

Morten O A Sommer

List of Publications by Year in descending order

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Version: 2024-02-01

95
papers

9,052
citations

57758

44
h-index

46799

89
g-index

107
all docs

107
docs citations

107
times ranked

11647
citing authors

#	ARTICLE	IF	CITATIONS
1	Comparison of non-invasive <i>Staphylococcus aureus</i> sampling methods on lesional skin in patients with atopic dermatitis. <i>European Journal of Clinical Microbiology and Infectious Diseases</i> , 2022, 41, 245-252.	2.9	6
2	Identification and Optimization of Novel Small-Molecule Cas9 Inhibitors by Cell-Based High-Throughput Screening. <i>Journal of Medicinal Chemistry</i> , 2022, 65, 3266-3305.	6.4	5
3	Niclosamide—A promising treatment for COVID-19. <i>British Journal of Pharmacology</i> , 2022, 179, 3250-3267.	5.4	31
4	Topical niclosamide (ATx201) reduces <i>Staphylococcus aureus</i> colonization and increases Shannon diversity of the skin microbiome in atopic dermatitis patients in a randomized, double-blind, placebo-controlled Phase 2 trial. <i>Clinical and Translational Medicine</i> , 2022, 12, e790.	4.0	15
5	Characterization of local gut microbiome and intestinal transcriptome responses to rosiglitazone treatment in diabetic db/db mice. <i>Biomedicine and Pharmacotherapy</i> , 2021, 133, 110966.	5.6	12
6	Short and long-read ultra-deep sequencing profiles emerging heterogeneity across five platform <i>Escherichia coli</i> strains. <i>Metabolic Engineering</i> , 2021, 65, 197-206.	7.0	13
7	Metabolic modeling predicts specific gut bacteria as key determinants for <i>Candida albicans</i> colonization levels. <i>ISME Journal</i> , 2021, 15, 1257-1270.	9.8	23
8	Expansion and persistence of antibiotic-specific resistance genes following antibiotic treatment. <i>Gut Microbes</i> , 2021, 13, 1-19.	9.8	24
9	Immersive virtual reality as a competitive training strategy for the biopharma industry. <i>Nature Biotechnology</i> , 2021, 39, 116-119.	17.5	16
10	Compatibility of Evolutionary Responses to Constituent Antibiotics Drive Resistance Evolution to Drug Pairs. <i>Molecular Biology and Evolution</i> , 2021, 38, 2057-2069.	8.9	18
11	Complex yeast-bacteria interactions affect the yield of industrial ethanol fermentation. <i>Nature Communications</i> , 2021, 12, 1498.	12.8	52
12	Forecasting the dissemination of antibiotic resistance genes across bacterial genomes. <i>Nature Communications</i> , 2021, 12, 2435.	12.8	111
13	A randomized, double-blind, placebo-controlled phase 1 trial of inhaled and intranasal niclosamide: A broad spectrum antiviral candidate for treatment of COVID-19. <i>Lancet Regional Health - Europe</i> , The, 2021, 4, 100084.	5.6	45
14	Distinct composition and metabolic functions of human gut microbiota are associated with cachexia in lung cancer patients. <i>ISME Journal</i> , 2021, 15, 3207-3220.	9.8	51
15	Bacterial resistance to CRISPR-Cas antimicrobials. <i>Scientific Reports</i> , 2021, 11, 17267.	3.3	28
16	The novel anti-CRISPR AcrIIA22 relieves DNA torsion in target plasmids and impairs SpyCas9 activity. <i>PLoS Biology</i> , 2021, 19, e3001428.	5.6	13
17	Exploring Selective Pressure Trade-Offs for Synthetic Addiction to Extend Metabolite Productive Lifetimes in Yeast. <i>ACS Synthetic Biology</i> , 2021, 10, 2842-2849.	3.8	4
18	<i>Escherichia coli</i> Promoters with Consistent Expression throughout the Murine Gut. <i>ACS Synthetic Biology</i> , 2021, 10, 3359-3368.	3.8	11

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19	Niclosamide shows strong antiviral activity in a human airway model of SARS-CoV-2 infection and a conserved potency against the Alpha (B.1.1.7), Beta (B.1.351) and Delta variant (B.1.617.2). PLoS ONE, 2021, 16, e0260958.	2.5	31
20	Regulatory control circuits for stabilizing long-term anabolic product formation in yeast. Metabolic Engineering, 2020, 61, 369-380.	7.0	17
21	Spatial and temporal dynamics of SARS-CoV-2 in COVID-19 patients: A systematic review and meta-analysis. EBioMedicine, 2020, 58, 102916.	6.1	95
22	Systematic Investigation of Resistance Evolution to Common Antibiotics Reveals Conserved Collateral Responses across Common Human Pathogens. Antimicrobial Agents and Chemotherapy, 2020, 65, .	3.2	9
23	Global responses to oxytetracycline treatment in tetracycline-resistant Escherichia coli. Scientific Reports, 2020, 10, 8438.	3.3	7
24	Improved biotin, thiamine, and lipoic acid biosynthesis by engineering the global regulator IscR. Metabolic Engineering, 2020, 60, 97-109.	7.0	15
25	Dominant resistance and negative epistasis can limit the co-selection of de novo resistance mutations and antibiotic resistance genes. Nature Communications, 2020, 11, 1199.	12.8	21
26	Overcoming genetic heterogeneity in industrial fermentations. Nature Biotechnology, 2019, 37, 869-876.	17.5	116
27	Metabolic and gut microbiome changes following GLP-1 or dual GLP-1/GLP-2 receptor agonist treatment in diet-induced obese mice. Scientific Reports, 2019, 9, 15582.	3.3	64
28	Mining, analyzing, and integrating viral signals from metagenomic data. Microbiome, 2019, 7, 42.	11.1	58
29	Discovery and Characterization of Cas9 Inhibitors Disseminated across Seven Bacterial Phyla. Cell Host and Microbe, 2019, 25, 233-241.e5.	11.0	63
30	Rapid diagnosis of lung infections. Nature Biotechnology, 2019, 37, 725-726.	17.5	3
31	Antibiotic Treatment Drives the Diversification of the Human Gut Resistome. Genomics, Proteomics and Bioinformatics, 2019, 17, 39-51.	6.9	51
32	Wiring cell growth to product formation. Current Opinion in Biotechnology, 2019, 59, 85-92.	6.6	13
33	Collateral sensitivity constrains resistance evolution of the CTX-M-15 β -lactamase. Nature Communications, 2019, 10, 618.	12.8	64
34	NetSurfPv2.0: Improved prediction of protein structural features by integrated deep learning. Proteins: Structure, Function and Bioinformatics, 2019, 87, 520-527.	2.6	439
35	Diverse genetic error modes constrain large-scale bio-based production. Nature Communications, 2018, 9, 787.	12.8	125
36	Directed Evolution of Membrane Transport Using Synthetic Selections. ACS Synthetic Biology, 2018, 7, 789-793.	3.8	18

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37	Synthetic addiction extends the productive life time of engineered <i>Escherichia coli</i> populations. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2347-2352.	7.1	98
38	Biochemical mechanisms determine the functional compatibility of heterologous genes. <i>Nature Communications</i> , 2018, 9, 522.	12.8	59
39	Drug-Driven Phenotypic Convergence Supports Rational Treatment Strategies of Chronic Infections. <i>Cell</i> , 2018, 172, 121-134.e14.	28.9	131
40	Chromosomal barcoding as a tool for multiplexed phenotypic characterization of laboratory evolved lineages. <i>Scientific Reports</i> , 2018, 8, 6961.	3.3	18
41	Shared strategies for β -lactam catabolism in the soil microbiome. <i>Nature Chemical Biology</i> , 2018, 14, 556-564.	8.0	67
42	Enhanced Metabolite Productivity of <i>Escherichia coli</i> Adapted to Glucose M9 Minimal Medium. <i>Frontiers in Bioengineering and Biotechnology</i> , 2018, 6, 166.	4.1	20
43	The Environmental Exposures and Inner- and Intercity Traffic Flows of the Metro System May Contribute to the Skin Microbiome and Resistome. <i>Cell Reports</i> , 2018, 24, 1190-1202.e5.	6.4	56
44	The evolving interface between synthetic biology and functional metagenomics. <i>Nature Chemical Biology</i> , 2018, 14, 752-759.	8.0	44
45	A synthetic medium to simulate sugarcane molasses. <i>Biotechnology for Biofuels</i> , 2018, 11, 221.	6.2	39
46	Rapid resistome mapping using nanopore sequencing. <i>Nucleic Acids Research</i> , 2017, 45, gkw1328.	14.5	62
47	Dissemination of antibiotic resistance genes from antibiotic producers to pathogens. <i>Nature Communications</i> , 2017, 8, 15784.	12.8	287
48	Development of a Bacterial Biosensor for Rapid Screening of Yeast <i>p</i> -Coumaric Acid Production. <i>ACS Synthetic Biology</i> , 2017, 6, 1860-1869.	3.8	120
49	Draft Genome Sequences of Three β -Lactam-Catabolizing Soil Proteobacteria. <i>Genome Announcements</i> , 2017, 5, .	0.8	11
50	Prediction of antibiotic resistance: time for a new preclinical paradigm?. <i>Nature Reviews Microbiology</i> , 2017, 15, 689-696.	28.6	221
51	Genetic-Metabolic Coupling for Targeted Metabolic Engineering. <i>Cell Reports</i> , 2017, 20, 1029-1037.	6.4	22
52	Assessing glycolytic flux alterations resulting from genetic perturbations in <i>E. coli</i> using a biosensor. <i>Metabolic Engineering</i> , 2017, 42, 194-202.	7.0	22
53	Genome Dynamics of <i>Escherichia coli</i> during Antibiotic Treatment: Transfer, Loss, and Persistence of Genetic Elements In situ of the Infant Gut. <i>Frontiers in Cellular and Infection Microbiology</i> , 2017, 7, 126.	3.9	46
54	Adaptive Laboratory Evolution of Antibiotic Resistance Using Different Selection Regimes Lead to Similar Phenotypes and Genotypes. <i>Frontiers in Microbiology</i> , 2017, 8, 816.	3.5	64

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55	Transfer and Persistence of a Multi-Drug Resistance Plasmid in situ of the Infant Gut Microbiota in the Absence of Antibiotic Treatment. <i>Frontiers in Microbiology</i> , 2017, 8, 1852.	3.5	63
56	Survival and Evolution of a Large Multidrug Resistance Plasmid in New Clinical Bacterial Hosts. <i>Molecular Biology and Evolution</i> , 2016, 33, 2860-2873.	8.9	212
57	Simulating Serial-Target Antibacterial Drug Synergies Using Flux Balance Analysis. <i>PLoS ONE</i> , 2016, 11, e0147651.	2.5	14
58	Oral supplementation of healthy adults with 2- <i>O</i> -fucosyllactose and lacto-N-neotetraose is well tolerated and shifts the intestinal microbiota. <i>British Journal of Nutrition</i> , 2016, 116, 1356-1368.	2.3	148
59	(Meta-)genome mining for new ribo-regulators. <i>Science</i> , 2016, 352, 144-145.	12.6	3
60	Molecular Buffers Permit Sensitivity Tuning and Inversion of Riboswitch Signals. <i>ACS Synthetic Biology</i> , 2016, 5, 632-638.	3.8	12
61	Functional mining of transporters using synthetic selections. <i>Nature Chemical Biology</i> , 2016, 12, 1015-1022.	8.0	64
62	Transcriptional interactions suggest niche segregation among microorganisms in the human gut. <i>Nature Microbiology</i> , 2016, 1, 16152.	13.3	56
63	Adaptive responses to cefotaxime treatment in ESBL-producing <i>Escherichia coli</i> and the possible use of significantly regulated pathways as novel secondary targets. <i>Journal of Antimicrobial Chemotherapy</i> , 2016, 71, 2449-2459.	3.0	9
64	Relation between tetR and tetA expression in tetracycline resistant <i>Escherichia coli</i> . <i>BMC Microbiology</i> , 2016, 16, 39.	3.3	69
65	Transient overexpression of DNA adenine methylase enables efficient and mobile genome engineering with reduced off-target effects. <i>Nucleic Acids Research</i> , 2016, 44, e36-e36.	14.5	41
66	Predictable tuning of protein expression in bacteria. <i>Nature Methods</i> , 2016, 13, 233-236.	19.0	116
67	Collateral Resistance and Sensitivity Modulate Evolution of High-Level Resistance to Drug Combination Treatment in <i>Staphylococcus aureus</i> . <i>Molecular Biology and Evolution</i> , 2015, 32, 1175-1185.	8.9	97
68	Recombination-stable multimeric green fluorescent protein for characterization of weak promoter outputs in <i>Saccharomyces cerevisiae</i> . <i>FEMS Yeast Research</i> , 2015, 15, fov085.	2.3	8
69	Advancing gut microbiome research using cultivation. <i>Current Opinion in Microbiology</i> , 2015, 27, 127-132.	5.1	44
70	Limited dissemination of the wastewater treatment plant core resistome. <i>Nature Communications</i> , 2015, 6, 8452.	12.8	173
71	deFUME: Dynamic exploration of functional metagenomic sequencing data. <i>BMC Research Notes</i> , 2015, 8, 328.	1.4	9
72	Software-Supported USER Cloning Strategies for Site-Directed Mutagenesis and DNA Assembly. <i>ACS Synthetic Biology</i> , 2015, 4, 342-349.	3.8	41

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73	Direct Mutagenesis of Thousands of Genomic Targets Using Microarray-Derived Oligonucleotides. ACS Synthetic Biology, 2015, 4, 17-22.	3.8	57
74	CTX-M-1 β -lactamase expression in Escherichia coli is dependent on cefotaxime concentration, growth phase and gene location. Journal of Antimicrobial Chemotherapy, 2015, 70, 62-70.	3.0	26
75	Human Intestinal Cells Modulate Conjugational Transfer of Multidrug Resistance Plasmids between Clinical Escherichia coli Isolates. PLoS ONE, 2014, 9, e100739.	2.5	22
76	MODEST: a web-based design tool for oligonucleotide-mediated genome engineering and recombineering. Nucleic Acids Research, 2014, 42, W408-W415.	14.5	60
77	Prediction of resistance development against drug combinations by collateral responses to component drugs. Science Translational Medicine, 2014, 6, 262ra156.	12.4	150
78	Barriers to the spread of resistance. Nature, 2014, 509, 567-568.	27.8	20
79	A sustainable route to produce the scytonemin precursor using Escherichia coli. Green Chemistry, 2014, 16, 3255-3265.	9.0	22
80	Cultivation-based multiplex phenotyping of human gut microbiota allows targeted recovery of previously uncultured bacteria. Nature Communications, 2014, 5, 4714.	12.8	123
81	Evolution of Escherichia coli to 42 $^{\circ}$ C and Subsequent Genetic Engineering Reveals Adaptive Mechanisms and Novel Mutations. Molecular Biology and Evolution, 2014, 31, 2647-2662.	8.9	145
82	Improving biotech education through gamified laboratory simulations. Nature Biotechnology, 2014, 32, 694-697.	17.5	164
83	Experimental Approaches for Defining Functional Roles of Microbes in the Human Gut. Annual Review of Microbiology, 2013, 67, 459-475.	7.3	39
84	Use of Collateral Sensitivity Networks to Design Drug Cycling Protocols That Avoid Resistance Development. Science Translational Medicine, 2013, 5, 204ra132.	12.4	368
85	The Shared Antibiotic Resistome of Soil Bacteria and Human Pathogens. Science, 2012, 337, 1107-1111.	12.6	1,314
86	Context matters – the complex interplay between resistome genotypes and resistance phenotypes. Current Opinion in Microbiology, 2012, 15, 577-582.	5.1	97
87	Antibiotics and the resistant microbiome. Current Opinion in Microbiology, 2011, 14, 556-563.	5.1	140
88	Functional Metagenomic Investigations of the Human Intestinal Microbiota. Frontiers in Microbiology, 2011, 2, 188.	3.5	44
89	Evolutionary dynamics of bacteria in a human host environment. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 7481-7486.	7.1	327
90	The human microbiome harbors a diverse reservoir of antibiotic resistance genes. Virulence, 2010, 1, 299-303.	4.4	166

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91	A functional metagenomic approach for expanding the synthetic biology toolbox for biomass conversion. <i>Molecular Systems Biology</i> , 2010, 6, 360.	7.2	64
92	Functional Characterization of the Antibiotic Resistance Reservoir in the Human Microflora. <i>Science</i> , 2009, 325, 1128-1131.	12.6	748
93	Bacteria Subsisting on Antibiotics. <i>Science</i> , 2008, 320, 100-103.	12.6	499
94	Crystallizing proteins on the basis of their precipitation diagram determined using a microfluidic formulator. <i>Journal of Synchrotron Radiation</i> , 2005, 12, 779-785.	2.4	13
95	From The Cover: Systematic investigation of protein phase behavior with a microfluidic formulator. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 14431-14436.	7.1	173