

# Marko Djordjevic

## List of Publications by Year in descending order

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Version: 2024-02-01

64  
papers

1,534  
citations

361045

20  
h-index

329751

37  
g-index

67  
all docs

67  
docs citations

67  
times ranked

2284  
citing authors

#	ARTICLE	IF	CITATIONS
1	Transcription, processing and function of CRISPR cassettes in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2010, 77, 1367-1379.	1.2	203
2	A Biophysical Approach to Transcription Factor Binding Site Discovery. <i>Genome Research</i> , 2003, 13, 2381-2390.	2.4	179
3	SELEX experiments: New prospects, applications and data analysis in inferring regulatory pathways. <i>New Biotechnology</i> , 2007, 24, 179-189.	2.7	120
4	Specificity and robustness in transcription control networks. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2072-2077.	3.3	76
5	LHC jet suppression of light and heavy flavor observables. <i>Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics</i> , 2014, 734, 286-289.	1.5	69
6	Predictions of heavy-flavor suppression at 5.1 TeV Pb-Pb collisions at the CERN Large Hadron Collider. <i>Physical Review C</i> , 2015, 92, .	1.1	55
7	Generalization of radiative jet energy loss to non-zero magnetic mass. <i>Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics</i> , 2012, 709, 229-233.	1.5	51
8	RHIC and LHC jet suppression in non-central collisions. <i>Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics</i> , 2014, 737, 298-302.	1.5	51
9	Transcription regulation of the type II restriction-modification system AhdI. <i>Nucleic Acids Research</i> , 2008, 36, 1429-1442.	6.5	48
10	DREENA-B framework: First predictions of R and $v_2$ within dynamical energy loss formalism in evolving QCD medium. <i>Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics</i> , 2019, 791, 236-241.	1.5	45
11	Redefining <i>Escherichia coli</i> $\sigma^{70}$ Promoter Elements: $\sigma^{15}$ Motif as a Complement of the $\sigma^{10}$ Motif. <i>Journal of Bacteriology</i> , 2011, 193, 6305-6314.	1.0	37
12	Quantitative modeling and data analysis of SELEX experiments. <i>Physical Biology</i> , 2006, 3, 13-28.	0.8	35
13	Temporal Regulation of Viral Transcription during Development of <i>Thermus thermophilus</i> Bacteriophage $\phi$ YS40. <i>Journal of Molecular Biology</i> , 2007, 366, 420-435.	2.0	32
14	The tale of two RNA polymerases: transcription profiling and gene expression strategy of bacteriophage Xp10. <i>Molecular Microbiology</i> , 2004, 55, 764-777.	1.2	29
15	Temporal dynamics of methyltransferase and restriction endonuclease accumulation in individual cells after introducing a restriction-modification system. <i>Nucleic Acids Research</i> , 2016, 44, 790-800.	6.5	28
16	Endogenous Gene Regulation as a Predicted Main Function of Type I-E CRISPR/Cas System in <i>E. coli</i> . <i>Molecules</i> , 2019, 24, 784.	1.7	26
17	Formation of the Open Complex by Bacterial RNA Polymerase: A Quantitative Model. <i>Biophysical Journal</i> , 2008, 94, 4233-4248.	0.2	25
18	PM2.5 as a major predictor of COVID-19 basic reproduction number in the USA. <i>Environmental Research</i> , 2021, 201, 111526.	3.7	24

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19	Effects of Demographic and Weather Parameters on COVID-19 Basic Reproduction Number. <i>Frontiers in Ecology and Evolution</i> , 2021, 8, .	1.1	23
20	CRISPR transcript processing: a mechanism for generating a large number of small interfering RNAs. <i>Biology Direct</i> , 2012, 7, 24.	1.9	22
21	Temporal Regulation of Gene Expression of the Escherichia coli Bacteriophage phiEco32. <i>Journal of Molecular Biology</i> , 2012, 416, 389-399.	2.0	21
22	Heavy flavor puzzle from data measured at the BNL Relativistic Heavy Ion Collider: Analysis of the underlying effects. <i>Physical Review C</i> , 2014, 90, .	1.1	20
23	DREENA-C framework: joint R AA and $v_2$ predictions and implications to QGP tomography. <i>Journal of Physics C: Nuclear and Particle Physics</i> , 2019, 46, 085101.	1.4	19
24	Calculating hard probe radiative energy loss beyond the soft-gluon approximation: Examining the approximation validity. <i>Physical Review C</i> , 2019, 99, .	1.1	18
25	Ribosome-controlled transcription termination is essential for the production of antibiotic microcin C. <i>Nucleic Acids Research</i> , 2014, 42, 11891-11902.	6.5	17
26	Exploring the initial stages in heavy-ion collisions with high- $p_T$ particles: theory and data. <i>Physical Review C</i> , 2020, 101, .	1.1	17
27	Inferring bacteriophage infection strategies from genome sequence: analysis of bacteriophage 7-11 and related phages. <i>BMC Evolutionary Biology</i> , 2015, 15, S1.	3.2	16
28	Understanding key features of bacterial restriction-modification systems through quantitative modeling. <i>BMC Systems Biology</i> , 2017, 11, 1-15.	3.0	16
29	Bioinformatics as a first-line approach for understanding bacteriophage transcription. <i>Bacteriophage</i> , 2015, 5, e1062588.	1.9	14
30	How to test path-length dependence in energy-loss mechanisms: Analysis leading to a new observable. <i>Physical Review C</i> , 2019, 99, .	1.1	13
31	Inferring the Main Drivers of SARS-CoV-2 Global Transmissibility by Feature Selection Methods. <i>GeoHealth</i> , 2021, 5, e2021GH000432.	1.9	13
32	Efficient transcription initiation in bacteria: an interplay of protein-DNA interaction parameters. <i>Integrative Biology (United Kingdom)</i> , 2013, 5, 796-806.	0.6	12
33	Promoter Recognition by Extracytoplasmic Function $\sigma$ Factors: Analyzing DNA and Protein Interaction Motifs. <i>Journal of Bacteriology</i> , 2016, 198, 1927-1938.	1.0	11
34	Avoidance of Trinucleotide Corresponding to Consensus Protospacer Adjacent Motif Controls the Efficiency of Prespacer Selection during Primed Adaptation. <i>MBio</i> , 2018, 9, .	1.8	11
35	Quantitative analysis of a virulent bacteriophage transcription strategy. <i>Virology</i> , 2006, 354, 240-251.	1.1	10
36	Controller protein of restriction-modification system Kpn2I affects transcription of its gene by acting as a transcription elongation roadblock. <i>Nucleic Acids Research</i> , 2018, 46, 10810-10826.	6.5	10

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37	From biophysics to omics and systems biology. <i>European Biophysics Journal</i> , 2019, 48, 413-424.	1.2	10
38	Understanding Infection Progression under Strong Control Measures through Universal COVID-19 Growth Signatures. <i>Global Challenges</i> , 2021, 5, 2000101.	1.8	10
39	Mix-and-matching as a promoter recognition mechanism by ECF $\sigma$ factors. <i>BMC Evolutionary Biology</i> , 2017, 17, 12.	3.2	9
40	Extracting the temperature dependence in high- $p$ particle energy loss. <i>Physical Review C</i> , 2021, 103, .		
41	COVID-19 severity determinants inferred through ecological and epidemiological modeling. <i>One Health</i> , 2021, 13, 100355.	1.5	9
42	In silico Analysis Suggests Common Appearance of scaRNAs in Type II Systems and Their Association With Bacterial Virulence. <i>Frontiers in Genetics</i> , 2018, 9, 474.	1.1	8
43	A Simple Criterion for Inferring CRISPR Array Direction. <i>Frontiers in Microbiology</i> , 2019, 10, 2054.	1.5	8
44	A systems biology approach to COVID-19 progression in population. <i>Advances in Protein Chemistry and Structural Biology</i> , 2021, 127, 291-314.	1.0	8
45	Early evolution constrained by high- $p$ quark-gluon plasma tomography. <i>Physical Review C</i> , 2022, 105, .		
46	Features of CRISPR-Cas Regulation Key to Highly Efficient and Temporally-Specific crRNA Production. <i>Frontiers in Microbiology</i> , 2017, 8, 2139.	1.5	5
47	Shape of the quark gluon plasma droplet reflected in the high- $p$ data. <i>Physical Review C</i> , 2019, 100, .		
48	Inferring Protein-DNA Interaction Parameters from SELEX Experiments. <i>Methods in Molecular Biology</i> , 2010, 674, 195-211.	0.4	4
49	Explaining the fine hierarchy in pion and kaon suppression at LHC: importance of fragmentation functions. <i>Journal of Physics C: Nuclear and Particle Physics</i> , 2014, 41, 055104.	1.4	4
50	Contribution of bacterial promoter elements to transcription start site detection accuracy. <i>Journal of Bioinformatics and Computational Biology</i> , 2017, 15, 1650038.	0.3	4
51	Modeling bacterial immune systems: Strategies for expression of toxic but useful molecules. <i>BioSystems</i> , 2013, 112, 139-144.	0.9	3
52	Dynamical energy loss formalism: from describing suppression patterns to implications for future experiments. <i>Nuclear Physics A</i> , 2019, 982, 699-702.	0.6	3
53	A simple biosynthetic pathway for large product generation from small substrate amounts. <i>Physical Biology</i> , 2012, 9, 056004.	0.8	2
54	Integrating Sequence Analysis with Biophysical Modelling for Accurate Transcription Start Site Prediction. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 58-67.	1.0	2

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55	Comparative Analysis of Diverse Acetyltransferase-Type Toxin-Antitoxin Loci in <i>Klebsiella pneumoniae</i> . <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	2
56	Scoring Targets of Transcription in Bacteria Rather than Focusing on Individual Binding Sites. <i>Frontiers in Microbiology</i> , 2017, 8, 2314.	1.5	1
57	Systems Biology of Bacterial Immune Systems: Regulation of Restriction-Modification and CRISPR-Cas Systems. <i>RNA Technologies</i> , 2018, , 37-58.	0.2	1
58	Effects of Population Dynamics on Establishment of a Restriction-Modification System in a Bacterial Host. <i>Molecules</i> , 2019, 24, 198.	1.7	1
59	Integrating sequence analysis with biophysical modelling for accurate transcription start site prediction. <i>Journal of Integrative Bioinformatics</i> , 2014, 11, 240.	1.0	1
60	Understanding the unexpected suppression patterns at RHIC and LHC. <i>Modern Physics Letters A</i> , 2014, 29, 1430035.	0.5	0
61	Testing the Reliability of the Soft-Gluon Approximation for High $p_{\perp}$ Particles. <i>Proceedings (mdpi)</i> , 2019, 10, 13.	0.2	0
62	From high $p_{\perp}$ theory and data to inferring anisotropy of Quark-Gluon Plasma. <i>Nuclear Physics A</i> , 2021, 1005, 121900.	0.6	0
63	CRISPR Transcript Processing: An Unusual Mechanism for Rapid Production of Desired Molecules. <i>Lecture Notes in Computer Science</i> , 2012, , 31-34.	1.0	0
64	Utilizing high- $p_{\perp}$ theory and data to constrain the initial stages of quark-gluon plasma. <i>International Journal of Modern Physics E</i> , 2021, 30, .	0.4	0