

# Raluca Gordãen

## List of Publications by Year in descending order

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Version: 2024-02-01

43  
papers

3,552  
citations

279798

23  
h-index

276875

41  
g-index

52  
all docs

52  
docs citations

52  
times ranked

5769  
citing authors

#	ARTICLE	IF	CITATIONS
1	MESH1 knockdown triggers proliferation arrest through TAZ repression. <i>Cell Death and Disease</i> , 2022, 13, 221.	6.3	6
2	Mutational processes in cancer preferentially affect binding of particular transcription factors. <i>Scientific Reports</i> , 2021, 11, 3339.	3.3	2
3	Competition for DNA binding between paralogous transcription factors determines their genomic occupancy and regulatory functions. <i>Genome Research</i> , 2021, 31, 1216-1229.	5.5	14
4	Sex dependent glial-specific changes in the chromatin accessibility landscape in late-onset Alzheimer's disease brains. <i>Molecular Neurodegeneration</i> , 2021, 16, 58.	10.8	10
5	DNA mismatches reveal conformational penalties in protein-DNA recognition. <i>Nature</i> , 2020, 587, 291-296.	27.8	74
6	Unexpected implications of STAT3 acetylation revealed by genetic encoding of acetyl-lysine. <i>Biochimica Et Biophysica Acta - General Subjects</i> , 2019, 1863, 1343-1350.	2.4	33
7	QBiC-Pred: quantitative predictions of transcription factor binding changes due to sequence variants. <i>Nucleic Acids Research</i> , 2019, 47, W127-W135.	14.5	26
8	DNA Sequence Recognition by DNA Primase Using High-Throughput Primase Profiling. <i>Journal of Visualized Experiments</i> , 2019, , .	0.3	2
9	Divergence in DNA Specificity among Paralogous Transcription Factors Contributes to Their Differential In Vivo Binding. <i>Cell Systems</i> , 2018, 6, 470-483.e8.	6.2	38
10	Genetic variation determines VEGF-A plasma levels in cancer patients. <i>Scientific Reports</i> , 2018, 8, 16332.	3.3	10
11	DNA Sequence Context Controls the Binding and Processivity of the T7 DNA Primase. <i>IScience</i> , 2018, 2, 141-147.	4.1	5
12	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.	1.4	7
13	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.	2.5	13
14	Expression level is a key determinant of E2F1-mediated cell fate. <i>Cell Death and Differentiation</i> , 2017, 24, 626-637.	11.2	42
15	Quantifying the Impact of Non-coding Variants on Transcription Factor-DNA Binding. <i>Lecture Notes in Computer Science</i> , 2017, 10229, 336-352.	1.3	16
16	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.	7.1	70
17	Whole-Genome and Epigenomic Landscapes of Etiologically Distinct Subtypes of Cholangiocarcinoma. <i>Cancer Discovery</i> , 2017, 7, 1116-1135.	9.4	637
18	Incomplete MyoD-induced transdifferentiation is associated with chromatin remodeling deficiencies. <i>Nucleic Acids Research</i> , 2017, 45, 11684-11699.	14.5	27

#	ARTICLE	IF	CITATIONS
19	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.	7.0	54
20	HDAC inhibitors cause site-specific chromatin remodeling at PU.1-bound enhancers in K562 cells. <i>Epigenetics and Chromatin</i> , 2016, 9, 15.	3.9	20
21	Survey of variation in human transcription factors reveals prevalent DNA binding changes. <i>Science</i> , 2016, 351, 1450-1454.	12.6	114
22	Punctuated evolution and transitional hybrid network in an ancestral cell cycle of fungi. <i>ELife</i> , 2016, 5, .	6.0	52
23	Human-Chimpanzee Differences in a FZD8 Enhancer Alter Cell-Cycle Dynamics in the Developing Neocortex. <i>Current Biology</i> , 2015, 25, 772-779.	3.9	214
24	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.	7.1	218
25	Nonconsensus Protein Binding to Repetitive DNA Sequence Elements Significantly Affects Eukaryotic Genomes. <i>PLoS Computational Biology</i> , 2015, 11, e1004429.	3.2	22
26	Protein-DNA binding: complexities and multi-protein codes. <i>Nucleic Acids Research</i> , 2014, 42, 2099-2111.	14.5	186
27	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.	7.1	96
28	TFBSshape: a motif database for DNA shape features of transcription factor binding sites. <i>Nucleic Acids Research</i> , 2014, 42, D148-D155.	14.5	111
29	COUGER-co-factors associated with uniquely-bound genomic regions. <i>Nucleic Acids Research</i> , 2014, 42, W461-W467.	14.5	0
30	Absence of a simple code: how transcription factors read the genome. <i>Trends in Biochemical Sciences</i> , 2014, 39, 381-399.	7.5	447
31	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.	6.4	280
32	Stability selection for regression-based models of transcription factor-DNA binding specificity. <i>Bioinformatics</i> , 2013, 29, i117-i125.	4.1	53
33	Identification of cell cycle-regulated, putative hyphal genes in <i>Candida albicans</i> . <i>Pacific Symposium on Biocomputing Pacific Symposium on Biocomputing</i> , 2012, , 299-310.	0.7	1
34	Curated collection of yeast transcription factor DNA binding specificity data reveals novel structural and gene regulatory insights. <i>Genome Biology</i> , 2011, 12, R125.	9.6	103
35	Identification of Tat-SF1 cellular targets by exon array analysis reveals dual roles in transcription and splicing. <i>Rna</i> , 2011, 17, 665-674.	3.5	16
36	Finding regulatory DNA motifs using alignment-free evolutionary conservation information. <i>Nucleic Acids Research</i> , 2010, 38, e90-e90.	14.5	38

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37	<i>Drosophila</i> ORC localizes to open chromatin and marks sites of cohesin complex loading. <i>Genome Research</i> , 2010, 20, 201-211.	5.5	248
38	Distinguishing direct versus indirect transcription factor-DNA interactions. <i>Genome Research</i> , 2009, 19, 2090-2100.	5.5	128
39	The role of local transcription and chromatin structure in establishing DNA replication origins. <i>FASEB Journal</i> , 2009, 23, 78.2.	0.5	0
40	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
41	A Nucleosome-Guided Map of Transcription Factor Binding Sites in Yeast. <i>PLoS Computational Biology</i> , 2007, 3, e215.	3.2	85
42	USING DNA DUPLEX STABILITY INFORMATION FOR TRANSCRIPTION FACTOR BINDING SITE DISCOVERY. , 2007, , .		9
43	A nucleosome-guided map of transcription factor binding sites in yeast. <i>PLoS Computational Biology</i> , 2005, preprint, e215.	3.2	0