

Dov J Stekel

List of Publications by Year in descending order

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Version: 2024-02-01

57
papers

2,317
citations

304743

22
h-index

254184

43
g-index

62
all docs

62
docs citations

62
times ranked

3751
citing authors

#	ARTICLE	IF	CITATIONS
1	Metal Resistance and Its Association With Antibiotic Resistance. <i>Advances in Microbial Physiology</i> , 2017, 70, 261-313.	2.4	276
2	Microbial mass movements. <i>Science</i> , 2017, 357, 1099-1100.	12.6	218
3	Hybrid assembly of an agricultural slurry virome reveals a diverse and stable community with the potential to alter the metabolism and virulence of veterinary pathogens. <i>Microbiome</i> , 2021, 9, 65.	11.1	182
4	The fatal fungal outbreak on Vancouver Island is characterized by enhanced intracellular parasitism driven by mitochondrial regulation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 12980-12985.	7.1	180
5	Molecular circuits for associative learning in single-celled organisms. <i>Journal of the Royal Society Interface</i> , 2009, 6, 463-469.	3.4	96
6	<i>AtMYB93</i> is a novel negative regulator of lateral root development in <i>Arabidopsis</i> . <i>New Phytologist</i> , 2014, 203, 1194-1207.	7.3	79
7	Comprehensive Identification of <i>Salmonella enterica</i> Serovar Typhimurium Genes Required for Infection of BALB/c Mice. <i>PLoS Pathogens</i> , 2009, 5, e1000529.	4.7	75
8	Human dissemination of genes and microorganisms in Earth's Critical Zone. <i>Global Change Biology</i> , 2018, 24, 1488-1499.	9.5	71
9	Multidrug resistant, extended spectrum β -lactamase (ESBL)-producing <i>Escherichia coli</i> isolated from a dairy farm. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw013.	2.7	69
10	A model of lymphocyte recirculation. <i>Trends in Immunology</i> , 1997, 18, 216-221.	7.5	63
11	Strong negative self regulation of Prokaryotic transcription factors increases the intrinsic noise of protein expression. <i>BMC Systems Biology</i> , 2008, 2, 6.	3.0	62
12	Wood identification of <i>Dalbergia nigra</i> (CITES Appendix I) using quantitative wood anatomy, principal components analysis and naive Bayes classification. <i>Annals of Botany</i> , 2010, 105, 45-56.	2.9	62
13	Contrasting Effects of in Vitro Fertilization and Nuclear Transfer on the Expression of mtDNA Replication Factors. <i>Genetics</i> , 2007, 176, 1511-1526.	2.9	55
14	A novel method of differential gene expression analysis using multiple cDNA libraries applied to the identification of tumour endothelial genes. <i>BMC Genomics</i> , 2008, 9, 153.	2.8	47
15	Mathematical modelling of antimicrobial resistance in agricultural waste highlights importance of gene transfer rate. <i>FEMS Microbiology Ecology</i> , 2016, 92, fiw040.	2.7	47
16	Lipidomic analysis of plasma samples from women with polycystic ovary syndrome. <i>Metabolomics</i> , 2015, 11, 657-666.	3.0	44
17	A machine learning heuristic to identify biologically relevant and minimal biomarker panels from omics data. <i>BMC Genomics</i> , 2015, 16, S2.	2.8	43
18	Investigating the Association Between the Caecal Microbiomes of Broilers and <i>Campylobacter</i> Burden. <i>Frontiers in Microbiology</i> , 2018, 9, 927.	3.5	43

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19	Is there a Liquid State Machine in the Bacterium Escherichia Coli?. , 2007, , .		31
20	Removal of copper from cattle footbath wastewater with layered double hydroxide adsorbents as a route to antimicrobial resistance mitigation on dairy farms. <i>Science of the Total Environment</i> , 2019, 655, 1139-1149.	8.0	30
21	Prediction of future BSE spread. <i>Nature</i> , 1996, 381, 119-119.	27.8	29
22	Inferring the Brassica rapa Interactome Using Proteinâ€“Protein Interaction Data from Arabidopsis thaliana. <i>Frontiers in Plant Science</i> , 2012, 3, 297.	3.6	25
23	Three-dimensional images of choanoflagellate loricae. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 3-11.	2.6	23
24	The Comparison of Gene Expression from Multiple cDNA Libraries. <i>Genome Research</i> , 2000, 10, 2055-2061.	5.5	23
25	De Novo Evolution of Complex, Global and Hierarchical Gene Regulatory Mechanisms. <i>Journal of Molecular Evolution</i> , 2010, 71, 128-140.	1.8	22
26	Towards a general model for predicting minimal metal concentrations co-selecting for antibiotic resistance plasmids. <i>Environmental Pollution</i> , 2021, 275, 116602.	7.5	22
27	Inclusion of neighboring base interdependencies substantially improves genome-wide prokaryotic transcription factor binding site prediction. <i>Nucleic Acids Research</i> , 2010, 38, e135-e135.	14.5	20
28	The dynamic balance of import and export of zinc in <i>Escherichia coli</i> suggests a heterogeneous population response to stress. <i>Journal of the Royal Society Interface</i> , 2015, 12, 20150069.	3.4	19
29	Whole-genome sequencing and gene sharing network analysis powered by machine learning identifies antibiotic resistance sharing between animals, humans and environment in livestock farming. <i>PLoS Computational Biology</i> , 2022, 18, e1010018.	3.2	19
30	Mathematical model of the Lux luminescence system in the terrestrial bacterium <i>Photobacterium luminescens</i> . <i>Molecular BioSystems</i> , 2009, 5, 68-76.	2.9	17
31	Analysis of Occludin Trafficking, Demonstrating Continuous Endocytosis, Degradation, Recycling and Biosynthetic Secretory Trafficking. <i>PLoS ONE</i> , 2014, 9, e111176.	2.5	17
32	So why have you added me? Adolescent girlsâ€™ technology-mediated attachments and relationships. <i>Computers in Human Behavior</i> , 2016, 63, 25-34.	8.5	16
33	Reconstructing promoter activity from Lux bioluminescent reporters. <i>PLoS Computational Biology</i> , 2017, 13, e1005731.	3.2	14
34	Laboratory Stock Variants of the Archetype Silver Resistance Plasmid pMG101 Demonstrate Plasmid Fusion, Loss of Transmissibility, and Transposition of Tn7/pco/sil Into the Host Chromosome. <i>Frontiers in Microbiology</i> , 2021, 12, 723322.	3.5	13
35	The Role of Inter-Cellular Adhesion in the Recirculation of T Lymphocytes. <i>Journal of Theoretical Biology</i> , 1997, 186, 491-501.	1.7	12
36	Stochasticity Versus Determinism: Consequences for Realistic Gene Regulatory Network Modelling and Evolution. <i>Journal of Molecular Evolution</i> , 2010, 70, 215-231.	1.8	12

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37	Global transcription regulation of RK2 plasmids: a case study in the combined use of dynamical mathematical models and statistical inference for integration of experimental data and hypothesis exploration. BMC Systems Biology, 2011, 5, 119.	3.0	12
38	Regulatory feedback response mechanisms to phosphate starvation in rice. Npj Systems Biology and Applications, 2018, 4, 4.	3.0	11
39	DirtyGenes: testing for significant changes in gene or bacterial population compositions from a small number of samples. Scientific Reports, 2019, 9, 2373.	3.3	11
40	EMBRACE-WATERS statement: Recommendations for reporting of studies on antimicrobial resistance in wastewater and related aquatic environments. One Health, 2021, 13, 100339.	3.4	11
41	A generalised model for generalised transduction: the importance of co-evolution and stochasticity in phage mediated antimicrobial resistance transfer. FEMS Microbiology Ecology, 2020, 96, .	2.7	10
42	THE USE OF A COMPUTER MODEL TO SIMULATE EPITHELIAL PATHOLOGIES. , 1996, 179, 333-339.		9
43	A New Model for Investigating the Evolution of Transcription Control Networks. Artificial Life, 2009, 15, 259-291.	1.3	9
44	Analysis of host response to bacterial infection using error model based gene expression microarray experiments. Nucleic Acids Research, 2005, 33, e53-e53.	14.5	8
45	A Model to Investigate the Impact of Farm Practice on Antimicrobial Resistance in UK Dairy Farms. Bulletin of Mathematical Biology, 2021, 83, 36.	1.9	6
46	Adaptation for Protein Synthesis Efficiency in a Naturally Occurring Self-Regulating Operon. PLoS ONE, 2012, 7, e49678.	2.5	5
47	Evolution of Resource and Energy Management in Biologically Realistic Gene Regulatory Network Models. Advances in Experimental Medicine and Biology, 2012, 751, 301-328.	1.6	4
48	Bioinformatic Methods for Finding Differentially Expressed Genes in cDNA Libraries, Applied to the Identification of Tumour Vascular Targets. Methods in Molecular Biology, 2011, 729, 99-119.	0.9	4
49	Antigenic diversity thresholds and hazard functions. Mathematical Biosciences, 1997, 139, 59-68.	1.9	2
50	A Bayesian approach to analyzing phenotype microarray data enables estimation of microbial growth parameters. Journal of Bioinformatics and Computational Biology, 2016, 14, 1650007.	0.8	2
51	Nonlinear Data Mining of Microarray Data Using Michaelis Menten Functions. BMC Bioinformatics, 2005, 6, S13.	2.6	1
52	DNA Traffic in the Environment and Antimicrobial Resistance. , 2019, , 245-271.		1
53	Modelling the evolution of transcriptional control networks using stochastic simulations and evolutionary computational methods. BMC Systems Biology, 2007, 1, .	3.0	0
54	<i>IN SILICO</i> BIOLOGY. , 2009, , 477-480.		0

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55	Modeling Plasmid Regulatory Systems. , 2014, , 1-6.		0
56	Computational Prediction of Domain-domain Interactions: Factor-graph Based Modelling and Inference. Current Chemical Biology, 2014, 7, 234-240.	0.5	0
57	Plasmid Regulatory Systems, Modeling. , 2018, , 956-961.		0