

Andrew L Goodman

List of Publications by Year in descending order

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53
papers

14,337
citations

81900

39
h-index

175258

52
g-index

55
all docs

55
docs citations

55
times ranked

18832
citing authors

#	ARTICLE	IF	CITATIONS
1	Cancer Microbiology. Journal of the National Cancer Institute, 2022, 114, 651-663.	6.3	4
2	Obeticholic Acid Decreases Intestinal Content of Enterococcus in Rats With Cirrhosis and Ascites. Hepatology Communications, 2021, 5, 1507-1517.	4.3	4
3	A Common Pathway for Activation of Host-Targeting and Bacteria-Targeting Toxins in Human Intestinal Bacteria. MBio, 2021, 12, e0065621.	4.1	5
4	Insights from pharmacokinetic models of host-microbiome drug metabolism. Gut Microbes, 2020, 11, 587-596.	9.8	27
5	Genetic Manipulation of Wild Human Gut <i>Bacteroides</i> . Journal of Bacteriology, 2020, 202, .	2.2	33
6	Sphingolipids produced by gut bacteria enter host metabolic pathways impacting ceramide levels. Nature Communications, 2020, 11, 2471.	12.8	172
7	A decade of advances in transposon-insertion sequencing. Nature Reviews Genetics, 2020, 21, 526-540.	16.3	228
8	B vitamin acquisition by gut commensal bacteria. PLoS Pathogens, 2020, 16, e1008208.	4.7	48
9	A Master Regulator of <i>Bacteroides thetaiotaomicron</i> Gut Colonization Controls Carbohydrate Utilization and an Alternative Protein Synthesis Factor. MBio, 2020, 11, .	4.1	22
10	Mapping human microbiome drug metabolism by gut bacteria and their genes. Nature, 2019, 570, 462-467.	27.8	666
11	Pathogenic Autoreactive T and B Cells Cross-React with Mimotopes Expressed by a Common Human Gut Commensal to Trigger Autoimmunity. Cell Host and Microbe, 2019, 26, 100-113.e8.	11.0	109
12	Genome-Wide Screening for Enteric Colonization Factors in Carbapenem-Resistant ST258 <i>Klebsiella pneumoniae</i> . MBio, 2019, 10, .	4.1	32
13	Separating host and microbiome contributions to drug pharmacokinetics and toxicity. Science, 2019, 363, .	12.6	281
14	Dietary sugar silences a colonization factor in a mammalian gut symbiont. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 233-238.	7.1	71
15	Topical application of aminoglycoside antibiotics enhances host resistance to viral infections in a microbiota-independent manner. Nature Microbiology, 2018, 3, 611-621.	13.3	80
16	Dot/Icm-Translocated Proteins Important for Biogenesis of the <i>Coxiella burnetii</i> -Containing Vacuole Identified by Screening of an Effector Mutant Sublibrary. Infection and Immunity, 2018, 86, .	2.2	33
17	Commensal orthologs of the human autoantigen Ro60 as triggers of autoimmunity in lupus. Science Translational Medicine, 2018, 10, .	12.4	226
18	The Stringent Response Determines the Ability of a Commensal Bacterium to Survive Starvation and to Persist in the Gut. Cell Host and Microbe, 2018, 24, 120-132.e6.	11.0	50

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19	Human gut <i>Bacteroides</i> capture vitamin B12 via cell surface-exposed lipoproteins. <i>ELife</i> , 2018, 7, .	6.0	81
20	Engineered Regulatory Systems Modulate Gene Expression of Human Commensals in the Gut. <i>Cell</i> , 2017, 169, 547-558.e15.	28.9	147
21	An insider's perspective: <i>Bacteroides</i> as a window into the microbiome. <i>Nature Microbiology</i> , 2017, 2, 17026.	13.3	416
22	Enhancement of IFN γ Production by Distinct Commensals Ameliorates Salmonella-Induced Disease. <i>Cell Host and Microbe</i> , 2017, 21, 682-694.e5.	11.0	91
23	The Landscape of Type VI Secretion across Human Gut Microbiomes Reveals Its Role in Community Composition. <i>Cell Host and Microbe</i> , 2017, 22, 411-419.e4.	11.0	137
24	Multiple <i>Legionella pneumophila</i> effector virulence phenotypes revealed through high-throughput analysis of targeted mutant libraries. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E10446-E10454.	7.1	81
25	Metabolic and fitness determinants for in vitro growth and intestinal colonization of the bacterial pathogen <i>Campylobacter jejuni</i> . <i>PLoS Biology</i> , 2017, 15, e2001390.	5.6	58
26	Human symbionts inject and neutralize antibacterial toxins to persist in the gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 3639-3644.	7.1	190
27	Characterizing the Interactions between a Naturally Primed Immunoglobulin A and Its Conserved <i>Bacteroides thetaiotaomicron</i> Species-specific Epitope in Gnotobiotic Mice. <i>Journal of Biological Chemistry</i> , 2015, 290, 12630-12649.	3.4	52
28	Novel Components of the Flagellar System in Epsilonproteobacteria. <i>MBio</i> , 2014, 5, e01349-14.	4.1	57
29	Global discovery of colonization determinants in the squid symbiont <i>Vibrio fischeri</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 17284-17289.	7.1	93
30	Vitamin B 12 as a Modulator of Gut Microbial Ecology. <i>Cell Metabolism</i> , 2014, 20, 769-778.	16.2	356
31	A Type VI Secretion-Related Pathway in Bacteroidetes Mediates Interbacterial Antagonism. <i>Cell Host and Microbe</i> , 2014, 16, 227-236.	11.0	311
32	Immunoglobulin A Coating Identifies Colitogenic Bacteria in Inflammatory Bowel Disease. <i>Cell</i> , 2014, 158, 1000-1010.	28.9	982
33	Human Gut Microbes Use Multiple Transporters to Distinguish Vitamin B12 Analogs and Compete in the Gut. <i>Cell Host and Microbe</i> , 2014, 15, 47-57.	11.0	225
34	The Long-Term Stability of the Human Gut Microbiota. <i>Science</i> , 2013, 341, 1237439.	12.6	1,696
35	Experimental Approaches for Defining Functional Roles of Microbes in the Human Gut. <i>Annual Review of Microbiology</i> , 2013, 67, 459-475.	7.3	39
36	Identifying microbial fitness determinants by insertion sequencing using genome-wide transposon mutant libraries. <i>Nature Protocols</i> , 2011, 6, 1969-1980.	12.0	156

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37	The Impact of a Consortium of Fermented Milk Strains on the Gut Microbiome of Gnotobiotic Mice and Monozygotic Twins. <i>Science Translational Medicine</i> , 2011, 3, 106ra106.	12.4	456
38	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.	7.1	656
39	Human nutrition, the gut microbiome and the immune system. <i>Nature</i> , 2011, 474, 327-336.	27.8	2,175
40	The two-component sensor response regulator RoxS/RoxR plays a role in <i>Pseudomonas aeruginosa</i> interactions with airway epithelial cells. <i>Microbes and Infection</i> , 2010, 12, 190-198.	1.9	18
41	Creating and characterizing communities of human gut microbes in gnotobiotic mice. <i>ISME Journal</i> , 2010, 4, 1094-1098.	9.8	116
42	Sit and Stay a While: How BfiSR Controls Irreversible Attachment in <i>Pseudomonas aeruginosa</i> Biofilms. <i>Journal of Bacteriology</i> , 2010, 192, 5273-5274.	2.2	5
43	Our Unindicted Coconspirators: Human Metabolism from a Microbial Perspective. <i>Cell Metabolism</i> , 2010, 12, 111-116.	16.2	64
44	Direct interaction between sensor kinase proteins mediates acute and chronic disease phenotypes in a bacterial pathogen. <i>Genes and Development</i> , 2009, 23, 249-259.	5.9	272
45	Identifying Genetic Determinants Needed to Establish a Human Gut Symbiont in Its Habitat. <i>Cell Host and Microbe</i> , 2009, 6, 279-289.	11.0	612
46	In vivo imaging and genetic analysis link bacterial motility and symbiosis in the zebrafish gut. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 7622-7627.	7.1	154
47	Modulation of Bacterial Lifestyles via Two-Component Regulatory Networks. , 2007, , 311-340.		0
48	A Virulence Locus of <i>Pseudomonas aeruginosa</i> Encodes a Protein Secretion Apparatus. <i>Science</i> , 2006, 312, 1526-1530.	12.6	984
49	Multiple sensors control reciprocal expression of <i>Pseudomonas aeruginosa</i> regulatory RNA and virulence genes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 171-176.	7.1	401
50	<i>Pseudomonas aeruginosa</i> regulates flagellin expression as part of a global response to airway fluid from cystic fibrosis patients. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 6664-6668.	7.1	131
51	A Signaling Network Reciprocally Regulates Genes Associated with Acute Infection and Chronic Persistence in <i>Pseudomonas aeruginosa</i> . <i>Developmental Cell</i> , 2004, 7, 745-754.	7.0	559
52	Analysis of regulatory networks in <i>Pseudomonas aeruginosa</i> by genomewide transcriptional profiling. <i>Current Opinion in Microbiology</i> , 2004, 7, 39-44.	5.1	64
53	A four-tiered transcriptional regulatory circuit controls flagellar biogenesis in <i>Pseudomonas aeruginosa</i> . <i>Molecular Microbiology</i> , 2003, 50, 809-824.	2.5	404