

David J Schneider

List of Publications by Year in descending order

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#	ARTICLE	IF	CITATIONS
1	Comparative analysis of transcriptomic points-of-departure (tPODs) and apical responses in embryo-larval fathead minnows exposed to fluoxetine. <i>Environmental Pollution</i> , 2022, 295, 118667.	3.7	10
2	Development of a Comprehensive Toxicity Pathway Model for 17 β -Ethinylestradiol in Early Life Stage Fathead Minnows (<i>Pimephales promelas</i>). <i>Environmental Science & Technology</i> , 2021, 55, 5024-5036.	4.6	13
3	Assessing the Toxicity of 17 β -Ethinylestradiol in Rainbow Trout Using a 4-Day Transcriptomics Benchmark Dose (BMD) Embryo Assay. <i>Environmental Science & Technology</i> , 2021, 55, 10608-10618.	4.6	14
4	Optimal transport and barycenters for dendritic measures. <i>Pure and Applied Analysis</i> , 2020, 2, 581-601.	0.4	1
5	Further experiments comparing direct vapor equilibration and cryogenic vacuum distillation for plant water stable isotope analysis. <i>Rapid Communications in Mass Spectrometry</i> , 2019, 33, 1850-1854.	0.7	6
6	Proteome Profile and Genome Refinement of the Tomato Pathogenic Bacterium <i>Clavibacter michiganensis</i> subsp. <i>michiganensis</i> . <i>Proteomics</i> , 2019, 19, 1800224.	1.3	6
7	A comparison of extraction systems for plant water stable isotope analysis. <i>Rapid Communications in Mass Spectrometry</i> , 2018, 32, 1031-1044.	0.7	75
8	The ECF sigma factor, PSPTO_1043, in <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000 is induced by oxidative stress and regulates genes involved in oxidative stress response. <i>PLoS ONE</i> , 2017, 12, e0180340.	1.1	4
9	Whole genome sequence of two <i>Rathayibacter toxicus</i> strains reveals a tunicamycin biosynthetic cluster similar to <i>Streptomyces chartreusis</i> . <i>PLoS ONE</i> , 2017, 12, e0183005.	1.1	13
10	Evolving technologies for growing, imaging and analyzing 3D root system architecture of crop plants. <i>Journal of Integrative Plant Biology</i> , 2016, 58, 230-241.	4.1	43
11	Analysis of the small RNA spf in the plant pathogen <i>Pseudomonas syringae</i> pv. <i>tomato</i> strain DC3000. <i>Microbiology (United Kingdom)</i> , 2014, 160, 941-953.	0.7	9
12	Using multitype branching processes to quantify statistics of disease outbreaks in zoonotic epidemics. <i>Physical Review E</i> , 2014, 89, 032702.	0.8	11
13	Two-strain competition in quasineutral stochastic disease dynamics. <i>Physical Review E</i> , 2014, 90, 042149.	0.8	34
14	Functional, structural and phylogenetic analysis of domains underlying the Al^{3+} sensitivity of the aluminum-activated malate/anion transporter, <i>AtALMT1</i> . <i>Plant Journal</i> , 2013, 76, 766-780.	2.8	50
15	Epidemic fronts in complex networks with metapopulation structure. <i>Physical Review E</i> , 2013, 88, 012809.	0.8	24
16	HopX1 in <i>Erwinia amylovora</i> Functions as an Avirulence Protein in Apple and Is Regulated by HrpL. <i>Journal of Bacteriology</i> , 2012, 194, 553-560.	1.0	18
17	Functional and Computational Analysis of Amino Acid Patterns Predictive of Type III Secretion System Substrates in <i>Pseudomonas syringae</i> . <i>PLoS ONE</i> , 2012, 7, e36038.	1.1	20
18	Creating a Buzz About Insect Genomes. <i>Science</i> , 2011, 331, 1386-1386.	6.0	185

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19	Saturation mutagenesis of a CepR binding site as a means to identify new quorum-regulated promoters in <i>Burkholderia cenocepacia</i> . <i>Molecular Microbiology</i> , 2011, 79, 616-632.	1.2	14
20	Parameter Estimation as a Problem in Statistical Thermodynamics. , 2011, 1305, 357-364.		0
21	Characterization of the Fur Regulon in <i>Pseudomonas syringae</i> pv. tomato DC3000. <i>Journal of Bacteriology</i> , 2011, 193, 4598-4611.	1.0	50
22	The Plant Pathogen <i>Pseudomonas syringae</i> pv. tomato Is Genetically Monomorphic and under Strong Selection to Evade Tomato Immunity. <i>PLoS Pathogens</i> , 2011, 7, e1002130.	2.1	186
23	Genome-Wide Identification of Transcriptional Start Sites in the Plant Pathogen <i>Pseudomonas syringae</i> pv. tomato str. DC3000. <i>PLoS ONE</i> , 2011, 6, e29335.	1.1	33
24	Studying Plant-Pathogen Interactions in the Genomics Era: Beyond Molecular Koch's Postulates to Systems Biology. <i>Annual Review of Phytopathology</i> , 2010, 48, 457-479.	3.5	57
25	Magnetic Resonance Spectra and Statistical Geometry. <i>Applied Magnetic Resonance</i> , 2010, 37, 865-880.	0.6	7
26	Complex responses to culture conditions in <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000 continuous cultures: The role of iron in cell growth and virulence factor induction. <i>Biotechnology and Bioengineering</i> , 2010, 105, 955-964.	1.7	6
27	Complete Genome Sequence of the Plant Pathogen <i>Erwinia amylovora</i> Strain ATCC 49946. <i>Journal of Bacteriology</i> , 2010, 192, 2020-2021.	1.0	112
28	Construction of an <i>rsmX</i> co-variance model and identification of five <i>rsmX</i> non-coding RNAs in <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000. <i>RNA Biology</i> , 2010, 7, 508-516.	1.5	54
29	Transcriptome Analysis of <i>Pseudomonas syringae</i> Identifies New Genes, Noncoding RNAs, and Antisense Activity. <i>Journal of Bacteriology</i> , 2010, 192, 2359-2372.	1.0	121
30	Effect of Iron Concentration on the Growth Rate of <i>Pseudomonas syringae</i> and the Expression of Virulence Factors in <i>hrp</i> -Inducing Minimal Medium. <i>Applied and Environmental Microbiology</i> , 2009, 75, 2720-2726.	1.4	51
31	Deletions in the Repertoire of <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000 Type III Secretion Effector Genes Reveal Functional Overlap among Effectors. <i>PLoS Pathogens</i> , 2009, 5, e1000388.	2.1	269
32	Lifestyles of the Effector Rich: Genome-Enabled Characterization of Bacterial Plant Pathogens. <i>Plant Physiology</i> , 2009, 150, 1623-1630.	2.3	28
33	The Effect of Target Vector Selection on the Invariance of Classifier Performance Measures. <i>IEEE Transactions on Neural Networks</i> , 2009, 20, 745-757.	4.8	1
34	A Draft Genome Sequence of <i>Pseudomonas syringae</i> pv. <i>tomato</i> T1 Reveals a Type III Effector Repertoire Significantly Divergent from That of <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000. <i>Molecular Plant-Microbe Interactions</i> , 2009, 22, 52-62.	1.4	134
35	Characterization of the PvdS-regulated promoter motif in <i>Pseudomonas syringae</i> pv. <i>tomato</i> DC3000 reveals regulon members and insights regarding PvdS function in other pseudomonads. <i>Molecular Microbiology</i> , 2008, 68, 871-889.	1.2	67
36	Global transcriptional responses of <i>Pseudomonas syringae</i> DC3000 to changes in iron bioavailability in vitro. <i>BMC Microbiology</i> , 2008, 8, 209.	1.3	54

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37	Elevated ozone affects the genetic composition of <i>Plantago lanceolata</i> L. populations. <i>Environmental Pollution</i> , 2008, 152, 380-386.	3.7	7
38	Roadmap to New Virulence Determinants in <i>Pseudomonas syringae</i> : Insights from Comparative Genomics and Genome Organization. <i>Molecular Plant-Microbe Interactions</i> , 2008, 21, 685-700.	1.4	109
39	Closing the Circle on the Discovery of Genes Encoding Hrp Regulon Members and Type III Secretion System Effectors in the Genomes of Three Model <i>Pseudomonas syringae</i> Strains. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1151-1158.	1.4	138
40	Whole-Genome Expression Profiling Defines the HrpL Regulon of <i>Pseudomonas syringae</i> pv. tomato DC3000, Allows de novo Reconstruction of the Hrp cis Element, and Identifies Novel Coregulated Genes. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1167-1179.	1.4	105
41	Bioinformatics-Enabled Identification of the HrpL Regulon and Type III Secretion System Effector Proteins of <i>Pseudomonas syringae</i> pv. phaseolicola 1448A. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1193-1206.	1.4	81
42	Multiple Approaches to a Complete Inventory of <i>Pseudomonas syringae</i> pv. tomato DC3000 Type III Secretion System Effector Proteins. <i>Molecular Plant-Microbe Interactions</i> , 2006, 19, 1180-1192.	1.4	119
43	Lineage-specific regions in <i>Pseudomonas syringae</i> pv. tomato DC3000. <i>Molecular Plant Pathology</i> , 2005, 6, 53-64.	2.0	14
44	Complete genome sequence of the plant commensal <i>Pseudomonas fluorescens</i> Pf-5. <i>Nature Biotechnology</i> , 2005, 23, 873-878.	9.4	615
45	Whole-Genome Sequence Analysis of <i>Pseudomonas syringae</i> pv. phaseolicola 1448A Reveals Divergence among Pathovars in Genes Involved in Virulence and Transposition. <i>Journal of Bacteriology</i> , 2005, 187, 6488-6498.	1.0	301
46	Identification of a Twin-Arginine Translocation System in <i>Pseudomonas syringae</i> pv. tomato DC3000 and Its Contribution to Pathogenicity and Fitness. <i>Journal of Bacteriology</i> , 2005, 187, 8450-8461.	1.0	68
47	The complete genome sequence of the Arabidopsis and tomato pathogen <i>Pseudomonas syringae</i> pv. tomato DC3000. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 10181-10186.	3.3	785
48	Development and Mapping of 2240 New SSR Markers for Rice (<i>Oryza sativa</i> L.) (Supplement). <i>DNA Research</i> , 2002, 9, 257-279.	1.5	121
49	Genomewide identification of <i>Pseudomonas syringae</i> pv. tomato DC3000 promoters controlled by the HrpL alternative sigma factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 2275-2280.	3.3	280
50	Genomewide identification of proteins secreted by the Hrp type III protein secretion system of <i>Pseudomonas syringae</i> pv. tomato DC3000. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 7652-7657.	3.3	266
51	Genomic mining type III secretion system effectors in <i>Pseudomonas syringae</i> yields new picks for all TTSS prospectors. <i>Trends in Microbiology</i> , 2002, 10, 462-469.	3.5	224
52	Development and Mapping of 2240 New SSR Markers for Rice (<i>Oryza sativa</i> L.). <i>DNA Research</i> , 2002, 9, 199-207.	1.5	1,203
53	Ab initio dynamics of rapid fracture. <i>Modelling and Simulation in Materials Science and Engineering</i> , 1998, 6, 639-670.	0.8	32
54	Charge Transfer Modeling for Charge-Coupled Devices. <i>Materials Research Society Symposia Proceedings</i> , 1997, 490, 251.	0.1	0

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55	Instability dynamics in three-dimensional fracture: An atomistic simulation. <i>Journal of the Mechanics and Physics of Solids</i> , 1997, 45, 1461-1471.	2.3	60
56	Molecular Dynamics of Ion~Chelate Complexes Attached to Dendrimers. <i>Journal of the American Chemical Society</i> , 1996, 118, 7774-7782.	6.6	110
57	Analysis of the early workload on the Cornell Theory Center IBM SP2. <i>Performance Evaluation Review</i> , 1996, 24, 272-273.	0.4	9
58	A theoretical approach to the analysis of arbitrary pulses in magnetic resonance. <i>Chemical Physics Letters</i> , 1996, 262, 17-26.	1.2	12
59	Theory for dynamic lineshapes of strongly correlated two-spin systems. <i>Journal of Magnetic Resonance</i> , 1989, 85, 275-293.	0.5	5
60	Rapid singular value decomposition for time-domain analysis of magnetic resonance signals by use of the lanczos algorithm. <i>Journal of Magnetic Resonance</i> , 1989, 82, 150-155.	0.5	5
61	The Perfect Club Benchmarks: Effective Performance Evaluation of Supercomputers. <i>The International Journal of Supercomputer Applications</i> , 1989, 3, 5-40.	0.6	312
62	Calculating Slow Motional Magnetic Resonance Spectra. <i>Biological Magnetic Resonance</i> , 1989, , 1-76.	0.4	179
63	Rapid determination of translational diffusion coefficients using ESR imaging. <i>Journal of Magnetic Resonance</i> , 1988, 79, 474-492.	0.5	9
64	Calculation of ESR spectra and related Fokker~Planck forms by the use of the Lanczos algorithm. II. Criteria for truncation of basis sets and recursive steps utilizing conjugate gradients. <i>Journal of Chemical Physics</i> , 1987, 86, 647-661.	1.2	46
65	Diffusion coefficients in anisotropic fluids by ESR imaging of concentration profiles. <i>Journal of Chemical Physics</i> , 1986, 84, 3387-3395.	1.2	65
66	Complexity of minor histocompatibility loci. <i>Human Immunology</i> , 1985, 14, 220-233.	1.2	4
67	Immune responses in vitro. <i>Immunogenetics</i> , 1984, 20, 301-310.	1.2	7
68	X-ray absorption spectroscopy of iron-tyrosinate proteins. <i>Journal of the American Chemical Society</i> , 1984, 106, 1676-1681.	6.6	281
69	Computational identi?cation and characterization of Type III secretion substrates. , 0, , .		1