

Gautam Dantas

List of Publications by Year in descending order

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Version: 2024-02-01

141
papers

16,750
citations

41627

51
h-index

18944

123
g-index

152
all docs

152
docs citations

152
times ranked

22047
citing authors

#	ARTICLE	IF	CITATIONS
1	Substantial overlap between symptomatic and asymptomatic genitourinary microbiota states. <i>Microbiome</i> , 2022, 10, 6.	4.9	3
2	Multi-omics investigation of <i>Clostridioides difficile</i> -colonized patients reveals pathogen and commensal correlates of <i>C. difficile</i> pathogenesis. <i>ELife</i> , 2022, 11, .	2.8	16
3	Comparative Genomics of <i>Bacteroides fragilis</i> Group Isolates Reveals Species-Dependent Resistance Mechanisms and Validates Clinical Tools for Resistance Prediction. <i>MBio</i> , 2022, 13, e0360321.	1.8	17
4	Comparative Genomics of Borderline Oxacillin-Resistant <i>Staphylococcus aureus</i> Detected during a Pseudo-outbreak of Methicillin-Resistant <i>S. aureus</i> in a Neonatal Intensive Care Unit. <i>MBio</i> , 2022, 13, e0319621.	1.8	7
5	Genetically stable CRISPR-based kill switches for engineered microbes. <i>Nature Communications</i> , 2022, 13, 672.	5.8	70
6	Structural and molecular rationale for the diversification of resistance mediated by the Antibiotic_NAT family. <i>Communications Biology</i> , 2022, 5, 263.	2.0	3
7	A Tunable and Expandable Transactivation System in Probiotic Yeast <i>Saccharomyces boulardii</i> . <i>ACS Synthetic Biology</i> , 2022, 11, 508-514.	1.9	5
8	Acute and persistent effects of commonly used antibiotics on the gut microbiome and resistome in healthy adults. <i>Cell Reports</i> , 2022, 39, 110649.	2.9	64
9	The resistance within: Antibiotic disruption of the gut microbiome and resistome dynamics in infancy. <i>Cell Host and Microbe</i> , 2022, 30, 675-683.	5.1	22
10	Persisting uropathogenic <i>Escherichia coli</i> lineages show signatures of niche-specific within-host adaptation mediated by mobile genetic elements. <i>Cell Host and Microbe</i> , 2022, 30, 1034-1047.e6.	5.1	13
11	Genomic Surveillance of Clinical <i>Pseudomonas aeruginosa</i> Isolates Reveals an Additive Effect of Carbapenemase Production on Carbapenem Resistance. <i>Microbiology Spectrum</i> , 2022, 10, .	1.2	4
12	Antibiotic-resistant organisms establish reservoirs in new hospital built environments and are related to patient blood infection isolates. <i>Communications Medicine</i> , 2022, 2, .	1.9	21
13	Draft Genome Sequence of a <i>Mycobacterium</i> Strain Isolated from a Clinical Wound Sample. <i>Microbiology Resource Announcements</i> , 2022, 11, .	0.3	1
14	Time for Some Group Therapy: Update on Identification, Antimicrobial Resistance, Taxonomy, and Clinical Significance of the <i>Bacteroides fragilis</i> Group. <i>Journal of Clinical Microbiology</i> , 2022, 60, .	1.8	7
15	The Gut Microbiome as a Reservoir for Antimicrobial Resistance. <i>Journal of Infectious Diseases</i> , 2021, 223, S209-S213.	1.9	55
16	Genomic Characterization of Emerging Bacterial Uropathogen <i>Neisseria meningitidis</i> , Which Was Misidentified as <i>Neisseria gonorrhoeae</i> by Nucleic Acid Amplification Testing. <i>Journal of Clinical Microbiology</i> , 2021, 59, .	1.8	13
17	Assessment of the Urinary Microbiota of MSM Using Urine Culturomics Reveals a Diverse Microbial Environment. <i>Clinical Chemistry</i> , 2021, 68, 192-203.	1.5	1
18	Improving ICI outcomes with a little help from my microbial friends. <i>Cell Host and Microbe</i> , 2021, 29, 155-157.	5.1	3

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19	Approaches for characterizing and tracking hospital-associated multidrug-resistant bacteria. Cellular and Molecular Life Sciences, 2021, 78, 2585-2606.	2.4	21
20	Microbiota restoration reduces antibiotic-resistant bacteria gut colonization in patients with recurrent Clostridioides difficile infection from the open-label PUNCH CD study. Genome Medicine, 2021, 13, 28.	3.6	51
21	Randomized Controlled Trial of Oral Vancomycin Treatment in Clostridioides difficile-Colonized Patients. MSphere, 2021, 6, .	1.3	20
22	Manure Microbial Communities and Resistance Profiles Reconfigure after Transition to Manure Pits and Differ from Those in Fertilized Field Soil. MBio, 2021, 12, .	1.8	13
23	Bacterial sepsis increases hippocampal fibrillar amyloid plaque load and neuroinflammation in a mouse model of Alzheimer's disease. Neurobiology of Disease, 2021, 152, 105292.	2.1	21
24	Destination shapes antibiotic resistance gene acquisitions, abundance increases, and diversity changes in Dutch travelers. Genome Medicine, 2021, 13, 79.	3.6	20
25	#8: Microbiome and immune disruption accompany mouse death in a gnotobiotic mouse model of neonatal sepsis. Journal of the Pediatric Infectious Diseases Society, 2021, 10, S6-S7.	0.6	0
26	Spontaneous Bacterial Peritonitis Caused by <i>Bordetella hinzii</i> . Emerging Infectious Diseases, 2021, 27, 2966-2968.	2.0	1
27	Antibiotic-driven intestinal dysbiosis in pediatric short bowel syndrome is associated with persistently altered microbiome functions and gut-derived bloodstream infections. Gut Microbes, 2021, 13, 1940792.	4.3	15
28	Necrotizing Enterocolitis and the Microbiome: Current Status and Future Directions. Journal of Infectious Diseases, 2021, 223, S257-S263.	1.9	32
29	Comparative Genomics of Mycobacterium avium Complex Reveals Signatures of Environment-Specific Adaptation and Community Acquisition. MSystems, 2021, 6, e0119421.	1.7	7
30	Staphylococcus aureus injection drug use-associated bloodstream infections are propagated by community outbreaks of diverse lineages. Communications Medicine, 2021, 1, .	1.9	9
31	Breakpoint beware: reliance on historical breakpoints for Enterobacteriaceae leads to discrepancies in interpretation of susceptibility testing for carbapenems and cephalosporins and gaps in detection of carbapenem-resistant organisms. European Journal of Clinical Microbiology and Infectious Diseases, 2020, 39, 187-195.	1.3	9
32	In vitro activity of meropenem/piperacillin/tazobactam triple combination therapy against clinical isolates of Staphylococcus aureus, Staphylococcus epidermidis, Staphylococcus pseudintermedius and vancomycin-resistant Enterococcus spp. International Journal of Antimicrobial Agents, 2020, 55, 105864.	1.1	5
33	Cotrimoxazole Prophylaxis Increases Resistance Gene Prevalence and α -Diversity but Decreases β -Diversity in the Gut Microbiome of Human Immunodeficiency Virus-Exposed, Uninfected Infants. Clinical Infectious Diseases, 2020, 71, 2858-2868.	2.9	35
34	Understanding the impact of antibiotic perturbation on the human microbiome. Genome Medicine, 2020, 12, 82.	3.6	148
35	The gut microbiome defines social group membership in honey bee colonies. Science Advances, 2020, 6, .	4.7	55
36	Antimicrobial resistance in enteric bacteria: current state and next-generation solutions. Gut Microbes, 2020, 12, 1799654.	4.3	41

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37	Unveiling the biodiversity of lipid species in Corynebacteria- characterization of the uncommon lipid families in <i>C.Âglutamicum</i> and pathogen <i>C. striatum</i> by mass spectrometry. <i>Biochimie</i> , 2020, 178, 158-169.	1.3	5
38	The Gut Microbiome and Resistome of Healthy Volunteers are Restructured After Short Courses of Antibiotics. <i>Infection Control and Hospital Epidemiology</i> , 2020, 41, s5-s6.	1.0	0
39	Impact of investigational microbiota therapeutic RBX2660 on the gut microbiome and resistome revealed by a placebo-controlled clinical trial. <i>Microbiome</i> , 2020, 8, 125.	4.9	41
40	Genomic Prediction of Antimicrobial Resistance: Ready or Not, Here It Comes!. <i>Clinical Chemistry</i> , 2020, 66, 1278-1289.	1.5	25
41	Tetracycline-inactivating enzymes from environmental, human commensal, and pathogenic bacteria cause broad-spectrum tetracycline resistance. <i>Communications Biology</i> , 2020, 3, 241.	2.0	97
42	Environmental remodeling of human gut microbiota and antibiotic resistome in livestock farms. <i>Nature Communications</i> , 2020, 11, 1427.	5.8	133
43	Microbiome Restoration by RBX2660 Does Not Preclude Recurrence of Multidrug-Resistant Urinary Tract Infection Following Subsequent Antibiotic Exposure: A Case Report. <i>Open Forum Infectious Diseases</i> , 2020, 7, ofaa042.	0.4	7
44	The microbiome and resistome of chimpanzees, gorillas, and humans across host lifestyle and geography. <i>ISME Journal</i> , 2020, 14, 1584-1599.	4.4	78
45	Prairie plants harbor distinct and beneficial root-endophytic bacterial communities. <i>PLoS ONE</i> , 2020, 15, e0234537.	1.1	0
46	Faropenem resistance causes in vitro cross-resistance to carbapenems in ESBL-producing <i>Escherichia coli</i> . <i>International Journal of Antimicrobial Agents</i> , 2020, 55, 105902.	1.1	9
47	Transcript Barcoding Illuminates the Expression Level of Synthetic Constructs in <i>E. coli</i> Nissle Residing in the Mammalian Gut. <i>ACS Synthetic Biology</i> , 2020, 9, 1010-1021.	1.9	15
48	Longitudinal Characterization and Transmission Dynamics of Antibiotic-Resistant Organisms in an ICU (LOCATE AROs). <i>Infection Control and Hospital Epidemiology</i> , 2020, 41, s42-s43.	1.0	0
49	Prairie plants harbor distinct and beneficial root-endophytic bacterial communities. , 2020, 15, e0234537.		0
50	Prairie plants harbor distinct and beneficial root-endophytic bacterial communities. , 2020, 15, e0234537.		0
51	Prairie plants harbor distinct and beneficial root-endophytic bacterial communities. , 2020, 15, e0234537.		0
52	Prairie plants harbor distinct and beneficial root-endophytic bacterial communities. , 2020, 15, e0234537.		0
53	Prairie plants harbor distinct and beneficial root-endophytic bacterial communities. , 2020, 15, e0234537.		0
54	Prairie plants harbor distinct and beneficial root-endophytic bacterial communities. , 2020, 15, e0234537.		0

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55	Development of <i>Rhodococcus opacus</i> as a chassis for lignin valorization and bioproduction of high-value compounds. <i>Biotechnology for Biofuels</i> , 2019, 12, 192.	6.2	35
56	Genotypic and Phenotypic Characterization of Antimicrobial Resistance in <i>Neisseria gonorrhoeae</i> : a Cross-Sectional Study of Isolates Recovered from Routine Urine Cultures in a High-Incidence Setting. <i>MSphere</i> , 2019, 4, .	1.3	8
57	A concerted systems biology analysis of phenol metabolism in <i>Rhodococcus opacus</i> PD630. <i>Metabolic Engineering</i> , 2019, 55, 120-130.	3.6	37
58	Spatiotemporal dynamics of multidrug resistant bacteria on intensive care unit surfaces. <i>Nature Communications</i> , 2019, 10, 4569.	5.8	39
59	Comparative Genomics of Antibiotic-Resistant Uropathogens Implicates Three Routes for Recurrence of Urinary Tract Infections. <i>MBio</i> , 2019, 10, .	1.8	73
60	Phenotypic and genotypic characterization of linezolid-resistant <i>Enterococcus faecium</i> from the USA and Pakistan. <i>Journal of Antimicrobial Chemotherapy</i> , 2019, 74, 3445-3452.	1.3	33
61	In Silico Analysis of <i>Gardnerella</i> Genomespecies Detected in the Setting of Bacterial Vaginosis. <i>Clinical Chemistry</i> , 2019, 65, 1375-1387.	1.5	24
62	Persistent metagenomic signatures of early-life hospitalization and antibiotic treatment in the infant gut microbiota and resistome. <i>Nature Microbiology</i> , 2019, 4, 2285-2297.	5.9	191
63	Bogotá River anthropogenic contamination alters microbial communities and promotes spread of antibiotic resistance genes. <i>Scientific Reports</i> , 2019, 9, 11764.	1.6	29
64	Complex interactions between the microbiome and cancer immune therapy. <i>Critical Reviews in Clinical Laboratory Sciences</i> , 2019, 56, 567-585.	2.7	28
65	Urinary tract colonization is enhanced by a plasmid that regulates uropathogenic <i>Acinetobacter baumannii</i> chromosomal genes. <i>Nature Communications</i> , 2019, 10, 2763.	5.8	80
66	Genomic and Metagenomic Approaches for Predictive Surveillance of Emerging Pathogens and Antibiotic Resistance. <i>Clinical Pharmacology and Therapeutics</i> , 2019, 106, 512-524.	2.3	33
67	Sequencing-based methods and resources to study antimicrobial resistance. <i>Nature Reviews Genetics</i> , 2019, 20, 356-370.	7.7	263
68	Semisynthetic Analogues of Anhydrotetracycline as Inhibitors of Tetracycline Destructase Enzymes. <i>ACS Infectious Diseases</i> , 2019, 5, 618-633.	1.8	24
69	Adaptive Strategies of the Candidate Probiotic <i>E. coli</i> Nissle in the Mammalian Gut. <i>Cell Host and Microbe</i> , 2019, 25, 499-512.e8.	5.1	94
70	Discovery and Characterization of a Nitroreductase Capable of Conferring Bacterial Resistance to Chloramphenicol. <i>Cell Chemical Biology</i> , 2019, 26, 559-570.e6.	2.5	45
71	2847. Comparative Genomics and Clonal Tracking of Multi-drug-Resistant Uropathogens Implicates the Fecal Microbiome as a Potential Reservoir for Recurrent Urinary Tract Infections. <i>Open Forum Infectious Diseases</i> , 2019, 6, S70-S71.	0.4	1
72	Insights into How Probiotics Colonize the Healthy Human Gut. <i>Gastroenterology</i> , 2019, 156, 820-822.	0.6	5

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73	Multidrug-resistant plasmids repress chromosomally encoded T6SS to enable their dissemination. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 1378-1383.	3.3	83
74	Genomic Characterization of Antibiotic Resistant <i>Escherichia coli</i> Isolated From Domestic Chickens in Pakistan. <i>Frontiers in Microbiology</i> , 2019, 10, 3052.	1.5	23
75	Multiscale Evolutionary Dynamics of Host-Associated Microbiomes. <i>Cell</i> , 2018, 172, 1216-1227.	13.5	85
76	bla _{IMP-27} on transferable plasmids in <i>Proteus mirabilis</i> and <i>Providencia rettgeri</i> . <i>Clinical Microbiology and Infection</i> , 2018, 24, 1019.e5-1019.e8.	2.8	22
77	Checkpoint Checkmate: Microbiota Modulation of Cancer Immunotherapy. <i>Clinical Chemistry</i> , 2018, 64, 1280-1283.	1.5	3
78	Shared strategies for β -lactam catabolism in the soil microbiome. <i>Nature Chemical Biology</i> , 2018, 14, 556-564.	3.9	67
79	Impact of Amoxicillin-Clavulanate followed by Autologous Fecal Microbiota Transplantation on Fecal Microbiome Structure and Metabolic Potential. <i>MSphere</i> , 2018, 3, .	1.3	17
80	Lipid metabolism of phenol-tolerant <i>Rhodococcus opacus</i> strains for lignin bioconversion. <i>Biotechnology for Biofuels</i> , 2018, 11, 339.	6.2	23
81	Population Structure, Antibiotic Resistance, and Uropathogenicity of <i>Klebsiella variicola</i> . <i>MBio</i> , 2018, 9, .	1.8	61
82	Infant diet and maternal gestational weight gain predict early metabolic maturation of gut microbiomes. <i>Nature Medicine</i> , 2018, 24, 1822-1829.	15.2	162
83	Characterization of Wild and Captive Baboon Gut Microbiota and Their Antibiotic Resistomes. <i>MSystems</i> , 2018, 3, .	1.7	51
84	Multi-omic elucidation of aromatic catabolism in adaptively evolved <i>Rhodococcus opacus</i> . <i>Metabolic Engineering</i> , 2018, 49, 69-83.	3.6	50
85	<i>Superficieibacter electus</i> gen. nov., sp. nov., an Extended-Spectrum β -Lactamase Possessing Member of the Enterobacteriaceae Family, Isolated From Intensive Care Unit Surfaces. <i>Frontiers in Microbiology</i> , 2018, 9, 1629.	1.5	14
86	Mechanism of High-Level Daptomycin Resistance in <i>Corynebacterium striatum</i> . <i>MSphere</i> , 2018, 3, .	1.3	28
87	Close Encounters of Three Kinds: Bacteriophages, Commensal Bacteria, and Host Immunity. <i>Trends in Microbiology</i> , 2018, 26, 943-954.	3.5	70
88	Plasticity, dynamics, and inhibition of emerging tetracycline resistance enzymes. <i>Nature Chemical Biology</i> , 2017, 13, 730-736.	3.9	93
89	Next-generation approaches to understand and combat the antibiotic resistome. <i>Nature Reviews Microbiology</i> , 2017, 15, 422-434.	13.6	438
90	Draft Genome Sequence of a <i>Salmonella enterica</i> Serovar Typhi Strain Resistant to Fourth-Generation Cephalosporin and Fluoroquinolone Antibiotics. <i>Genome Announcements</i> , 2017, 5, .	0.8	9

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91	Draft Genome Sequences of Three β -Lactam-Catabolizing Soil Proteobacteria. <i>Genome Announcements</i> , 2017, 5, .	0.8	11
92	Draft Genome Sequence of the bla OXA-436 - and bla NDM-1 -Harboring <i>Shewanella putrefaciens</i> SA70 Isolate. <i>Genome Announcements</i> , 2017, 5, .	0.8	5
93	Structural and Functional Survey of Environmental Aminoglycoside Acetyltransferases Reveals Functionality of Resistance Enzymes. <i>ACS Infectious Diseases</i> , 2017, 3, 653-665.	1.8	9
94	Genomic and functional techniques to mine the microbiome for novel antimicrobials and antimicrobial resistance genes. <i>Annals of the New York Academy of Sciences</i> , 2017, 1388, 42-58.	1.8	38
95	Functional Metagenomics to Study Antibiotic Resistance. <i>Methods in Molecular Biology</i> , 2017, 1520, 307-329.	0.4	29
96	Draft Genome Sequence of the Naturally Competent <i>Bacillus simplex</i> Strain WY10. <i>Genome Announcements</i> , 2017, 5, .	0.8	1
97	2322. <i>Journal of Clinical and Translational Science</i> , 2017, 1, 35-35.	0.3	0
98	Evaluation of Machine Learning and Rules-Based Approaches for Predicting Antimicrobial Resistance Profiles in Gram-negative Bacilli from Whole Genome Sequence Data. <i>Frontiers in Microbiology</i> , 2016, 7, 1887.	1.5	88
99	Simulating Serial-Target Antibacterial Drug Synergies Using Flux Balance Analysis. <i>PLoS ONE</i> , 2016, 11, e0147651.	1.1	14
100	Transcriptomic analysis illuminates genes involved in chlorophyll synthesis after nitrogen starvation in <i>Acaryochloris</i> sp. CCME 5410. <i>Photosynthesis Research</i> , 2016, 129, 171-182.	1.6	27
101	The effects of antibiotics on the microbiome throughout development and alternative approaches for therapeutic modulation. <i>Genome Medicine</i> , 2016, 8, 39.	3.6	676
102	Interconnected microbiomes and resistomes in low-income human habitats. <i>Nature</i> , 2016, 533, 212-216.	13.7	425
103	Contextual organismality: Beyond pattern to process in the emergence of organisms. <i>Evolution; International Journal of Organic Evolution</i> , 2016, 70, 2669-2677.	1.1	10
104	The rapid spread of carbapenem-resistant Enterobacteriaceae. <i>Drug Resistance Updates</i> , 2016, 29, 30-46.	6.5	282
105	Antibiotic perturbation of the preterm infant gut microbiome and resistome. <i>Gut Microbes</i> , 2016, 7, 443-449.	4.3	102
106	Developmental dynamics of the preterm infant gut microbiota and antibiotic resistome. <i>Nature Microbiology</i> , 2016, 1, 16024.	5.9	346
107	Comparative transcriptomics elucidates adaptive phenol tolerance and utilization in lipid-accumulating <i>Rhodococcus opacus</i> PD630. <i>Nucleic Acids Research</i> , 2016, 44, 2240-2254.	6.5	105
108	Identification of Genes Conferring Tolerance to Lignocellulose-Derived Inhibitors by Functional Selections in Soil Metagenomes. <i>Applied and Environmental Microbiology</i> , 2016, 82, 528-537.	1.4	20

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109	Gut resistome development in healthy twin pairs in the first year of life. <i>Microbiome</i> , 2015, 3, 27.	4.9	88
110	Functional Characterization of Bacteria Isolated from Ancient Arctic Soil Exposes Diverse Resistance Mechanisms to Modern Antibiotics. <i>PLoS ONE</i> , 2015, 10, e0069533.	1.1	202
111	The Tetracycline Destructases: A Novel Family of Tetracycline-Inactivating Enzymes. <i>Chemistry and Biology</i> , 2015, 22, 888-897.	6.2	140
112	Antibiotics and the developing infant gut microbiota and resistome. <i>Current Opinion in Microbiology</i> , 2015, 27, 51-56.	2.3	184
113	The microbiome of uncontacted Amerindians. <i>Science Advances</i> , 2015, 1, .	4.7	721
114	KPC and NDM-1 Genes in Related <i>Enterobacteriaceae</i> Strains and Plasmids from Pakistan and the United States. <i>Emerging Infectious Diseases</i> , 2015, 21, 1034-1037.	2.0	55
115	Synergistic, collaterally sensitive β -lactam combinations suppress resistance in MRSA. <i>Nature Chemical Biology</i> , 2015, 11, 855-861.	3.9	126
116	Improved annotation of antibiotic resistance determinants reveals microbial resistomes cluster by ecology. <i>ISME Journal</i> , 2015, 9, 207-216.	4.4	540
117	High-Specificity Targeted Functional Profiling in Microbial Communities with ShortBRED. <i>PLoS Computational Biology</i> , 2015, 11, e1004557.	1.5	235
118	Bacterial phylogeny structures soil resistomes across habitats. <i>Nature</i> , 2014, 509, 612-616.	13.7	973
119	Longitudinal analysis of microbial interaction between humans and the indoor environment. <i>Science</i> , 2014, 345, 1048-1052.	6.0	751
120	The Yin and Yang of Bacterial Resilience in the Human Gut Microbiota. <i>Journal of Molecular Biology</i> , 2014, 426, 3866-3876.	2.0	58
121	How to Fight Back Against Antibiotic Resistance. <i>American Scientist</i> , 2014, 102, 42.	0.1	51
122	Experimental Approaches for Defining Functional Roles of Microbes in the Human Gut. <i>Annual Review of Microbiology</i> , 2013, 67, 459-475.	2.9	39
123	Novel resistance functions uncovered using functional metagenomic investigations of resistance reservoirs. <i>Frontiers in Microbiology</i> , 2013, 4, 145.	1.5	79
124	Pediatric Fecal Microbiota Harbor Diverse and Novel Antibiotic Resistance Genes. <i>PLoS ONE</i> , 2013, 8, e78822.	1.1	150
125	The Shared Antibiotic Resistome of Soil Bacteria and Human Pathogens. <i>Science</i> , 2012, 337, 1107-1111.	6.0	1,314
126	Context matters – the complex interplay between resistome genotypes and resistance phenotypes. <i>Current Opinion in Microbiology</i> , 2012, 15, 577-582.	2.3	97

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127	Antibiotics and the resistant microbiome. <i>Current Opinion in Microbiology</i> , 2011, 14, 556-563.	2.3	140
128	Tackling antibiotic resistance. <i>Nature Reviews Microbiology</i> , 2011, 9, 894-896.	13.6	919
129	Extensive personal human gut microbiota culture collections characterized and manipulated in gnotobiotic mice. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 6252-6257.	3.3	656
130	Functional Metagenomic Investigations of the Human Intestinal Microbiota. <i>Frontiers in Microbiology</i> , 2011, 2, 188.	1.5	44
131	The human microbiome harbors a diverse reservoir of antibiotic resistance genes. <i>Virulence</i> , 2010, 1, 299-303.	1.8	166
132	A functional metagenomic approach for expanding the synthetic biology toolbox for biomass conversion. <i>Molecular Systems Biology</i> , 2010, 6, 360.	3.2	64
133	Functional Characterization of the Antibiotic Resistance Reservoir in the Human Microflora. <i>Science</i> , 2009, 325, 1128-1131.	6.0	748
134	Bacteria Subsisting on Antibiotics. <i>Science</i> , 2008, 320, 100-103.	6.0	499
135	High-resolution Structural and Thermodynamic Analysis of Extreme Stabilization of Human Procarboxypeptidase by Computational Protein Design. <i>Journal of Molecular Biology</i> , 2007, 366, 1209-1221.	2.0	84
136	Mis-translation of a Computationally Designed Protein Yields an Exceptionally Stable Homodimer: Implications for Protein Engineering and Evolution. <i>Journal of Molecular Biology</i> , 2006, 362, 1004-1024.	2.0	29
137	High-Resolution Structural Validation of the Computational Redesign of Human U1A Protein. <i>Structure</i> , 2006, 14, 847-856.	1.6	19
138	¹ H, ¹³ C and ¹⁵ N Resonance Assignments of URNdesign, a Computationally Redesigned RRM Protein. <i>Journal of Biomolecular NMR</i> , 2005, 33, 135-135.	1.6	0
139	Design of a Novel Globular Protein Fold with Atomic-Level Accuracy. <i>Science</i> , 2003, 302, 1364-1368.	6.0	1,471
140	A Large Scale Test of Computational Protein Design: Folding and Stability of Nine Completely Redesigned Globular Proteins. <i>Journal of Molecular Biology</i> , 2003, 332, 449-460.	2.0	293
141	Synthesis of Polyazamacrocyclic Compounds via Modified Richman's Atkins Cyclization of β^2 -Trimethylsilylethanesulfonamides. <i>Journal of Organic Chemistry</i> , 2001, 66, 2722-2725.	1.7	34