

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	Whole-genome sequencing and gene sharing network analysis powered by machine learning identifies antibiotic resistance sharing between animals, humans and environment in livestock farming. PLoS Computational Biology, 2022, 18, e1010018.	3.2	19
2	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
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. Microbiome, 2021, 9, 65.	11.1	182
4	Towards a general model for predicting minimal metal concentrations co-selecting for antibiotic resistance plasmids. Environmental Pollution, 2021, 275, 116602.	7.5	22
5	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. Frontiers in Microbiology, 2021, 12, 723322.	3.5	13
6	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
7	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
8	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
9	DNA Traffic in the Environment and Antimicrobial Resistance. , 2019, , 245-271.		1
10	Removal of copper from cattle footbath wastewater with layered double hydroxide adsorbents as a route to antimicrobial resistance mitigation on dairy farms. Science of the Total Environment, 2019, 655, 1139-1149.	8.0	30
11	Regulatory feedback response mechanisms to phosphate starvation in rice. Npj Systems Biology and Applications, 2018, 4, 4.	3.0	11
12	Human dissemination of genes and microorganisms in Earth's Critical Zone. Global Change Biology, 2018, 24, 1488-1499.	9.5	71
13	Investigating the Association Between the Caecal Microbiomes of Broilers and Campylobacter Burden. Frontiers in Microbiology, 2018, 9, 927.	3.5	43
14	Plasmid Regulatory Systems, Modeling. , 2018, , 956-961.		0
15	Metal Resistance and Its Association With Antibiotic Resistance. Advances in Microbial Physiology, 2017, 70, 261-313.	2.4	276
16	Microbial mass movements. Science, 2017, 357, 1099-1100.	12.6	218
17	Reconstructing promoter activity from Lux bioluminescent reporters. PLoS Computational Biology, 2017, 13, e1005731.	3.2	14
18	So why have you added me? Adolescent girlsâ€™ technology-mediated attachments and relationships. Computers in Human Behavior, 2016, 63, 25-34.	8.5	16

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19	A Bayesian approach to analyzing phenotype microarray data enables estimation of microbial growth parameters. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1650007.	0.8	2
20	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
21	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
22	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
23	Lipidomic analysis of plasma samples from women with polycystic ovary syndrome. <i>Metabolomics</i> , 2015, 11, 657-666.	3.0	44
24	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
25	<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
26	Analysis of Occludin Trafficking, Demonstrating Continuous Endocytosis, Degradation, Recycling and Biosynthetic Secretory Trafficking. <i>PLoS ONE</i> , 2014, 9, e111176.	2.5	17
27	Modeling Plasmid Regulatory Systems. , 2014, , 1-6.		0
28	Computational Prediction of Domain-domain Interactions: Factor-graph Based Modelling and Inference. <i>Current Chemical Biology</i> , 2014, 7, 234-240.	0.5	0
29	Inferring the <i>Brassica rapa</i> Interactome Using Protein-Protein Interaction Data from <i>Arabidopsis thaliana</i> . <i>Frontiers in Plant Science</i> , 2012, 3, 297.	3.6	25
30	Evolution of Resource and Energy Management in Biologically Realistic Gene Regulatory Network Models. <i>Advances in Experimental Medicine and Biology</i> , 2012, 751, 301-328.	1.6	4
31	Adaptation for Protein Synthesis Efficiency in a Naturally Occurring Self-Regulating Operon. <i>PLoS ONE</i> , 2012, 7, e49678.	2.5	5
32	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. <i>BMC Systems Biology</i> , 2011, 5, 119.	3.0	12
33	Bioinformatic Methods for Finding Differentially Expressed Genes in cDNA Libraries, Applied to the Identification of Tumour Vascular Targets. <i>Methods in Molecular Biology</i> , 2011, 729, 99-119.	0.9	4
34	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
35	De Novo Evolution of Complex, Global and Hierarchical Gene Regulatory Mechanisms. <i>Journal of Molecular Evolution</i> , 2010, 71, 128-140.	1.8	22
36	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

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37	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
38	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
39	A New Model for Investigating the Evolution of Transcription Control Networks. <i>Artificial Life</i> , 2009, 15, 259-291.	1.3	9
40	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
41	Three-dimensional images of choanoflagellate loricae. <i>Proceedings of the Royal Society B: Biological Sciences</i> , 2009, 276, 3-11.	2.6	23
42	Molecular circuits for associative learning in single-celled organisms. <i>Journal of the Royal Society Interface</i> , 2009, 6, 463-469.	3.4	96
43	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
44	<i>IN SILICO</i> BIOLOGY. , 2009, , 477-480.		0
45	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
46	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
47	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
48	Is there a Liquid State Machine in the Bacterium <i>Escherichia Coli</i> ? , 2007, , .		31
49	Modelling the evolution of transcriptional control networks using stochastic simulations and evolutionary computational methods. <i>BMC Systems Biology</i> , 2007, 1, .	3.0	0
50	Nonlinear Data Mining of Microarray Data Using Michaelis Menten Functions. <i>BMC Bioinformatics</i> , 2005, 6, S13.	2.6	1
51	Analysis of host response to bacterial infection using error model based gene expression microarray experiments. <i>Nucleic Acids Research</i> , 2005, 33, e53-e53.	14.5	8
52	The Comparison of Gene Expression from Multiple cDNA Libraries. <i>Genome Research</i> , 2000, 10, 2055-2061.	5.5	23
53	Antigenic diversity thresholds and hazard functions. <i>Mathematical Biosciences</i> , 1997, 139, 59-68.	1.9	2
54	A model of lymphocyte recirculation. <i>Trends in Immunology</i> , 1997, 18, 216-221.	7.5	63

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55	The Role of Inter-Cellular Adhesion in the Recirculation of T Lymphocytes. Journal of Theoretical Biology, 1997, 186, 491-501.	1.7	12
56	THE USE OF A COMPUTER MODEL TO SIMULATE EPITHELIAL PATHOLOGIES. , 1996, 179, 333-339.		9
57	Prediction of future BSE spread. Nature, 1996, 381, 119-119.	27.8	29