

# Jon L Hobman

## List of Publications by Year in descending order

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72  
papers

6,040  
citations

87888

38  
h-index

106344

65  
g-index

80  
all docs

80  
docs citations

80  
times ranked

7320  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	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
3	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
4	Occurrence and distribution of antibiotics and antibiotic resistance determinants in coastal environments. , 2021, , 121-167.		0
5	Infrastructure for a PHAge REference Database: Identification of Large-Scale Biases in the Current Collection of Cultured Phage Genomes. <i>Phage</i> , 2021, 2, 214-223.	1.7	121
6	Genome Sequence and Characterization of Coliphage vB_Eco_SLUR29. <i>Phage</i> , 2020, 1, 38-44.	1.7	3
7	Antibiotic and Metal Resistance in <i>Escherichia coli</i> Isolated from Pig Slaughterhouses in the United Kingdom. <i>Antibiotics</i> , 2020, 9, 746.	3.7	15
8	A generalised model for generalised transduction: the importance of co-evolution and stochasticity in phage mediated antimicrobial resistance transfer. <i>FEMS Microbiology Ecology</i> , 2020, 96, .	2.7	10
9	Metagenomics of the Viral Community in Three Cattle Slurry Samples. <i>Microbiology Resource Announcements</i> , 2019, 8, .	0.6	2
10	DNA Traffic in the Environment and Antimicrobial Resistance. , 2019, , 245-271.		1
11	Anthropogenic environmental drivers of antimicrobial resistance in wildlife. <i>Science of the Total Environment</i> , 2019, 649, 12-20.	8.0	108
12	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
13	Comparative Genomics of Bacteriophage of the Genus Seuratvirus. <i>Genome Biology and Evolution</i> , 2018, 10, 72-76.	2.5	41
14	Transposable Elements and Plasmid Genomes. , 2018, , 1220-1223.		0
15	Bacterial resistance to arsenic protects against protist killing. <i>BioMetals</i> , 2017, 30, 307-311.	4.1	13
16	Metal Resistance and Its Association With Antibiotic Resistance. <i>Advances in Microbial Physiology</i> , 2017, 70, 261-313.	2.4	276
17	SilE is an intrinsically disordered periplasmic $\alpha$ -molecular sponge $\alpha$ -involved in bacterial silver resistance. <i>Molecular Microbiology</i> , 2016, 101, 731-742.	2.5	38
18	Draft Genome Sequence of the Bacteriophage vB_Eco_slurp01. <i>Genome Announcements</i> , 2016, 4, .	0.8	5

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19	Multidrug resistant, extended spectrum $\beta$ -lactamase (ESBL)-producing <i>Escherichia coli</i> isolated from a dairy farm. FEMS Microbiology Ecology, 2016, 92, fiw013.	2.7	69
20	Mathematical modelling of antimicrobial resistance in agricultural waste highlights importance of gene transfer rate. FEMS Microbiology Ecology, 2016, 92, fiw040.	2.7	47
21	Draft Genome Sequences of 14 <i>Escherichia coli</i> Phages Isolated from Cattle Slurry. Genome Announcements, 2015, 3, .	0.8	21
22	Survival in amoeba—a major selection pressure on the presence of bacterial copper and zinc resistance determinants? Identification of a copper pathogenicity island. Applied Microbiology and Biotechnology, 2015, 99, 5817-5824.	3.6	42
23	The dynamic balance of import and export of zinc in <i>Escherichia coli</i> suggests a heterogeneous population response to stress. Journal of the Royal Society Interface, 2015, 12, 20150069.	3.4	19
24	Bacterial antimicrobial metal ion resistance. Journal of Medical Microbiology, 2015, 64, 471-497.	1.8	294
25	Response of <i>Cupriavidus metallidurans</i> CH34 to Metals. Springer Briefs in Molecular Science, 2015, , 45-89.	0.1	5
26	Microbial Mercury Reduction. , 2014, , 175-197.		23
27	Transposable Elements and Plasmid Genomes. , 2014, , 1-4.		0
28	High-Resolution Mapping of In vivo Genomic Transcription Factor Binding Sites Using In situ DNase I Footprinting and ChIP-seq. DNA Research, 2013, 20, 325-338.	3.4	24
29	Laboratory adapted <i>Escherichia coli</i> K12 becomes a pathogen of <i>Caenorhabditis elegans</i> upon restoration of <i>O</i> antigen biosynthesis. Molecular Microbiology, 2013, 87, 939-950.	2.5	72
30	Cysteine coordination of Pb(II) is involved in the PbrR-dependent activation of the lead-resistance promoter, PpbrA, from <i>Cupriavidus metallidurans</i> CH34. BMC Microbiology, 2012, 12, 109.	3.3	28
31	Complete Genome Sequence and Comparative Metabolic Profiling of the Prototypical Enterotoxigenic <i>Escherichia coli</i> Strain 042. PLoS ONE, 2010, 5, e8801.	2.5	165
32	YieJ (CbrC) Mediates CreBC-Dependent Colicin E2 Tolerance in <i>Escherichia coli</i> . Journal of Bacteriology, 2010, 192, 3329-3336.	2.2	17
33	A Commensal Gene Bad: Complete Genome Sequence of the Prototypical Enterotoxigenic <i>Escherichia coli</i> Strain H10407. Journal of Bacteriology, 2010, 192, 5822-5831.	2.2	168
34	Exposure of <i>Escherichia coli</i> and <i>Salmonella enterica</i> serovar Typhimurium to triclosan induces a species-specific response, including drug detoxification. Journal of Antimicrobial Chemotherapy, 2009, 64, 973-985.	3.0	65
35	Gene doctoring: a method for recombineering in laboratory and pathogenic <i>Escherichia coli</i> strains. BMC Microbiology, 2009, 9, 252.	3.3	143
36	Transcriptional activation of MerR family promoters in <i>Cupriavidus metallidurans</i> CH34. Antonie Van Leeuwenhoek, 2009, 96, 149-159.	1.7	23

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37	Global responses of <i>Escherichia coli</i> to adverse conditions determined by microarrays and FT-IR spectroscopy. <i>Canadian Journal of Microbiology</i> , 2009, 55, 714-728.	1.7	44
38	Evidence for direct interactions between the mercuric ion transporter (MerT) and mercuric reductase (MerA) from the Tn501 mer operon. <i>BioMetals</i> , 2008, 21, 107-116.	4.1	16
39	Probing bactericidal mechanisms induced by cold atmospheric plasmas with <i>Escherichia coli</i> mutants. <i>Applied Physics Letters</i> , 2007, 90, 073902.	3.3	147
40	The <i>Escherichia coli</i> Regulator of Sigma 70 Protein, Rsd, Can Up-Regulate Some Stress-Dependent Promoters by Sequestering Sigma 70. <i>Journal of Bacteriology</i> , 2007, 189, 3489-3495.	2.2	43
41	Comparative Genomic Hybridization Detects Secondary Chromosomal Deletions in <i>Escherichia coli</i> K-12 MG1655 Mutants and Highlights Instability in the <i>flhDC</i> Region. <i>Journal of Bacteriology</i> , 2007, 189, 8786-8792.	2.2	15
42	Zinc dependence of <i>zinT</i> ( <i>yodA</i> ) mutants and binding of zinc, cadmium and mercury by <i>ZinT</i> . <i>Biochemical and Biophysical Research Communications</i> , 2007, 364, 66-71.	2.1	36
43	Mercury Microbiology: Resistance Systems, Environmental Aspects, Methylation, and Human Health. , 2007, , 357-370.		21
44	Transcriptomic Responses of Bacterial Cells to Sublethal Metal Ion Stress. , 2007, , 73-115.		22
45	The multicopper oxidase (CueO) and cell aggregation in <i>Escherichia coli</i> . <i>Environmental Microbiology</i> , 2007, 9, 2110-2116.	3.8	24
46	MerR family transcription activators: similar designs, different specificities. <i>Molecular Microbiology</i> , 2007, 63, 1275-1278.	2.5	62
47	Laboratory strains of <i>Escherichia coli</i> : model citizens or deceitful delinquents growing old disgracefully?. <i>Molecular Microbiology</i> , 2007, 64, 881-885.	2.5	64
48	Microarray analysis of gene regulation by oxygen, nitrate, nitrite, FNR, NarL and NarP during anaerobic growth of <i>Escherichia coli</i> : new insights into microbial physiology. <i>Biochemical Society Transactions</i> , 2006, 34, 104-107.	3.4	52
49	Analysis of fimbrial gene clusters and their expression in enterohaemorrhagic <i>Escherichia coli</i> O157:H7. <i>Environmental Microbiology</i> , 2006, 8, 1033-1047.	3.8	98
50	A Reassessment of the FNR Regulon and Transcriptomic Analysis of the Effects of Nitrate, Nitrite, NarXL, and NarQP as <i>Escherichia coli</i> K12 Adapts from Aerobic to Anaerobic Growth. <i>Journal of Biological Chemistry</i> , 2006, 281, 4802-4815.	3.4	234
51	Climate factors influencing bacterial count in background air samples. <i>International Journal of Biometeorology</i> , 2005, 49, 167-178.	3.0	124
52	A Design for Life: Prokaryotic Metal-binding MerR Family Regulators. <i>BioMetals</i> , 2005, 18, 429-436.	4.1	95
53	The expression profile of <i>Escherichia coli</i> K-12 in response to minimal, optimal and excess copper concentrations. <i>Microbiology (United Kingdom)</i> , 2005, 151, 1187-1198.	1.8	131
54	Genomic Studies with <i>Escherichia coli</i> MerR Protein: Applications of Chromatin Immunoprecipitation and Microarrays. <i>Journal of Bacteriology</i> , 2004, 186, 6938-6943.	2.2	92

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55	Regulators Encoded in the Escherichia coli Type III Secretion System 2 Gene Cluster Influence Expression of Genes within the Locus for Enterocyte Effacement in Enterohemorrhagic E. coli O157:H7. <i>Infection and Immunity</i> , 2004, 72, 7282-7293.	2.2	89
56	Translocation of transposition-deficient (Tnd PKLH2-like) transposons in the natural environment: mechanistic insights from the study of adjacent DNA sequences. <i>Microbiology (United Kingdom)</i> , 2004, 150, 979-992.	1.8	36
57	Identification of the CRP regulon using in vitro and in vivo transcriptional profiling. <i>Nucleic Acids Research</i> , 2004, 32, 5874-5893.	14.5	358
58	The MerR family of transcriptional regulators. <i>FEMS Microbiology Reviews</i> , 2003, 27, 145-163.	8.6	628
59	Mercury Resistance Determinants Related to Tn 21 , Tn 1696 , and Tn 5053 in Enterobacteria from the Preantibiotic Era. <i>Antimicrobial Agents and Chemotherapy</i> , 2003, 47, 1115-1119.	3.2	47
60	Mercury transport and resistance. <i>Biochemical Society Transactions</i> , 2002, 30, 715-718.	3.4	45
61	Class II broad-spectrum mercury resistance transposons in Gram-positive bacteria from natural environments. <i>Research in Microbiology</i> , 2001, 152, 503-514.	2.1	31
62	CueR (YbbI) of Escherichia coli is a MerR family regulator controlling expression of the copper exporter CopA. <i>Molecular Microbiology</i> , 2001, 39, 502-512.	2.5	225
63	Cloning and Functional Analysis of the <i>pbr</i> Lead Resistance Determinant of <i>Ralstonia metallidurans</i> CH34. <i>Journal of Bacteriology</i> , 2001, 183, 5651-5658.	2.2	254
64	Bacterial metal-resistance proteins and their use in biosensors for the detection of bioavailable heavy metals. <i>Journal of Inorganic Biochemistry</i> , 2000, 79, 225-229.	3.5	76
65	MerF is a mercury transport protein: different structures but a common mechanism for mercuric ion transporters?. <i>FEBS Letters</i> , 2000, 472, 78-82.	2.8	82
66	ZntR is a Zn(II)-responsive MerR-like transcriptional regulator of zntA in Escherichia coli. <i>Molecular Microbiology</i> , 1999, 31, 893-902.	2.5	235
67	Whole cell- and protein-based biosensors for the detection of bioavailable heavy metals in environmental samples. <i>Analytica Chimica Acta</i> , 1999, 387, 235-244.	5.4	248
68	Overexpression of MerT, the mercuric ion transport protein of transposon Tn. <i>Molecular Genetics and Genomics</i> , 1996, 250, 129.	2.4	0
69	The role of cysteine residues in the transport of mercuric ions by the Tn501 MerT and MerP mercury-resistance proteins. <i>Molecular Microbiology</i> , 1995, 17, 25-35.	2.5	87
70	Accumulation and intracellular fate of tellurite in tellurite-resistant Escherichia coli: A model for the mechanism of resistance. <i>FEMS Microbiology Letters</i> , 1994, 118, 113-119.	1.8	61
71	The sequence of the mer operon of pMER327/419 and transposon ends of pMER327/419, 330 and 05. <i>Gene</i> , 1994, 146, 73-78.	2.2	35
72	Novel mercury resistance determinants carried by IncJ plasmids pMERPH and R391. <i>Molecular Genetics and Genomics</i> , 1991, 228, 294-299.	2.4	58