

Raluca Gordãen

List of Publications by Year in descending order

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Version: 2024-02-01

43
papers

3,552
citations

279487

23
h-index

276539

41
g-index

52
all docs

52
docs citations

52
times ranked

5769
citing authors

#	ARTICLE	IF	CITATIONS
1	Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. <i>Cancer Discovery</i> , 2017, 7, 1116-1135.	7.7	637
2	Absence of a simple code: how transcription factors read the genome. <i>Trends in Biochemical Sciences</i> , 2014, 39, 381-399.	3.7	447
3	Genomic Regions Flanking E-Box Binding Sites Influence DNA Binding Specificity of bHLH Transcription Factors through DNA Shape. <i>Cell Reports</i> , 2013, 3, 1093-1104.	2.9	280
4	<i>Drosophila</i> ORC localizes to open chromatin and marks sites of cohesin complex loading. <i>Genome Research</i> , 2010, 20, 201-211.	2.4	248
5	Quantitative modeling of transcription factor binding specificities using DNA shape. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 4654-4659.	3.3	218
6	Human-Chimpanzee Differences in a FZD8 Enhancer Alter Cell-Cycle Dynamics in the Developing Neocortex. <i>Current Biology</i> , 2015, 25, 772-779.	1.8	214
7	Protein-DNA binding: complexities and multi-protein codes. <i>Nucleic Acids Research</i> , 2014, 42, 2099-2111.	6.5	186
8	Distinguishing direct versus indirect transcription factor-DNA interactions. <i>Genome Research</i> , 2009, 19, 2090-2100.	2.4	128
9	Survey of variation in human transcription factors reveals prevalent DNA binding changes. <i>Science</i> , 2016, 351, 1450-1454.	6.0	114
10	TFBSshape: a motif database for DNA shape features of transcription factor binding sites. <i>Nucleic Acids Research</i> , 2014, 42, D148-D155.	6.5	111
11	Curated collection of yeast transcription factor DNA binding specificity data reveals novel structural and gene regulatory insights. <i>Genome Biology</i> , 2011, 12, R125.	13.9	103
12	Protein-DNA binding in the absence of specific base-pair recognition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17140-17145.	3.3	96
13	A Nucleosome-Guided Map of Transcription Factor Binding Sites in Yeast. <i>PLoS Computational Biology</i> , 2007, 3, e215.	1.5	85
14	DNA mismatches reveal conformational penalties in protein-DNA recognition. <i>Nature</i> , 2020, 587, 291-296.	13.7	74
15	Inkjet-printed point-of-care immunoassay on a nanoscale polymer brush enables subpicomolar detection of analytes in blood. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E7054-E7062.	3.3	70
16	Establishment of Expression in the SHORTROOT-SCARECROW Transcriptional Cascade through Opposing Activities of Both Activators and Repressors. <i>Developmental Cell</i> , 2016, 39, 585-596.	3.1	54
17	Stability selection for regression-based models of transcription factor-DNA binding specificity. <i>Bioinformatics</i> , 2013, 29, i117-i125.	1.8	53
18	Punctuated evolution and transitional hybrid network in an ancestral cell cycle of fungi. <i>ELife</i> , 2016, 5, .	2.8	52

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19	Expression level is a key determinant of E2F1-mediated cell fate. <i>Cell Death and Differentiation</i> , 2017, 24, 626-637.	5.0	42
20	Finding regulatory DNA motifs using alignment-free evolutionary conservation information. <i>Nucleic Acids Research</i> , 2010, 38, e90-e90.	6.5	38
21	Divergence in DNA Specificity among Paralogous Transcription Factors Contributes to Their Differential In Vivo Binding. <i>Cell Systems</i> , 2018, 6, 470-483.e8.	2.9	38
22	Unexpected implications of STAT3 acetylation revealed by genetic encoding of acetyl-lysine. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 1343-1350.	1.1	33
23	Incomplete MyoD-induced transdifferentiation is associated with chromatin remodeling deficiencies. <i>Nucleic Acids Research</i> , 2017, 45, 11684-11699.	6.5	27
24	QBIC-Pred: quantitative predictions of transcription factor binding changes due to sequence variants. <i>Nucleic Acids Research</i> , 2019, 47, W127-W135.	6.5	26
25	Nonconsensus Protein Binding to Repetitive DNA Sequence Elements Significantly Affects Eukaryotic Genomes. <i>PLoS Computational Biology</i> , 2015, 11, e1004429.	1.5	22
26	HDAC inhibitors cause site-specific chromatin remodeling at PU.1-bound enhancers in K562 cells. <i>Epigenetics and Chromatin</i> , 2016, 9, 15.	1.8	20
27	Identification of Tat-SF1 cellular targets by exon array analysis reveals dual roles in transcription and splicing. <i>Rna</i> , 2011, 17, 665-674.	1.6	16
28	Quantifying the Impact of Non-coding Variants on Transcription Factor-DNA Binding. <i>Lecture Notes in Computer Science</i> , 2017, 10229, 336-352.	1.0	16
29	Competition for DNA binding between paralogous transcription factors determines their genomic occupancy and regulatory functions. <i>Genome Research</i> , 2021, 31, 1216-1229.	2.4	14
30	The vitamin D receptor gene as a determinant of survival in pancreatic cancer patients: Genomic analysis and experimental validation. <i>PLoS ONE</i> , 2018, 13, e0202272.	1.1	13
31	Genetic variation determines VEGF-A plasma levels in cancer patients. <i>Scientific Reports</i> , 2018, 8, 16332.	1.6	10
32	Sex dependent glial-specific changes in the chromatin accessibility landscape in late-onset Alzheimer's disease brains. <i>Molecular Neurodegeneration</i> , 2021, 16, 58.	4.4	10
33	USING DNA DUPLEX STABILITY INFORMATION FOR TRANSCRIPTION FACTOR BINDING SITE DISCOVERY. , 2007, , .		9
34	Toward deciphering the mechanistic role of variations in the Rep1 repeat site in the transcription regulation of SNCA gene. <i>Neurogenetics</i> , 2018, 19, 135-144.	0.7	7
35	Using DNA duplex stability information for transcription factor binding site discovery. <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2008, , 453-64.	0.7	6
36	MESH1 knockdown triggers proliferation arrest through TAZ repression. <i>Cell Death and Disease</i> , 2022, 13, 221.	2.7	6

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37	DNA Sequence Context Controls the Binding and Processivity of the T7 DNA Primase. IScience, 2018, 2, 141-147.	1.9	5
38	DNA Sequence Recognition by DNA Primase Using High-Throughput Primase Profiling. Journal of Visualized Experiments, 2019, , .	0.2	2
39	Mutational processes in cancer preferentially affect binding of particular transcription factors. Scientific Reports, 2021, 11, 3339.	1.6	2
40	Identification of cell cycle-regulated, putative hyphal genes in Candida albicans. Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing, 2012, , 299-310.	0.7	1
41	COUGERâ€™co-factors associated with uniquely-bound genomic regions. Nucleic Acids Research, 2014, 42, W461-W467.	6.5	0
42	A nucleosome-guided map of transcription factor binding sites in yeast. PLoS Computational Biology, 2005, preprint, e215.	1.5	0
43	The role of local transcription and chromatin structure in establishing DNA replication origins. FASEB Journal, 2009, 23, 78.2.	0.2	0