Morten O A Sommer

List of Publications by Year
in descending order

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	The Shared Antibiotic Resistome of Soil Bacteria and Human Pathogens. Science, 2012, 337, 1107-1111.	12.6	1,314
2	Functional Characterization of the Antibiotic Resistance Reservoir in the Human Microflora. Science, 2009, 325, 1128-1131.	12.6	748
3	Bacteria Subsisting on Antibiotics. Science, 2008, 320, 100-103.	12.6	499
4	NetSurfPâ€2.0: Improved prediction of protein structural features by integrated deep learning. Proteins: Structure, Function and Bioinformatics, 2019, 87, 520-527.	2.6	439
5	Use of Collateral Sensitivity Networks to Design Drug Cycling Protocols That Avoid Resistance Development. Science Translational Medicine, 2013, 5, 204ra132.	12.4	368
6	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
7	Dissemination of antibiotic resistance genes from antibiotic producers to pathogens. Nature Communications, 2017, 8, 15784.	12.8	287
8	Prediction of antibiotic resistance: time for a new preclinical paradigm?. Nature Reviews Microbiology, 2017, 15, 689-696.	28.6	221
9	Survival and Evolution of a Large Multidrug Resistance Plasmid in New Clinical Bacterial Hosts. Molecular Biology and Evolution, 2016, 33, 2860-2873.	8.9	212
10	From The Cover: Systematic investigation of protein phase behavior with a microfluidic formulator. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 14431-14436.	7.1	173
11	Limited dissemination of the wastewater treatment plant core resistome. Nature Communications, 2015, 6, 8452.	12.8	173
12	The human microbiome harbors a diverse reservoir of antibiotic resistance genes. Virulence, 2010, 1, 299-303.	4.4	166
13	Improving biotech education through gamified laboratory simulations. Nature Biotechnology, 2014, 32, 694-697.	17.5	164
14	Prediction of resistance development against drug combinations by collateral responses to component drugs. Science Translational Medicine, 2014, 6, 262ra156.	12.4	150
15	Oral supplementation of healthy adults with 2â€²-O-fucosyllactose and lacto-N-neotetraose is well tolerated and shifts the intestinal microbiota. British Journal of Nutrition, 2016, 116, 1356-1368.	2.3	148
16	Evolution of Escherichia coli to 42 Â°C and Subsequent Genetic Engineering Reveals Adaptive Mechanisms and Novel Mutations. Molecular Biology and Evolution, 2014, 31, 2647-2662.	8.9	145
17	Antibiotics and the resistant microbiome. Current Opinion in Microbiology, 2011, 14, 556-563.	5.1	140
18	Drug-Driven Phenotypic Convergence Supports Rational Treatment Strategies of Chronic Infections. Cell, 2018, 172, 121-134.e14.	28.9	131

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19	Diverse genetic error modes constrain large-scale bio-based production. Nature Communications, 2018, 9, 787.	12.8	125
20	Cultivation-based multiplex phenotyping of human gut microbiota allows targeted recovery of previously uncultured bacteria. Nature Communications, 2014, 5, 4714.	12.8	123
21	Development of a Bacterial Biosensor for Rapid Screening of Yeast p-Coumaric Acid Production. ACS Synthetic Biology, 2017, 6, 1860-1869.	3.8	120
22	Predictable tuning of protein expression in bacteria. Nature Methods, 2016, 13, 233-236.	19.0	116
23	Overcoming genetic heterogeneity in industrial fermentations. Nature Biotechnology, 2019, 37, 869-876.	17.5	116
24	Forecasting the dissemination of antibiotic resistance genes across bacterial genomes. Nature Communications, 2021, 12, 2435.	12.8	111
25	Synthetic addiction extends the productive life time of engineered Escherichia coli populations. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 2347-2352.	7.1	98
26	Context matters â€" the complex interplay between resistome genotypes and resistance phenotypes. Current Opinion in Microbiology, 2012, 15, 577-582.	5.1	97
27	Collateral Resistance and Sensitivity Modulate Evolution of High-Level Resistance to Drug Combination Treatment in Staphylococcus aureus. Molecular Biology and Evolution, 2015, 32, 1175-1185.	8.9	97
28	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
29	Relation between tetR and tetA expression in tetracycline resistant Escherichia coli. BMC Microbiology, 2016, 16, 39.	3.3	69
30	Shared strategies for Î²-lactam catabolism in the soil microbiome. Nature Chemical Biology, 2018, 14, 556-564.	8.0	67
31	A functional metagenomic approach for expanding the synthetic biology toolbox for biomass conversion. Molecular Systems Biology, 2010, 6, 360.	7.2	64
32	Functional mining of transporters using synthetic selections. Nature Chemical Biology, 2016, 12, 1015-1022.	8.0	64
33	Adaptive Laboratory Evolution of Antibiotic Resistance Using Different Selection Regimes Lead to Similar Phenotypes and Genotypes. Frontiers in Microbiology, 2017, 8, 816.	3.5	64
34	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
35	Collateral sensitivity constrains resistance evolution of the CTX-M-15 Î²-lactamase. Nature Communications, 2019, 10, 618.	12.8	64
36	Transfer and Persistence of a Multi-Drug Resistance Plasmid in situ of the Infant Gut Microbiota in the Absence of Antibiotic Treatment. Frontiers in Microbiology, 2017, 8, 1852.	3.5	63

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37	Discovery and Characterization of Cas9 Inhibitors Disseminated across Seven Bacterial Phyla. Cell Host and Microbe, 2019, 25, 233-241.e5.	11.0	63
38	Rapid resistome mapping using nanopore sequencing. Nucleic Acids Research, 2017, 45, gkw1328.	14.5	62
39	MODEST: a web-based design tool for oligonucleotide-mediated genome engineering and recombineering. Nucleic Acids Research, 2014, 42, W408-W415.	14.5	60
40	Biochemical mechanisms determine the functional compatibility of heterologous genes. Nature Communications, 2018, 9, 522.	12.8	59
41	Mining, analyzing, and integrating viral signals from metagenomic data. Microbiome, 2019, 7, 42.	11.1	58
42	Direct Mutagenesis of Thousands of Genomic Targets Using Microarray-Derived Oligonucleotides. ACS Synthetic Biology, 2015, 4, 17-22.	3.8	57
43	Transcriptional interactions suggest niche segregation among microorganisms in the human gut. Nature Microbiology, 2016, 1, 16152.	13.3	56
44	The Environmental Exposures and Inner- and Intercity Traffic Flows of the Metro System May Contribute to the Skin Microbiome and Resistome. Cell Reports, 2018, 24, 1190-1202.e5.	6.4	56
45	Complex yeastâ€“bacteria interactions affect the yield of industrial ethanol fermentation. Nature Communications, 2021, 12, 1498.	12.8	52
46	Antibiotic Treatment Drives the Diversification of the Human Gut Resistome. Genomics, Proteomics and Bioinformatics, 2019, 17, 39-51.	6.9	51
47	Distinct composition and metabolic functions of human gut microbiota are associated with cachexia in lung cancer patients. ISME Journal, 2021, 15, 3207-3220.	9.8	51
48	Genome Dynamics of Escherichia coli during Antibiotic Treatment: Transfer, Loss, and Persistence of Genetic Elements In situ of the Infant Gut. Frontiers in Cellular and Infection Microbiology, 2017, 7, 126.	3.9	46
49	A randomized, double-blind, placebo-controlled phase 1 trial of inhaled and intranasal niclosamide: A broad spectrum antiviral candidate for treatment of COVID-19. Lancet Regional Health - Europe, The, 2021, 4, 100084.	5.6	45
50	Functional Metagenomic Investigations of the Human Intestinal Microbiota. Frontiers in Microbiology, 2011, 2, 188.	3.5	44
51	Advancing gut microbiome research using cultivation. Current Opinion in Microbiology, 2015, 27, 127-132.	5.1	44
52	The evolving interface between synthetic biology and functional metagenomics. Nature Chemical Biology, 2018, 14, 752-759.	8.0	44
53	Software-Supported USER Cloning Strategies for Site-Directed Mutagenesis and DNA Assembly. ACS Synthetic Biology, 2015, 4, 342-349.	3.8	41
54	Transient overexpression of DNA adenine methylase enables efficient and mobile genome engineering with reduced off-target effects. Nucleic Acids Research, 2016, 44, e36-e36.	14.5	41

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55	Experimental Approaches for Defining Functional Roles of Microbes in the Human Gut. Annual Review of Microbiology, 2013, 67, 459-475.	7.3	39
56	A synthetic medium to simulate sugarcane molasses. Biotechnology for Biofuels, 2018, 11, 221.	6.2	39
57	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
58	Niclosamideâ€"A promising treatment for COVIDâ€19. British Journal of Pharmacology, 2022, 179, 3250-3267.	5.4	31
59	Bacterial resistance to CRISPR-Cas antimicrobials. Scientific Reports, 2021, 11, 17267.	3.3	28
60	CTX-M-1 Î²-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
61	Expansion and persistence of antibiotic-specific resistance genes following antibiotic treatment. Gut Microbes, 2021, 13, 1-19.	9.8	24
62	Metabolic modeling predicts specific gut bacteria as key determinants for Candida albicans colonization levels. ISME Journal, 2021, 15, 1257-1270.	9.8	23
63	Human Intestinal Cells Modulate Conjugational Transfer of Multidrug Resistance Plasmids between Clinical Escherichia coli Isolates. PLoS ONE, 2014, 9, e100739.	2.5	22
64	A sustainable route to produce the scytonemin precursor usingEscherichia coli. Green Chemistry, 2014, 16, 3255-3265.	9.0	22
65	Genetic-Metabolic Coupling for Targeted Metabolic Engineering. Cell Reports, 2017, 20, 1029-1037.	6.4	22
66	Assessing glycolytic flux alterations resulting from genetic perturbations in E. coli using a biosensor. Metabolic Engineering, 2017, 42, 194-202.	7.0	22
67	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
68	Barriers to the spread of resistance. Nature, 2014, 509, 567-568.	27.8	20
69	Enhanced Metabolite Productivity of Escherichia coli Adapted to Glucose M9 Minimal Medium. Frontiers in Bioengineering and Biotechnology, 2018, 6, 166.	4.1	20
70	Directed Evolution of Membrane Transport Using Synthetic Selections. ACS Synthetic Biology, 2018, 7, 789-793.	3.8	18
71	Chromosomal barcoding as a tool for multiplexed phenotypic characterization of laboratory evolved lineages. Scientific Reports, 2018, 8, 6961.	3.3	18
72	Compatibility of Evolutionary Responses to Constituent Antibiotics Drive Resistance Evolution to Drug Pairs. Molecular Biology and Evolution, 2021, 38, 2057-2069.	8.9	18

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73	Regulatory control circuits for stabilizing long-term anabolic product formation in yeast. Metabolic Engineering, 2020, 61, 369-380.	7.0	17
74	Immersive virtual reality as a competitive training strategy for the biopharma industry. Nature Biotechnology, 2021, 39, 116-119.	17.5	16
75	Improved biotin, thiamine, and lipoic acid biosynthesis by engineering the global regulator IscR. Metabolic Engineering, 2020, 60, 97-109.	7.0	15
76	Topical niclosamide (ATx201) reduces Staphylococcus aureus colonization and increases Shannon diversity of the skin microbiome in atopic dermatitis patients in a randomized, doubleâ€blind, placeboâ€controlled Phase 2 trial. Clinical and Translational Medicine, 2022, 12, e790.	4.0	15
77	Simulating Serial-Target Antibacterial Drug Synergies Using Flux Balance Analysis. PLoS ONE, 2016, 11, e0147651.	2.5	14
78	Crystallizing proteins on the basis of their precipitation diagram determined using a microfluidic formulator. Journal of Synchrotron Radiation, 2005, 12, 779-785.	2.4	13
79	Wiring cell growth to product formation. Current Opinion in Biotechnology, 2019, 59, 85-92.	6.6	13
80	Short and long-read ultra-deep sequencing profiles emerging heterogeneity across five platform Escherichia coli strains. Metabolic Engineering, 2021, 65, 197-206.	7.0	13
81	The novel anti-CRISPR AcrIIA22 relieves DNA torsion in target plasmids and impairs SpyCas9 activity. PLoS Biology, 2021, 19, e3001428.	5.6	13
82	Molecular Buffers Permit Sensitivity Tuning and Inversion of Riboswitch Signals. ACS Synthetic Biology, 2016, 5, 632-638.	3.8	12
83	Characterization of local gut microbiome and intestinal transcriptome responses to rosiglitazone treatment in diabetic db/db mice. Biomedicine and Pharmacotherapy, 2021, 133, 110966.	5.6	12
84	Draft Genome Sequences of Three Î²-Lactam-Catabolizing Soil Proteobacteria. Genome Announcements, 2017, 5, .	0.8	11
85	Escherichia coli Promoters with Consistent Expression throughout the Murine Gut. ACS Synthetic Biology, 2021, 10, 3359-3368.	3.8	11
86	deFUME: Dynamic exploration of functional metagenomic sequencing data. BMC Research Notes, 2015, 8, 328.	1.4	9
87	Adaptive responses to cefotaxime treatment in ESBL-producingEscherichia coliand the possible use of significantly regulated pathways as novel secondary targets. Journal of Antimicrobial Chemotherapy, 2016, 71, 2449-2459.	3.0	9
88	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
89	Recombination-stable multimeric green fluorescent protein for characterization of weak promoter outputs inSaccharomyces cerevisiae. FEMS Yeast Research, 2015, 15, fov085.	2.3	8
90	Global responses to oxytetracycline treatment in tetracycline-resistant Escherichia coli. Scientific Reports, 2020, 10, 8438.	3.3	7

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91	Comparison of non-invasive Staphylococcus aureus sampling methods on lesional skin in patients with atopic dermatitis. European Journal of Clinical Microbiology and Infectious Diseases, 2022, 41, 245-252.	2.9	6
92	Identification and Optimization of Novel Small-Molecule Cas9 Inhibitors by Cell-Based High-Throughput Screening. Journal of Medicinal Chemistry, 2022, 65, 3266-3305.	6.4	5
93	Exploring Selective Pressure Trade-Offs for Synthetic Addiction to Extend Metabolite Productive Lifetimes in Yeast. ACS Synthetic Biology, 2021, 10, 2842-2849.	3.8	4
94	(Meta-)genome mining for new ribo-regulators. Science, 2016, 352, 144-145.	12.6	3
95	Rapid diagnosis of lung infections. Nature Biotechnology, 2019, 37, 725-726.	17.5	3