

S Cenk Sahinalp

List of Publications by Year in descending order

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134
papers

18,972
citations

46918

47
h-index

18075

120
g-index

157
all docs

157
docs citations

157
times ranked

34939
citing authors

#	ARTICLE	IF	CITATIONS
1	CYP2C8, CYP2C9, and CYP2C19 Characterization Using Next-Generation Sequencing and Haplotype Analysis. <i>Journal of Molecular Diagnostics</i> , 2022, 24, 337-350.	1.2	23
2	Analytical Validation of a Computational Method for Pharmacogenetic Genotyping from Clinical Whole Exome Sequencing. <i>Journal of Molecular Diagnostics</i> , 2022, 24, 576-585.	1.2	7
3	Characterizing genetic intra-tumor heterogeneity across 2,658 human cancer genomes. <i>Cell</i> , 2021, 184, 2239-2254.e39.	13.5	260
4	Privacy-preserving genotype imputation in a trusted execution environment. <i>Cell Systems</i> , 2021, 12, 983-993.e7.	2.9	13
5	Identification of conserved evolutionary trajectories in tumors. <i>Bioinformatics</i> , 2020, 36, i427-i435.	1.8	9
6	PhISCS-BnB: a fast branch and bound algorithm for the perfect tumor phylogeny reconstruction problem. <i>Bioinformatics</i> , 2020, 36, i169-i176.	1.8	19
7	Tumor Phylogeny Topology Inference via Deep Learning. <i>IScience</i> , 2020, 23, 101655.	1.9	11
8	Sketching algorithms for genomic data analysis and querying in a secure enclave. <i>Nature Methods</i> , 2020, 17, 295-301.	9.0	35
9	Graph Traversal Edit Distance and Extensions. <i>Journal of Computational Biology</i> , 2020, 27, 317-329.	0.8	4
10	The evolutionary history of 2,658 cancers. <i>Nature</i> , 2020, 578, 122-128.	13.7	690
11	Clonal Evolution and Heterogeneity of Osimertinib Acquired Resistance Mechanisms in EGFR Mutant Lung Cancer. <i>Cell Reports Medicine</i> , 2020, 1, 100007.	3.3	78
12	lordFAST: sensitive and Fast Alignment Search Tool for LOng noisy Read sequencing Data. <i>Bioinformatics</i> , 2019, 35, 20-27.	1.8	23
13	PhISCS: a combinatorial approach for subperfect tumor phylogeny reconstruction via integrative use of single-cell and bulk sequencing data. <i>Genome Research</i> , 2019, 29, 1860-1877.	2.4	73
14	A multi-labeled tree dissimilarity measure for comparing "clonal trees" of tumor progression. <i>Algorithms for Molecular Biology</i> , 2019, 14, 17.	0.3	25
15	Integrative inference of subclonal tumour evolution from single-cell and bulk sequencing data. <i>Nature Communications</i> , 2019, 10, 2750.	5.8	101
16	The Proteogenomic Landscape of Curable Prostate Cancer. <i>Cancer Cell</i> , 2019, 35, 414-427.e6.	7.7	168
17	Combinatorial Detection of Conserved Alteration Patterns for Identifying Cancer Subnetworks. <i>GigaScience</i> , 2019, 8, .	3.3	9
18	Widespread and Functional RNA Circularization in Localized Prostate Cancer. <i>Cell</i> , 2019, 176, 831-843.e22.	13.5	317

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19	BAP1 haploinsufficiency predicts a distinct immunogenic class of malignant peritoneal mesothelioma. <i>Genome Medicine</i> , 2019, 11, 8.	3.6	88
20	Structural variation and fusion detection using targeted sequencing data from circulating cell free DNA. <i>Nucleic Acids Research</i> , 2019, 47, e38-e38.	6.5	17
21	SubGraph2Vec: Highly-Vectorized Tree-like Subgraph Counting. , 2019, , .		3
22	Genomic Data Compression. , 2019, , 783-783.		1
23	Protecting Genomic Data Privacy with Probabilistic Modeling. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2019, 24, 403-414.	0.7	1
24	GTED: Graph Traversal Edit Distance. <i>Lecture Notes in Computer Science</i> , 2018, , 37-53.	1.0	1
25	MechRNA: prediction of lncRNA mechanisms from RNA-RNA and RNA-protein interactions. <i>Bioinformatics</i> , 2018, 34, 3101-3110.	1.8	48
26	Optimal compressed representation of high throughput sequence data via light assembly. <i>Nature Communications</i> , 2018, 9, 566.	5.8	14
27	Computational identification of micro-structural variations and their proteogenomic consequences in cancer. <i>Bioinformatics</i> , 2018, 34, 1672-1681.	1.8	8
28	Allelic decomposition and exact genotyping of highly polymorphic and structurally variant genes. <i>Nature Communications</i> , 2018, 9, 828.	5.8	67
29	Ultra High-Dimensional Nonlinear Feature Selection for Big Biological Data. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2018, 30, 1352-1365.	4.0	48
30	Stromal Gene Expression is Predictive for Metastatic Primary Prostate Cancer. <i>European Urology</i> , 2018, 73, 524-532.	0.9	60
31	Analysis of the androgen receptor-regulated lncRNA landscape identifies a role for ARLNC1 in prostate cancer progression. <i>Nature Genetics</i> , 2018, 50, 814-824.	9.4	196
32	The long noncoding RNA landscape of neuroendocrine prostate cancer and its clinical implications. <i>GigaScience</i> , 2018, 7, .	3.3	54
33	Preface: Selected Articles from RECOMB 2017. <i>Journal of Computational Biology</i> , 2018, 25, 623-623.	0.8	0
34	Protecting Genomic Data Privacy with Probabilistic Modeling. , 2018, , .		5
35	SRRM4 Drives Neuroendocrine Transdifferentiation of Prostate Adenocarcinoma Under Androgen Receptor Pathway Inhibition. <i>European Urology</i> , 2017, 71, 68-78.	0.9	136
36	Genomic hallmarks of localized, non-indolent prostate cancer. <i>Nature</i> , 2017, 541, 359-364.	13.7	462

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37	PRINCESS: Privacy-protecting Rare disease International Network Collaboration via Encryption through Software guard extensionS. <i>Bioinformatics</i> , 2017, 33, 871-878.	1.8	75
38	Clonality Inference from Single Tumor Samples Using Low-Coverage Sequence Data. <i>Journal of Computational Biology</i> , 2017, 24, 515-523.	0.8	20
39	Mutational Analysis of Gene Fusions Predicts Novel MHC Class Iâ€“Restricted T-Cell Epitopes and Immune Signatures in a Subset of Prostate Cancer. <i>Clinical Cancer Research</i> , 2017, 23, 7596-7607.	3.2	14
40	HIT'nDRIVE: patient-specific multidriver gene prioritization for precision oncology. <i>Genome Research</i> , 2017, 27, 1573-1588.	2.4	78
41	SiNVICT: ultra-sensitive detection of single nucleotide variants and indels in circulating tumour DNA. <i>Bioinformatics</i> , 2017, 33, 26-34.	1.8	48
42	PRESAGE: PRivacy-preserving gEnetic testing via SoftwAre Guard Extension. <i>BMC Medical Genomics</i> , 2017, 10, 48.	0.7	32
43	ReMixT: clone-specific genomic structure estimation in cancer. <i>Genome Biology</i> , 2017, 18, 140.	3.8	29
44	Abstract 378: The Cancer Genome Collaboratory. <i>Cancer Research</i> , 2017, 77, 378-378.	0.4	1
45	Edit Distance Under Block Operations. , 2016, , 611-614.		0
46	Enabling Privacy-Preserving GWASs in Heterogeneous Human Populations. <i>Cell Systems</i> , 2016, 3, 54-61.	2.9	62
47	CoLoRMap: Correcting Long Reads by Mapping short reads. <i>Bioinformatics</i> , 2016, 32, i545-i551.	1.8	49
48	Comparison of high-throughput sequencing data compression tools. <i>Nature Methods</i> , 2016, 13, 1005-1008.	9.0	91
49	Spatial genomic heterogeneity within localized, multifocal prostate cancer. <i>Nature Genetics</i> , 2015, 47, 736-745.	9.4	395
50	Cypiripi: exact genotyping of <i>CYP2D6</i> using high-throughput sequencing data. <i>Bioinformatics</i> , 2015, 31, i27-i34.	1.8	37
51	Robustness of Massively Parallel Sequencing Platforms. <i>PLoS ONE</i> , 2015, 10, e0138259.	1.1	3
52	mrsFAST-Ultra: a compact, SNP-aware mapper for high performance sequencing applications. <i>Nucleic Acids Research</i> , 2014, 42, W494-W500.	6.5	54
53	ORMAN: Optimal resolution of ambiguous RNA-Seq multimappings in the presence of novel isoforms. <i>Bioinformatics</i> , 2014, 30, 644-651.	1.8	17
54	Whole genome sequencing of Turkish genomes reveals functional private alleles and impact of genetic interactions with Europe, Asia and Africa. <i>BMC Genomics</i> , 2014, 15, 963.	1.2	46

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55	DeeZ: reference-based compression by local assembly. <i>Nature Methods</i> , 2014, 11, 1082-1084.	9.0	45
56	HITâ€™nDRIVE: Multi-driver Gene Prioritization Based on Hitting Time. <i>Lecture Notes in Computer Science</i> , 2014, , 293-306.	1.0	35
57	Barnacle: detecting and characterizing tandem duplications and fusions in transcriptome assemblies. <i>BMC Genomics</i> , 2013, 14, 550.	1.2	12
58	Abstract B129: Clinical implications of inter- and intra- prostatic heterogeneity.. , 2013, , .		0
59	nFuse: Discovery of complex genomic rearrangements in cancer using high-throughput sequencing. <i>Genome Research</i> , 2012, 22, 2250-2261.	2.4	67
60	SCALCE: boosting sequence compression algorithms using locally consistent encoding. <i>Bioinformatics</i> , 2012, 28, 3051-3057.	1.8	129
61	Mirroring co-evolving trees in the light of their topologies. <i>Bioinformatics</i> , 2012, 28, 1202-1208.	1.8	4
62	Dissect: detection and characterization of novel structural alterations in transcribed sequences. <i>Bioinformatics</i> , 2012, 28, i179-i187.	1.8	13
63	Polyâ€™gene fusion transcripts and chromothripsis in prostate cancer. <i>Genes Chromosomes and Cancer</i> , 2012, 51, 1144-1153.	1.5	46
64	Integrated genome and transcriptome sequencing identifies a novel form of hybrid and aggressive prostate cancer. <i>Journal of Pathology</i> , 2012, 227, 53-61.	2.1	63
65	From sequence to molecular pathology, and a mechanism driving the neuroendocrine phenotype in prostate cancer. <i>Journal of Pathology</i> , 2012, 227, 286-297.	2.1	161
66	CLIQ: Accurate Comparative Detection and Quantification of Expressed Isoforms in a Population. <i>Lecture Notes in Computer Science</i> , 2012, , 178-189.	1.0	32
67	Proteome Network Emulating Models. , 2012, , 69-95.		0
68	Mapping the Protein Interaction Network in Methicillin-Resistant <i>Staphylococcus aureus</i>. <i>Journal of Proteome Research</i> , 2011, 10, 1139-1150.	1.8	55
69	Demographic history and rare allele sharing among human populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 11983-11988.	3.3	589
70	Comrad: detection of expressed rearrangements by integrated analysis of RNA-Seq and low coverage genome sequence data. <i>Bioinformatics</i> , 2011, 27, 1481-1488.	1.8	39
71	<i>Alu</i> repeat discovery and characterization within human genomes. <i>Genome Research</i> , 2011, 21, 840-849.	2.4	94
72	Optimally discriminative subnetwork markers predict response to chemotherapy. <i>Bioinformatics</i> , 2011, 27, i205-i213.	1.8	81

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73	deFuse: An Algorithm for Gene Fusion Discovery in Tumor RNA-Seq Data. PLoS Computational Biology, 2011, 7, e1001138.	1.5	477
74	Simultaneous structural variation discovery among multiple paired-end sequenced genomes. Genome Research, 2011, 21, 2203-2212.	2.4	60
75	Sensitive and fast mapping of di-base encoded reads. Bioinformatics, 2011, 27, 1915-1921.	1.8	16
76	Simultaneous Structural Variation Discovery in Multiple Paired-End Sequenced Genomes. Lecture Notes in Computer Science, 2011, , 104-105.	1.0	4
77	Applicability Domains for Classification Problems: Benchmarking of Distance to Models for Ames Mutagenicity Set. Journal of Chemical Information and Modeling, 2010, 50, 2094-2111.	2.5	202
78	Fast prediction of RNA-RNA interaction. Algorithms for Molecular Biology, 2010, 5, 5.	0.3	44
79	A map of human genome variation from population-scale sequencing. Nature, 2010, 467, 1061-1073.	13.7	7,209
80	mrsFAST: a cache-oblivious algorithm for short-read mapping. Nature Methods, 2010, 7, 576-577.	9.0	248
81	Detection and characterization of novel sequence insertions using paired-end next-generation sequencing. Bioinformatics, 2010, 26, 1277-1283.	1.8	98
82	Sparsification of RNA structure prediction including pseudoknots. Algorithms for Molecular Biology, 2010, 5, 39.	0.3	17
83	Towards Improved Assessment of Functional Similarity in Large-Scale Screens: A Study on Indel Length. Journal of Computational Biology, 2010, 17, 1-20.	0.8	15
84	Protein-Protein Interaction Network Evaluation for Identifying Potential Drug Targets. Journal of Computational Biology, 2010, 17, 669-684.	0.8	30
85	Next-generation VariationHunter: combinatorial algorithms for transposon insertion discovery. Bioinformatics, 2010, 26, i350-i357.	1.8	190
86	Periodicity testing with sublinear samples and space. ACM Transactions on Algorithms, 2010, 6, 1-14.	0.9	3
87	PSORTb 3.0: improved protein subcellular localization prediction with refined localization subcategories and predictive capabilities for all prokaryotes. Bioinformatics, 2010, 26, 1608-1615.	1.8	2,044
88	Time and Space Efficient RNA-RNA Interaction Prediction via Sparse Folding. Lecture Notes in Computer Science, 2010, , 473-490.	1.0	18
89	Sparsification of RNA Structure Prediction Including Pseudoknots. Lecture Notes in Computer Science, 2010, , 40-51.	1.0	3
90	Pair HMM Based Gap Statistics for Re-evaluation of Indels in Alignments with Affine Gap Penalties. Lecture Notes in Computer Science, 2010, , 350-361.	1.0	0

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91	A partition function algorithm for interacting nucleic acid strands. <i>Bioinformatics</i> , 2009, 25, i365-i373.	1.8	85
92	Personalized copy number and segmental duplication maps using next-generation sequencing. <i>Nature Genetics</i> , 2009, 41, 1061-1067.	9.4	656
93	Combinatorial algorithms for structural variation detection in high-throughput sequenced genomes. <i>Genome Research</i> , 2009, 19, 1270-1278.	2.4	266
94	The Effect of Insertions and Deletions on Wirings in Protein-Protein Interaction Networks: A Large-Scale Study. <i>Journal of Computational Biology</i> , 2009, 16, 159-167.	0.8	25
95	Fast Prediction of RNA-RNA Interaction. <i>Lecture Notes in Computer Science</i> , 2009, , 261-272.	1.0	6
96	biRNA: Fast RNA-RNA Binding Sites Prediction. <i>Lecture Notes in Computer Science</i> , 2009, , 25-36.	1.0	26
97	smyRNA: A Novel Ab Initio ncRNA Gene Finder. <i>PLoS ONE</i> , 2009, 4, e5433.	1.1	13
98	Combinatorial Algorithms for Structural Variation Detection in High Throughput Sequenced Genomes. <i>Lecture Notes in Computer Science</i> , 2009, , 218-219.	1.0	3
99	Quantifying Systemic Evolutionary Changes by Color Coding Confidence-Scored PPI Networks. <i>Lecture Notes in Computer Science</i> , 2009, , 37-48.	1.0	4
100	COMPUTATIONAL STUDIES OF NON-CODING RNAs – Session Introduction. , 2009, , 54-56.		0
101	PERSONAL GENOMICS – Session Introduction. , 2009, , 302-304.		0
102	Biomolecular network motif counting and discovery by color coding. <i>Bioinformatics</i> , 2008, 24, i241-i249.	1.8	155
103	Comparative analysis of the small RNA transcriptomes of <i>Pinus contorta</i> and <i>Oryza sativa</i> . <i>Genome Research</i> , 2008, 18, 571-584.	2.4	305
104	Conifers have a unique small RNA silencing signature. <i>Rna</i> , 2008, 14, 1508-1515.	1.6	108
105	Optimal pooling for genome re-sequencing with ultra-high-throughput short-read technologies. <i>Bioinformatics</i> , 2008, 24, i32-i40.	1.8	16
106	Edit Distance Under Block Operations. , 2008, , 265-267.		2
107	The Relation between Indel Length and Functional Divergence: A Formal Study. <i>Lecture Notes in Computer Science</i> , 2008, , 330-341.	1.0	1
108	Not All Scale-Free Networks Are Born Equal: The Role of the Seed Graph in PPI Network Evolution. <i>PLoS Computational Biology</i> , 2007, 3, e118.	1.5	77

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109	Organization and Evolution of Primate Centromeric DNA from Whole-Genome Shotgun Sequence Data. PLoS Computational Biology, 2007, 3, e181.	1.5	80
110	taveRNA: a web suite for RNA algorithms and applications. Nucleic Acids Research, 2007, 35, W325-W329.	6.5	14
111	Optimal spaced seeds for faster approximate string matching. Journal of Computer and System Sciences, 2007, 73, 1035-1044.	0.9	17
112	Novel approaches for small biomolecule classification and structural similarity search. SIGKDD Explorations: Newsletter of the Special Interest Group (SIG) on Knowledge Discovery & Data Mining, 2007, 9, 14-21.	3.2	7
113	Comparative QSAR- and Fragments Distribution Analysis of Drugs, Druglikes, Metabolic Substances, and Antimicrobial Compounds. Journal of Chemical Information and Modeling, 2006, 46, 2167-2182.	2.5	50
114	Distance based algorithms for small biomolecule classification and structural similarity search. Bioinformatics, 2006, 22, e243-e251.	1.8	41
115	RNA-RNA Interaction Prediction and Antisense RNA Target Search. Journal of Computational Biology, 2006, 13, 267-282.	0.8	106
116	RNA Secondary Structure Prediction Via Energy Density Minimization. Lecture Notes in Computer Science, 2006, , 130-142.	1.0	9
117	Oblivious string embeddings and edit distance approximations. , 2006, , .		46
118	COMPARATIVE QSAR ANALYSIS OF BACTERIAL, FUNGAL PLANT AND HUMAN METABOLITES. , 2006, , .		0
119	Not All Scale Free Networks Are Born Equal: The Role of the Seed Graph in PPI Network Emulation. Lecture Notes in Computer Science, 2006, , 1-13.	1.0	0
120	Locally Consistent Parsing and Applications to Approximate String Comparisons. Lecture Notes in Computer Science, 2005, , 22-35.	1.0	2
121	Manipulating multiple sequence alignments via MaM and WebMaM. Nucleic Acids Research, 2005, 33, W295-W298.	6.5	5
122	Improved Duplication Models for Proteome Network Evolution. , 2005, , 119-137.		7
123	IDENTIFYING UNIFORMLY MUTATED SEGMENTS WITHIN REPEATS. Journal of Bioinformatics and Computational Biology, 2004, 02, 657-668.	0.3	0
124	The Role of Unequal Crossover in Alpha-Satellite DNA Evolution: A Computational Analysis. Journal of Computational Biology, 2004, 11, 933-944.	0.8	20
125	The structure and evolution of centromeric transition regions within the human genome. Nature, 2004, 430, 857-864.	13.7	179
126	Sublinear Methods for Detecting Periodic Trends in Data Streams. Lecture Notes in Computer Science, 2004, , 16-28.	1.0	11

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127	Hardness of String Similarity Search and Other Indexing Problems. Lecture Notes in Computer Science, 2004, , 1080-1098.	1.0	4
128	Analysis of Primate Genomic Variation Reveals a Repeat-Driven Expansion of the Human Genome. Genome Research, 2003, 13, 358-368.	2.4	127
129	Simple and Practical Sequence Nearest Neighbors with Block Operations. Lecture Notes in Computer Science, 2002, , 262-278.	1.0	9
130	The Complexity of Gene Placement. Journal of Algorithms, 2001, 41, 225-243.	0.9	3
131	Divergent Origins and Concerted Expansion of Two Segmental Duplications on Chromosome 16. Journal of Heredity, 2001, 92, 462-468.	1.0	25
132	Permutation Editing and Matching via Embeddings. Lecture Notes in Computer Science, 2001, , 481-492.	1.0	14
133	Approximate nearest neighbors and sequence comparison with block operations. , 2000, , .		58
134	On a parallel-algorithms method for string matching problems (overview). Lecture Notes in Computer Science, 1994, , 22-32.	1.0	6