

Yaron Orenstein

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4111362/publications.pdf>

Version: 2024-02-01

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	Evaluation of methods for modeling transcription factor sequence specificity. <i>Nature Biotechnology</i> , 2013, 31, 126-134.	17.5	341
2	Transcription factor family-specific <scp>DNA</scp> shape readout revealed by quantitative specificity models. <i>Molecular Systems Biology</i> , 2017, 13, 910.	7.2	105
3	A comparative analysis of transcription factor binding models learned from PBM, HT-SELEX and ChIP data. <i>Nucleic Acids Research</i> , 2014, 42, e63-e63.	14.5	89
4	Comprehensive, high-resolution binding energy landscapes reveal context dependencies of transcription factor binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E3702-E3711.	7.1	69
5	A deep neural network approach for learning intrinsic protein-RNA binding preferences. <i>Bioinformatics</i> , 2018, 34, i638-i646.	4.1	68
6	RCK: accurate and efficient inference of sequence- and structure-based protein-RNA binding models from RNAcomplete data. <i>Bioinformatics</i> , 2016, 32, i351-i359.	4.1	67
7	ElemE: a computational tool for detecting core promoter elements. <i>Transcription</i> , 2015, 6, 41-50.	3.1	66
8	Improving the performance of minimizers and winnowing schemes. <i>Bioinformatics</i> , 2017, 33, i110-i117.	4.1	62
9	<i>Drosophila</i> TRF2 is a preferential core promoter regulator. <i>Genes and Development</i> , 2014, 28, 2163-2174.	5.9	45
10	Designing small universal k-mer hitting sets for improved analysis of high-throughput sequencing. <i>PLoS Computational Biology</i> , 2017, 13, e1005777.	3.2	42
11	Custom DNA Microarrays Reveal Diverse Binding Preferences of Proteins and Small Molecules to Thousands of G-Quadruplexes. <i>ACS Chemical Biology</i> , 2020, 15, 925-935.	3.4	39
12	Compact Universal k-mer Hitting Sets. <i>Lecture Notes in Computer Science</i> , 2016, , 257-268.	1.3	24
13	Assessment of Algorithms for Inferring Positional Weight Matrix Motifs of Transcription Factor Binding Sites Using Protein Binding Microarray Data. <i>PLoS ONE</i> , 2012, 7, e46145.	2.5	21
14	Integrated microfluidic approach for quantitative high-throughput measurements of transcription factor binding affinities. <i>Nucleic Acids Research</i> , 2016, 44, e51-e51.	14.5	18
15	SELMAP - SELEX affinity landscape MAPPING of transcription factor binding sites using integrated microfluidics. <i>Scientific Reports</i> , 2016, 6, 33351.	3.3	17
16	A Randomized Parallel Algorithm for Efficiently Finding Near-Optimal Universal Hitting Sets. <i>Lecture Notes in Computer Science</i> , 2020, , 37-53.	1.3	16
17	DeepSELEX: inferring DNA-binding preferences from HT-SELEX data using multi-class CNNs. <i>Bioinformatics</i> , 2020, 36, i634-i642.	4.1	15
18	RAP: Accurate and Fast Motif Finding Based on Protein-Binding Microarray Data. <i>Journal of Computational Biology</i> , 2013, 20, 375-382.	1.6	14

#	ARTICLE	IF	CITATIONS
19	Modeling protein-DNA binding via high-throughput <i>in vitro</i> technologies. Briefings in Functional Genomics, 2017, 16, elw030.	2.7	14
20	Identifying Regulatory Elements via Deep Learning. Annual Review of Biomedical Data Science, 2020, 3, 315-338.	6.5	14
21	Design of shortest double-stranded DNA sequences covering all <i>k</i> -mers with applications to protein-binding microarrays and synthetic enhancers. Bioinformatics, 2013, 29, i71-i79.	4.1	13
22	G4detector: Convolutional Neural Network to Predict DNA G-Quadruplexes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 1946-1955.	3.0	10
23	DeCoDe: degenerate codon design for complete protein-coding DNA libraries. Bioinformatics, 2020, 36, 3357-3364.	4.1	8
24	Overcoming the design, build, test bottleneck for synthesis of nonrepetitive protein-RNA cassettes. Nature Communications, 2021, 12, 1576.	12.8	8
25	Finding RNA structure in the unstructured RBPome. BMC Genomics, 2018, 19, 154.	2.8	7
26	Testing Eulerianity and connectivity in directed sparse graphs. Theoretical Computer Science, 2011, 412, 6390-6408.	0.9	6
27	A systematic evaluation of data processing and problem formulation of CRISPR off-target site prediction. Briefings in Bioinformatics, 2022, 23, .	6.5	6
28	Efficient Design of Compact Unstructured RNA Libraries Covering All <i>k</i> -mers. Journal of Computational Biology, 2016, 23, 67-79.	1.6	5
29	Quantitative Analysis of Differential Expression of HOX Genes in Multiple Cancers. Cancers, 2020, 12, 1572.	3.7	4
30	Improving the efficiency of de Bruijn graph construction using compact universal hitting sets. , 2021, , .		4
31	MultiRBP. , 2021, , .		3
32	Computational modeling of mRNA degradation dynamics using deep neural networks. Bioinformatics, 2022, 38, 1087-1101.	4.1	3
33	Optimized Sequence Library Design for Efficient <i>In Vitro</i> Interaction Mapping. Cell Systems, 2017, 5, 230-236.e5.	6.2	0
34	Joker de Bruijn: Covering <i>k</i> -Mers Using Joker Characters. Journal of Computational Biology, 2018, 25, 1171-1178.	1.6	0
35	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
36	Improved Analysis of High-Throughput Sequencing Data Using Small Universal <i>k</i> -Mer Hitting Sets. Methods in Molecular Biology, 2021, 2243, 95-105.	0.9	0

#	ARTICLE	IF	CITATIONS
37	Efficient Design of Compact Unstructured RNA Libraries Covering All k-mers. Lecture Notes in Computer Science, 2015, , 308-325.	1.3	0
38	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