks: Experiments and Modeling. , 1992, , 257-270.		0
164	An algorithm for point clustering and grid generation. IEEE Transactions on Systems, Man, and Cybernetics, 1991, 21, 1278-1286.	0.9	241
165	Implementation of geometric hashing on the Connection Machine. , 0, , .		14
166	Well-behaved, tunable 3D-affine invariants. , 0, , .		2
167	Comments on: "A comprehensive repertoire of tRNA-derived fragments in prostate cancer", , 0, , .		1