Yaron Orenstein

List of Publications by Year
in descending order

38 papers	1,238 citations	623734 14 h-index	434195 31 g-index
47 all docs	47 docs citations	47 times ranked	1668 citing authors

#	ARTICLE	IF	CITATIONS
1	G4detector: Convolutional Neural Network to Predict DNA G-Quadruplexes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1946-1955.	3.0	10
2	Computational modeling of mRNA degradation dynamics using deep neural networks. Bioinformatics, 2022, 38, 1087-1101.	4.1	3
3	A systematic evaluation of data processing and problem formulation of CRISPR off-target site prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	6
4	Overcoming the design, build, test bottleneck for synthesis of nonrepetitive protein-RNA cassettes. Nature Communications, 2021, 12, 1576.	12.8	8
5	A comparative analysis of RNA-binding proteins binding models learned from RNAcompete, RNA Bind-n-Seq and eCLIP data. Briefings in Bioinformatics, 2021, 22, .	6.5	0
6	Improving the efficiency of de Bruijn graph construction using compact universal hitting sets. , 2021, , .		4
7	MultiRBP. , 2021, , .		3
8	Improved Analysis of High-Throughput Sequencing Data Using Small Universal k-Mer Hitting Sets. Methods in Molecular Biology, 2021, 2243, 95-105.	0.9	0
9	Identifying Regulatory Elements via Deep Learning. Annual Review of Biomedical Data Science, 2020, 3, 315-338.	6.5	14
10	Quantitative Analysis of Differential Expression of HOX Genes in Multiple Cancers. Cancers, 2020, 12, 1572.	3.7	4
11	DeCoDe: degenerate codon design for complete protein-coding DNA libraries. Bioinformatics, 2020, 36, 3357-3364.	4.1	8
12	Custom DNA Microarrays Reveal Diverse Binding Preferences of Proteins and Small Molecules to Thousands of G-Quadruplexes. ACS Chemical Biology, 2020, 15, 925-935.	3.4	39
13	A Randomized Parallel Algorithm for Efficiently Finding Near-Optimal Universal Hitting Sets. Lecture Notes in Computer Science, 2020, , 37-53.	1.3	16
14	DeepSELEX: inferring DNA-binding preferences from HT-SELEX data using multi-class CNNs. Bioinformatics, 2020, 36, i634-i642.	4.1	15
15	Reverse de Bruijn: Utilizing Reverse Peptide Synthesis to Cover All Amino Acid k-mers. Journal of Computational Biology, 2020, 27, 376-385.	1.6	0
16	Finding RNA structure in the unstructured RBPome. BMC Genomics, 2018, 19, 154.	2.8	7
17	Comprehensive, high-resolution binding energy landscapes reveal context dependencies of transcription factor binding. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E3702-E3711.	7.1	69
18	Joker de Bruijn: Covering k-Mers Using Joker Characters. Journal of Computational Biology, 2018, 25, 1171-1178.	1.6	0

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19	A deep neural network approach for learning intrinsic protein-RNA binding preferences. Bioinformatics, 2018, 34, i638-i646.	4.1	68
20	Modeling protein–DNA binding via high-throughput *in vitro* technologies. Briefings in Functional Genomics, 2017, 16, elw030.	2.7	14
21	Transcription factor family-specific <scp>DNA</scp> shape readout revealed by quantitative specificity models. Molecular Systems Biology, 2017, 13, 910.	7.2	105
22	Optimized Sequence Library Design for Efficient In Vitro Interaction Mapping. Cell Systems, 2017, 5, 230-236.e5.	6.2	0
23	Improving the performance of minimizers and winnowing schemes. Bioinformatics, 2017, 33, i110-i117.	4.1	62
24	Designing small universal k-mer hitting sets for improved analysis of high-throughput sequencing. PLoS Computational Biology, 2017, 13, e1005777.	3.2	42
25	Efficient Design of Compact Unstructured RNA Libraries Covering All *k*-mers. Journal of Computational Biology, 2016, 23, 67-79.	1.6	5
26	Compact Universal k-mer Hitting Sets. Lecture Notes in Computer Science, 2016, , 257-268.	1.3	24
27	SELMAP - SELEX affinity landscape MAPping of transcription factor binding sites using integrated microfluidics. Scientific Reports, 2016, 6, 33351.	3.3	17
28	RCK: accurate and efficient inference of sequence- and structure-based protein–RNA binding models from RNAcompete data. Bioinformatics, 2016, 32, i351-i359.	4.1	67
29	Integrated microfluidic approach for quantitative high-throughput measurements of transcription factor binding affinities. Nucleic Acids Research, 2016, 44, e51-e51.	14.5	18
30	ElemeNT: a computational tool for detecting core promoter elements. Transcription, 2015, 6, 41-50.	3.1	66
31	Efficient Design of Compact Unstructured RNA Libraries Covering All k-mers. Lecture Notes in Computer Science, 2015, , 308-325.	1.3	0
32	A comparative analysis of transcription factor binding models learned from PBM, HT-SELEX and ChIP data. Nucleic Acids Research, 2014, 42, e63-e63.	14.5	89
33	*Drosophila* TRF2 is a preferential core promoter regulator. Genes and Development, 2014, 28, 2163-2174.	5.9	45
34	Evaluation of methods for modeling transcription factor sequence specificity. Nature Biotechnology, 2013, 31, 126-134.	17.5	341
35	Design of shortest double-stranded DNA sequences covering all *k*-mers with applications to protein-binding microarrays and synthetic enhancers. Bioinformatics, 2013, 29, i71-i79.	4.1	13
36	RAP: Accurate and Fast Motif Finding Based on Protein-Binding Microarray Data. Journal of Computational Biology, 2013, 20, 375-382.	1.6	14

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37	Assessment of Algorithms for Inferring Positional Weight Matrix Motifs of Transcription Factor Binding Sites Using Protein Binding Microarray Data. PLoS ONE, 2012, 7, e46145.	2.5	21
38	Testing Eulerianity and connectivity in directed sparse graphs. Theoretical Computer Science, 2011, 412, 6390-6408.	0.9	6