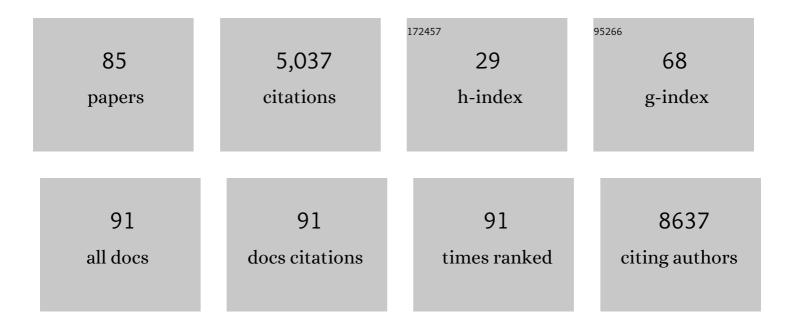
Daniel N Frank

List of Publications by Year in descending order

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DANIEL N EDANK

#	Article	IF	CITATIONS
1	A dysbiotic microbiome promotes head and neck squamous cell carcinoma. Oncogene, 2022, 41, 1269-1280.	5.9	32
2	Age and Injury Size Influence the Magnitude of Fecal Dysbiosis in Adult Burn Patients. Journal of Burn Care and Research, 2022, , .	0.4	6
3	Granzyme B ⁺ CD4 T cells accumulate in the colon during chronic HIV-1 infection. Gut Microbes, 2022, 14, 2045852.	9.8	3
4	Microbiota Associated With Cholesteatoma Tissue in Chronic Suppurative Otitis Media. Frontiers in Cellular and Infection Microbiology, 2022, 12, 746428.	3.9	3
5	Infection and inflammation in chronic rhinosinusitis: Gene ontology/pathway analysis perspective. International Forum of Allergy and Rhinology, 2022, 12, 1566-1569.	2.8	1
6	Otitis media susceptibility and shifts in the head and neck microbiome due to <i>SPINK5</i> variants. Journal of Medical Genetics, 2021, 58, 442-452.	3.2	14
7	Altered tissue specialized pro-resolving mediators in chronic rhinosinusitis. Prostaglandins Leukotrienes and Essential Fatty Acids, 2021, 164, 102218.	2.2	18
8	tidyMicro: a pipeline for microbiome data analysis and visualization using the tidyverse in R. BMC Bioinformatics, 2021, 22, 41.	2.6	12
9	A Unique Gut Microbiome–Physical Function Axis Exists in Older People with HIV: An Exploratory Study. AIDS Research and Human Retroviruses, 2021, 37, 542-550.	1.1	4
10	Impact of preoperative antibiotics and other variables on integrated microbiome-host transcriptomic data generated from colorectal cancer resections. World Journal of Gastroenterology, 2021, 27, 1465-1482.	3.3	4
11	Multiomic Predictors of Shortâ€Term Weight Loss and Clinical Outcomes During a Behavioralâ€Based Weight Loss Intervention. Obesity, 2021, 29, 859-869.	3.0	9
12	Combined Oral Contraceptive Treatment Does Not Alter the Gut Microbiome or Serum Metabolomic Profile in Obese Girls with Polycystic Ovary Syndrome. Journal of the Endocrine Society, 2021, 5, A711-A712.	0.2	0
13	Specialized pro-resolving mediator lipidome and 16S rRNA bacterial microbiome data associated with human chronic rhinosinusitis. Data in Brief, 2021, 36, 107023.	1.0	2
14	The role of CDHR3 in susceptibility to otitis media. Journal of Molecular Medicine, 2021, 99, 1571-1583.	3.9	4
15	The Short-Chain Fatty Acid Butyrate Attenuates Pulmonary Vascular Remodeling and Inflammation in Hypoxia-Induced Pulmonary Hypertension. International Journal of Molecular Sciences, 2021, 22, 9916.	4.1	28
16	The Gut Microbiota during a Behavioral Weight Loss Intervention. Nutrients, 2021, 13, 3248.	4.1	23
17	An exercise intervention alters stool microbiota and metabolites among older, sedentary adults. Therapeutic Advances in Infectious Disease, 2021, 8, 204993612110270.	1.8	16
18	Hepatic steatosis relates to gastrointestinal microbiota changes in obese girls with polycystic ovary syndrome. PLoS ONE, 2021, 16, e0245219.	2.5	14

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19	The FUT2 Variant c.461G>A (p.Trp154*) Is Associated With Differentially Expressed Genes and Nasopharyngeal Microbiota Shifts in Patients With Otitis Media. Frontiers in Cellular and Infection Microbiology, 2021, 11, 798246.	3.9	6
20	Effects of Complementary Feeding With Different Protein-Rich Foods on Infant Growth and Gut Health: Study Protocol. Frontiers in Pediatrics, 2021, 9, 793215.	1.9	4
21	Advanced Age Impairs Intestinal Antimicrobial Peptide Response and Worsens Fecal Microbiome Dysbiosis Following Burn Injury in Mice. Shock, 2020, 53, 71-77.	2.1	24
22	Gestational Diabetes Is Uniquely Associated With Altered Early Seeding of the Infant Gut Microbiota. Frontiers in Endocrinology, 2020, 11, 603021.	3.5	41
23	Multi-omic studies on missense PLG variants in families with otitis media. Scientific Reports, 2020, 10, 15035.	3.3	4
24	Randomized, Placebo-Controlled Trial of Rifaximin Therapy for Lowering Gut-Derived Cardiovascular Toxins and Inflammation in CKD. Kidney360, 2020, 1, 1206-1216.	2.1	10
25	Muc5ac Expression Protects the Colonic Barrier in Experimental Colitis. Inflammatory Bowel Diseases, 2020, 26, 1353-1367.	1.9	30
26	Crohn's Disease Differentially Affects Region-Specific Composition and Aerotolerance Profiles of Mucosally Adherent Bacteria. Inflammatory Bowel Diseases, 2020, 26, 1843-1855.	1.9	9
27	Bile acid sequestration reverses liver injury and prevents progression of nonalcoholic steatohepatitis in Western diet–fed mice. Journal of Biological Chemistry, 2020, 295, 4733-4747.	3.4	37
28	Obese Adolescents With PCOS Have Altered Biodiversity and Relative Abundance in Gastrointestinal Microbiota. Journal of Clinical Endocrinology and Metabolism, 2020, 105, e2134-e2144.	3.6	83
29	Nutrimetabolomics reveals food-specific compounds in urine of adults consuming a DASH-style diet. Scientific Reports, 2020, 10, 1157.	3.3	18
30	Different Gut Microbial Profiles in Sub-Saharan African and South Asian Women of Childbearing Age Are Primarily Associated With Dietary Intakes. Frontiers in Microbiology, 2019, 10, 1848.	3.5	16
31	Expression of Bitter Taste Receptors and Solitary Chemosensory Cell Markers in the Human Sinonasal Cavity. Chemical Senses, 2019, 44, 483-495.	2.0	17
32	Among older adults, age-related changes in the stool microbiome differ by HIV-1 serostatus. EBioMedicine, 2019, 40, 583-594.	6.1	23
33	Oral vitamin B ₁₂ supplement is delivered to the distal gut, altering the corrinoid profile and selectively depleting <i>Bacteroides</i> in C57BL/6 mice. Gut Microbes, 2019, 10, 654-662.	9.8	28
34	Influence of Crohn's disease related polymorphisms in innate immune function on ileal microbiome. PLoS ONE, 2019, 14, e0213108.	2.5	13
35	The Acute Influence of Acid Suppression with Esomeprazole on Gastrointestinal Microbiota and Brain Gene Expression Profiles in a Murine Model of Restraint Stress. Neuroscience, 2019, 398, 206-217.	2.3	11
36	High-fat diet exacerbates SIV pathogenesis and accelerates disease progression. Journal of Clinical Investigation, 2019, 129, 5474-5488.	8.2	31

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37	Identification of Novel Genes and Biological Pathways That Overlap in Infectious and Nonallergic Diseases of the Upper and Lower Airways Using Network Analyses. Frontiers in Genetics, 2019, 10, 1352.	2.3	9
38	Time Course of C-Reactive Protein and Procalcitonin Levels During the Treatment of Acute Bacterial Skin Infections. Open Forum Infectious Diseases, 2018, 5, ofy029.	0.9	7
39	Modulation of Inflammatory Arthritis in Mice by Gut Microbiota Through Mucosal Inflammation and Autoantibody Generation. Arthritis and Rheumatology, 2018, 70, 1220-1233.	5.6	126
40	Genomic evolution of Staphylococcus aureus isolates colonizing the nares and progressing to bacteremia. PLoS ONE, 2018, 13, e0195860.	2.5	17
41	The gut microbiota in infants of obese mothers increases inflammation and susceptibility to NAFLD. Nature Communications, 2018, 9, 4462.	12.8	205
42	Microbiome in patients with upper airway disease: Moving from taxonomic findings to mechanisms and causality. Journal of Allergy and Clinical Immunology, 2018, 142, 73-75.	2.9	14
43	Functional intraepithelial lymphocyte changes in inflammatory bowel disease and spondyloarthritis have disease specific correlations with intestinal microbiota. Arthritis Research and Therapy, 2018, 20, 149.	3.5	39
44	Probiotic supplements prevented oxonic acid-induced hyperuricemia and renal damage. PLoS ONE, 2018, 13, e0202901.	2.5	57
45	Determinants of the Nasal Microbiome: Pilot Study of Effects of Intranasal Medication Use. Allergy and Rhinology, 2018, 9, 215265671878951.	1.6	21
46	Longitudinal microbiome analysis of single donor fecal microbiota transplantation in patients with recurrent Clostridium difficile infection and/or ulcerative colitis. PLoS ONE, 2018, 13, e0190997.	2.5	29
47	Evaluation of bloodstream infections, Clostridium difficile infections, and gut microbiota in pediatric oncology patients. PLoS ONE, 2018, 13, e0191232.	2.5	22
48	Reply to M Gotteland and F Magne. American Journal of Clinical Nutrition, 2017, 105, 234-236.	4.7	0
49	Expression of immunoglobulin D is increased in chronic rhinosinusitis. Annals of Allergy, Asthma and Immunology, 2017, 119, 317-323.e1.	1.0	11
50	Low abundance of colonic butyrate-producing bacteria in HIV infection is associated with microbial translocation and immune activation. Aids, 2017, 31, 511-521.	2.2	123
51	Investigation of sinonasal microbiome spatial organization in chronic rhinosinusitis. International Forum of Allergy and Rhinology, 2017, 7, 16-23.	2.8	43
52	Iron in Micronutrient Powder Promotes an Unfavorable Gut Microbiota in Kenyan Infants. Nutrients, 2017, 9, 776.	4.1	65
53	Early Microbes Modify Immune System Development and Metabolic Homeostasis—The "Restaurant― Hypothesis Revisited. Frontiers in Endocrinology, 2017, 8, 349.	3.5	86
54	Group B Streptococci Colonization in Pregnant Guatemalan Women: Prevalence, Risk Factors, and Vaginal Microbiome. Open Forum Infectious Diseases, 2017, 4, ofx020.	0.9	37

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55	Implication of the intestinal microbiome as a potential surrogate marker of immune responsiveness to experimental therapies in autoimmune diabetes. PLoS ONE, 2017, 12, e0173968.	2.5	7
56	Maternal treatment with short-chain fatty acids modulates the intestinal microbiota and immunity and ameliorates type 1 diabetes in the offspring. PLoS ONE, 2017, 12, e0183786.	2.5	46
57	Influence of Gelatin-Thrombin Matrix Tissue Sealant on Bacterial Colony Formation and Risk of Pelvic Infection. Infectious Diseases in Obstetrics and Gynecology, 2016, 2016, 1-6.	1.5	0
58	Immune Responses to Circulating and Vaccine Viral Strains in HIV-Infected and Uninfected Children and Youth Who Received the 2013/2014 Quadrivalent Live-Attenuated Influenza Vaccine. Frontiers in Immunology, 2016, 7, 142.	4.8	3
59	Antibody responses to influenza a H1N1 vaccine compared to the circulating strain in influenza vaccine recipients during the 2013/2014 season in North America. Journal of Clinical Virology, 2016, 83, 56-60.	3.1	1
60	Whole-Genome Sequencing Identifies <i>In Vivo</i> Acquisition of a <i>bla</i> _{CTX-M-27} -Carrying IncFII Transmissible Plasmid as the Cause of Ceftriaxone Treatment Failure for an Invasive Salmonella enterica Serovar Typhimurium Infection. Antimicrobial Agents and Chemotherapy, 2016, 60, 7224-7235.	3.2	26
61	Complete Genome Sequence of <i>Escherichia coli</i> ER1821R, a Laboratory K-12 Derivative Engineered To Be Deficient in All Methylcytosine and Methyladenine Restriction Systems. Genome Announcements, 2016, 4, .	0.8	4
62	Mode of Delivery Determines Neonatal Pharyngeal Bacterial Composition and Early Intestinal Colonization. Journal of Pediatric Gastroenterology and Nutrition, 2016, 63, 320-328.	1.8	43
63	Enhancement of HIV-1 infection and intestinal CD4+ T cell depletion ex vivo by gut microbes altered during chronic HIV-1 infection. Retrovirology, 2016, 13, 5.	2.0	60
64	Comparison of Whole-Genome Sequencing and Molecular-Epidemiological Techniques for <i>Clostridium difficile</i> Strain Typing. Journal of the Pediatric Infectious Diseases Society, 2016, 5, 329-332.	1.3	12
65	Antibiotic and Antiinflammatory Therapy Transiently Reduces Inflammation and Hypercoagulation in Acutely SIV-Infected Pigtailed Macaques. PLoS Pathogens, 2016, 12, e1005384.	4.7	38
66	Impact of cigarette smoking on the middle meatus microbiome in health and chronic rhinosinusitis. International Forum of Allergy and Rhinology, 2015, 5, 981-989.	2.8	46
67	Comparison of Fecal Microbiota in Children with Autism Spectrum Disorders and Neurotypical Siblings in the Simons Simplex Collection. PLoS ONE, 2015, 10, e0137725.	2.5	173
68	Effects of Vaccination with 10-Valent Pneumococcal Non-Typeable Haemophilus influenza Protein D Conjugate Vaccine (PHiD-CV) on the Nasopharyngeal Microbiome of Kenyan Toddlers. PLoS ONE, 2015, 10, e0128064.	2.5	26
69	Identification of Candidate Adherent-Invasive E. coli Signature Transcripts by Genomic/Transcriptomic Analysis. PLoS ONE, 2015, 10, e0130902.	2.5	40
70	Perilipin-2 Modulates Lipid Absorption and Microbiome Responses in the Mouse Intestine. PLoS ONE, 2015, 10, e0131944.	2.5	43
71	Molecular analysis of single room humidifier bacteriology. Water Research, 2015, 69, 318-327.	11.3	9
72	Alterations in Intestinal Microbiota Correlate With Susceptibility to Type 1 Diabetes. Diabetes, 2015, 64, 3510-3520.	0.6	246

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73	High-Resolution Microbial Community Succession of Microbially Induced Concrete Corrosion in Working Sanitary Manholes. PLoS ONE, 2015, 10, e0116400.	2.5	30
74	Sinus microbiota varies among chronic rhinosinusitis phenotypes and predicts surgical outcome. Journal of Allergy and Clinical Immunology, 2015, 136, 334-342.e1.	2.9	158
75	Response to Comment on Alkanani et al. Alterations in Intestinal Microbiota Correlate With Susceptibility to Type 1 Diabetes. Diabetes 2015;64:3510–3520. Diabetes, 2015, 64, e41-e41.	0.6	2
76	Altered Interactions between the Gut Microbiome and Colonic Mucosa Precede Polyposis in APCMin/+ Mice. PLoS ONE, 2015, 10, e0127985.	2.5	48
77	High Colonization Rate and Prolonged Shedding of Clostridium difficile in Pediatric Oncology Patients. Clinical Infectious Diseases, 2014, 59, 401-403.	5.8	64
78	Explicet: graphical user interface software for metadata-driven management, analysis and visualization of microbiome data. Bioinformatics, 2013, 29, 3100-3101.	4.1	261
79	Sex Differences in the Gut Microbiome Drive Hormone-Dependent Regulation of Autoimmunity. Science, 2013, 339, 1084-1088.	12.6	1,565
80	Molecular Analysis of Bacterial and Circovirus Bioaerosols in Concentrated Animal Feeding Operations. Aerosol Science and Technology, 2013, 47, 755-766.	3.1	6
81	Altered Vaginal Microbiota Are Associated With Perinatal Mother-to-Child Transmission of HIV in African Women From Burkina Faso. Journal of Acquired Immune Deficiency Syndromes (1999), 2012, 60, 299-306.	2.1	42
82	Microbiome complexity and <i>Staphylococcus aureus</i> in chronic rhinosinusitis. Laryngoscope, 2012, 122, 467-472.	2.0	212
83	Investigating the biological and clinical significance of human dysbioses. Trends in Microbiology, 2011, 19, 427-434.	7.7	157
84	Cluster analysis of genome-wide expression differences in disease-unaffected ileal mucosa in inflammatory bowel diseases. , 2011, , .		1
85	BARCRAWL and BARTAB: software tools for the design and implementation of barcoded primers for highly multiplexed DNA sequencing. BMC Bioinformatics, 2009, 10, 362.	2.6	146