Marko Djordjevic

List of Publications by Year
in descending order

| 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	Early evolution constrained by high-$p_\perp$ quark-gluon plasma tomography. Physical Review C, 2022, 105, .	1.1	0
2	Comparative Analysis of Diverse Acetyltransferase-Type Toxin-Antitoxin Loci in Klebsiella pneumoniae. Microbiology Spectrum, 2022, 10, .	1.2	2
3	From high $p_\perp$ theory and data to inferring anisotropy of Quark-Gluon Plasma. Nuclear Physics A, 2021, 1005, 121900.	0.6	0
4	A systems biology approach to COVID-19 progression in population. Advances in Protein Chemistry and Structural Biology, 2021, 127, 291-314.	1.0	8
5	Effects of Demographic and Weather Parameters on COVID-19 Basic Reproduction Number. Frontiers in Ecology and Evolution, 2021, 8, .	1.1	23
6	Extracting the temperature dependence in high-$p_\perp$ particle energy loss. Physical Review C, 2021, 103, .	1.1	3
7	Understanding Infection Progression under Strong Control Measures through Universal COVID-19 Growth Signatures. Global Challenges, 2021, 5, 2000101.	1.8	10
8	Inferring the Main Drivers of SARS-CoV-2 Global Transmissibility by Feature Selection Methods. GeoHealth, 2021, 5, e2021GH000432.	1.9	13
9	PM2.5 as a major predictor of COVID-19 basic reproduction number in the USA. Environmental Research, 2021, 201, 111526.	3.7	24
10	COVID-19 severity determinants inferred through ecological and epidemiological modeling. One Health, 2021, 13, 100355.	1.5	9
11	Utilizing high-$p_\perp$ theory and data to constrain the initial stages of quark-gluon plasma. International Journal of Modern Physics E, 2021, 30, .	0.4	0
12	Exploring the initial stages in heavy-ion collisions with high-$p_\perp$ theory and data. Physical Review C, 2020, 101, .	1.1	17
13	How to test path-length dependence in energy-loss mechanisms: Analysis leading to a new observable. Physical Review C, 2019, 99, .	1.1	13
14	Shape of the quark gluon plasma droplet reflected in the high-$p_\perp$ data. Physical Review C, 2019, 100, .	1.1	19
15	DREENA-C framework: joint R AA and v 2 predictions and implications to QGP tomography. Journal of Physics G: Nuclear and Particle Physics, 2019, 46, 085101.	1.4	19
16	Dynamical energy loss formalism: from describing suppression patterns to implications for future experiments. Nuclear Physics A, 2019, 982, 699-702.	0.6	3
17	A Simple Criterion for Inferring CRISPR Array Direction. Frontiers in Microbiology, 2019, 10, 2054.	1.5	8
18	DREENA-B framework: First predictions of R and v2 within dynamical energy loss formalism in evolving QCD medium. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 2019, 791, 236-241.	1.5	45

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19	Testing the Reliability of the Soft-Gluon Approximation for High p⊥ Particles. Proceedings (mdpi), 2019, 10, 13.	0.2	0
20	Calculating hard probe radiative energy loss beyond the soft-gluon approximation: Examining the approximation validity. Physical Review C, 2019, 99, .	1.1	18
21	From biophysics to ̃omics and systems biology. European Biophysics Journal, 2019, 48, 413-424.	1.2	10
22	Effects of Population Dynamics on Establishment of a Restriction-Modification System in a Bacterial Host. Molecules, 2019, 24, 198.	1.7	1
23	Endogenous Gene Regulation as a Predicted Main Function of Type I-E CRISPR/Cas System in E. coli. Molecules, 2019, 24, 784.	1.7	26
24	Avoidance of Trinucleotide Corresponding to Consensus Protospacer Adjacent Motif Controls the Efficiency of Prespacer Selection during Primed Adaptation. MBio, 2018, 9, .	1.8	11
25	In silico Analysis Suggests Common Appearance of scaRNAs in Type II Systems and Their Association With Bacterial Virulence. Frontiers in Genetics, 2018, 9, 474.	1.1	8
26	Controller protein of restriction–modification system Kpn2I affects transcription of its gene by acting as a transcription elongation roadblock. Nucleic Acids Research, 2018, 46, 10810-10826.	6.5	10
27	Systems Biology of Bacterial Immune Systems: Regulation of Restriction-Modification and CRISPR-Cas Systems. RNA Technologies, 2018, , 37-58.	0.2	1
28	Mix-and-matching as a promoter recognition mechanism by ECF σ factors. BMC Evolutionary Biology, 2017, 17, 12.	3.2	9
29	Understanding key features of bacterial restriction-modification systems through quantitative modeling. BMC Systems Biology, 2017, 11, 1-15.	3.0	16
30	Contribution of bacterial promoter elements to transcription start site detection accuracy. Journal of Bioinformatics and Computational Biology, 2017, 15, 1650038.	0.3	4
31	Features of CRISPR-Cas Regulation Key to Highly Efficient and Temporally-Specific crRNA Production. Frontiers in Microbiology, 2017, 8, 2139.	1.5	5
32	Scoring Targets of Transcription in Bacteria Rather than Focusing on Individual Binding Sites. Frontiers in Microbiology, 2017, 8, 2314.	1.5	1
33	Promoter Recognition by Extracytoplasmic Function σ Factors: Analyzing DNA and Protein Interaction Motifs. Journal of Bacteriology, 2016, 198, 1927-1938.	1.0	11
34	Temporal dynamics of methyltransferase and restriction endonuclease accumulation in individual cells after introducing a restriction-modification system. Nucleic Acids Research, 2016, 44, 790-800.	6.5	28
35	Inferring bacteriophage infection strategies from genome sequence: analysis of bacteriophage 7-11 and related phages. BMC Evolutionary Biology, 2015, 15, S1.	3.2	16
36	Predictions of heavy-flavor suppression at 5.1 TeV Pb+Pb collisions at the CERN Large Hadron Collider. Physical Review C, 2015, 92, .	1.1	55

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37	Bioinformatics as a first-line approach for understanding bacteriophage transcription. Bacteriophage, 2015, 5, e1062588.	1.9	14
38	Understanding the unexpected suppression patterns at RHIC and LHC. Modern Physics Letters A, 2014, 29, 1430035.	0.5	0
39	Explaining the fine hierarchy in pion and kaon suppression at LHC: importance of fragmentation functions. Journal of Physics G: Nuclear and Particle Physics, 2014, 41, 055104.	1.4	4
40	RHIC and LHC jet suppression in non-central collisions. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 2014, 737, 298-302.	1.5	51
41	Heavy flavor puzzle from data measured at the BNL Relativistic Heavy Ion Collider: Analysis of the underlying effects. Physical Review C, 2014, 90, .	1.1	20
42	Ribosome-controlled transcription termination is essential for the production of antibiotic microcin C. Nucleic Acids Research, 2014, 42, 11891-11902.	6.5	17
43	LHC jet suppression of light and heavy flavor observables. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 2014, 734, 286-289.	1.5	69
44	Integrating Sequence Analysis with Biophysical Modelling for Accurate Transcription Start Site Prediction. Journal of Integrative Bioinformatics, 2014, 11, 58-67.	1.0	2
45	Integrating sequence analysis with biophysical modelling for accurate transcription start site prediction. Journal of Integrative Bioinformatics, 2014, 11, 240.	1.0	1
46	Modeling bacterial immune systems: Strategies for expression of toxic â€" but useful â€" molecules. BioSystems, 2013, 112, 139-144.	0.9	3
47	Efficient transcription initiation in bacteria: an interplay of proteinâ€"DNA interaction parameters. Integrative Biology (United Kingdom), 2013, 5, 796-806.	0.6	12
48	CRISPR transcript processing: a mechanism for generating a large number of small interfering RNAs. Biology Direct, 2012, 7, 24.	1.9	22
49	Temporal Regulation of Gene Expression of the Escherichia coli Bacteriophage phiEco32. Journal of Molecular Biology, 2012, 416, 389-399.	2.0	21
50	A simple biosynthetic pathway for large product generation from small substrate amounts. Physical Biology, 2012, 9, 056004.	0.8	2
51	Generalization of radiative jet energy loss to non-zero magnetic mass. Physics Letters, Section B: Nuclear, Elementary Particle and High-Energy Physics, 2012, 709, 229-233.	1.5	51
52	CRISPR Transcript Processing: An Unusual Mechanism for Rapid Production of Desired Molecules. Lecture Notes in Computer Science, 2012, , 31-34.	1.0	0
53	Redefining Escherichia coli $Ïƒ^{70}$ Promoter Elements: â̂'15 Motif as a Complement of the â̂'10 Motif. Journal of Bacteriology, 2011, 193, 6305-6314.	1.0	37
54	Transcription, processing and function of CRISPR cassettes in Escherichia coli. Molecular Microbiology, 2010, 77, 1367-1379.	1.2	203

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55	Inferring Protein–DNA Interaction Parameters from SELEX Experiments. Methods in Molecular Biology, 2010, 674, 195-211.	0.4	4
56	Formation of the Open Complex by Bacterial RNA Polymerase–A Quantitative Model. Biophysical Journal, 2008, 94, 4233-4248.	0.2	25
57	Transcription regulation of the type II restriction-modification system AhdI. Nucleic Acids Research, 2008, 36, 1429-1442.	6.5	48
58	Temporal Regulation of Viral Transcription during Development of Thermus thermophilus Bacteriophage Ï•YS40. Journal of Molecular Biology, 2007, 366, 420-435.	2.0	32
59	SELEX experiments: New prospects, applications and data analysis in inferring regulatory pathways. New Biotechnology, 2007, 24, 179-189.	2.7	120
60	Quantitative analysis of a virulent bacteriophage transcription strategy. Virology, 2006, 354, 240-251.	1.1	10
61	Quantitative modeling and data analysis of SELEX experiments. Physical Biology, 2006, 3, 13-28.	0.8	35
62	The tale of two RNA polymerases: transcription profiling and gene expression strategy of bacteriophage Xp10. Molecular Microbiology, 2004, 55, 764-777.	1.2	29
63	A Biophysical Approach to Transcription Factor Binding Site Discovery. Genome Research, 2003, 13, 2381-2390.	2.4	179
64	Specificity and robustness in transcription control networks. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 2072-2077.	3.3	76