David A Sela

List of Publications by Year
in descending order

53	4,473	172386	214721
papers	citations	29 h-index	47 g-index

56	56	56	5606
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Difference in levels of SARS-CoV-2 S1 and S2 subunits- and nucleocapsid protein-reactive SIgM/IgM, IgG and SIgA/IgA antibodies in human milk. Journal of Perinatology, 2021, 41, 850-859.	0.9	69
2	Nonprotein nitrogen and protein-derived peptides in human milk. , 2021, , 299-336.		0
3	Human Milk Antibodies against S1 and S2 Subunits from SARS-CoV-2, HCoV-OC43, and HCoV-229E in Mothers with a Confirmed COVID-19 PCR, Viral SYMPTOMS, and Unexposed Mothers. International Journal of Molecular Sciences, 2021, 22, 1749.	1.8	30
4	Cranberry Proanthocyanidins and Dietary Oligosaccharides Synergistically Modulate Lactobacillus plantarum Physiology. Microorganisms, 2021, 9, 656.	1.6	11
5	Prediagnostic White Blood Cell DNA Methylation and Risk of Breast Cancer in the Prostate Lung, Colorectal, and Ovarian Cancer Screening Trial (PLCO) Cohort. Cancer Epidemiology Biomarkers and Prevention, 2021, 30, 1575-1581.	1.1	1
6	Encapsulation of bifidobacterium in alginate microgels improves viability and targeted gut release. Food Hydrocolloids, 2021, 116, 106634.	5.6	57
7	Comparative Pangenomics of the Mammalian Gut Commensal Bifidobacterium longum. Microorganisms, 2020, 8, 7.	1.6	23
8	Bifidobacterium infantis Metabolizes 2â€²Fucosyllactose-Derived and Free Fucose Through a Common Catabolic Pathway Resulting in 1,2-Propanediol Secretion. Frontiers in Nutrition, 2020, 7, 583397.	1.6	22
9	The gastrointestinal fate of limonin and its effect on gut microbiota in mice. Food and Function, 2019, 10, 5521-5530.	2.1	12
10	Unveiling Genomic Diversity among Members of the Species Bifidobacterium pseudolongum , a Widely Distributed Gut Commensal of the Animal Kingdom. Applied and Environmental Microbiology, 2019, 85, .	1.4	44
11	Nutritional Requirements ofÂBifidobacteria. , 2018, , 115-129.		3
12	Peyer's patch-specificLactobacillus reuteristrains increase extracellular microbial DNA and antimicrobial peptide expression in the mouse small intestine. Food and Function, 2018, 9, 2989-2997.	2.1	4
13	Extending viability of Lactobacillus plantarum and Lactobacillus johnsonii by microencapsulation in alginate microgels. International Journal of Food Sciences and Nutrition, 2018, 69, 155-164.	1.3	13
14	Influence of sprouting environment on the microbiota of sprouts. Journal of Food Safety, 2018, 38, e12380.	1.1	7
15	A Vegetable Fermentation Facility Hosts Distinct Microbiomes Reflecting the Production Environment. Applied and Environmental Microbiology, 2018, 84, .	1.4	27
16	Draft Genome Sequence of Bifidobacterium longum UMA026, Isolated from Holstein Dairy Cow Feces. Genome Announcements, 2018, 6, .	0.8	0
17	Inefficient Metabolism of the Human Milk Oligosaccharides Lacto-N-tetraose and Lacto-N-neotetraose Shifts Bifidobacterium longum subsp. infantis Physiology. Frontiers in Nutrition, 2018, 5, 46.	1.6	41
18	The comparative genomics of Bifidobacterium callitrichos reflects dietary carbohydrate utilization within the common marmoset gut. Microbial Genomics, 2018, 4, .	1.0	16

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19	The Host Microbiome Regulates and Maintains Human Health: A Primer and Perspective for Non-Microbiologists. Cancer Research, 2017, 77, 1783-1812.	0.4	270
20	A Human Gut Commensal Ferments Cranberry Carbohydrates To Produce Formate. Applied and Environmental Microbiology, 2017, 83, .	1.4	35
21	Food-grade cationic antimicrobial Îµ-polylysine transiently alters the gut microbial community and predicted metagenome function in CD-1 mice. Npj Science of Food, 2017, 1, 8.	2.5	31
22	Draft Genome Sequences of Alloscardovia macacae UMA81211 and UMA81212, Isolated from the Feces of a Rhesus Macaque (Macaca mulatta). Genome Announcements, 2017, 5, .	0.8	0
23	The Role of Human Milk Oligosaccharides in Hostâ€“Microbial Interactions. , 2017, , 185-206.		1
24	Handling stress may confound murine gut microbiota studies. PeerJ, 2017, 5, e2876.	0.9	18
25	Microencapsulation in Alginate and Chitosan Microgels to Enhance Viability of Bifidobacterium longum for Oral Delivery. Frontiers in Microbiology, 2016, 7, 494.	1.5	125
26	The Reciprocal Interactions between Polyphenols and Gut Microbiota and Effects on Bioaccessibility. Nutrients, 2016, 8, 78.	1.7	573
27	Bioengineering bacteriophages to enhance the sensitivity of phage amplification-based paper fluidic detection of bacteria. Biosensors and Bioelectronics, 2016, 82, 14-19.	5.3	46
28	Rapid screening of waterborne pathogens using phage-mediated separation coupled with real-time PCR detection. Analytical and Bioanalytical Chemistry, 2016, 408, 4169-4178.	1.9	33
29	Genetic optimization of a bacteriophage-delivered alkaline phosphatase reporter to detect Escherichia coli. Analyst, The, 2016, 141, 5543-5548.	1.7	21
30	Correction: Microencapsulation of probiotics in hydrogel particles: enhancing Lactococcus lactis subsp. cremoris LM0230 viability using calcium alginate beads. Food and Function, 2016, 7, 2909-2909.	2.1	6
31	Development of a novel bacteriophage based biomagnetic separation method as an aid for sensitive detection of viable Escherichia coli. Analyst, The, 2016, 141, 1009-1016.	1.7	43
32	Microencapsulation of probiotics in hydrogel particles: enhancing Lactococcus lactis subsp. cremoris LM0230 viability using calcium alginate beads. Food and Function, 2016, 7, 1797-1804.	2.1	69
33	Validating bifidobacterial species and subspecies identity in commercial probiotic products. Pediatric Research, 2016, 79, 445-452.	1.1	125
34	Impact of Îµ-polylysine and pectin on the potential gastrointestinal fate of emulsified lipids: In vitro mouth, stomach and small intestine model. Food Chemistry, 2016, 192, 857-864.	4.2	23
35	Foodâ€grade antimicrobial É›â€polylysine transiently perturbs the structure of the murine gut microbiome. FASEB Journal, 2016, 30, 683.3.	0.2	0
36	Comparative transcriptomics reveals key differences in the response to milk oligosaccharides of infant gut-associated bifidobacteria. Scientific Reports, 2015, 5, 13517.	1.6	144

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37	Glycan cross-feeding activities between bifidobacteria under in vitro conditions. Frontiers in Microbiology, 2015, 6, 1030.	1.5	74
38	Phage & phosphatase: a novel phage-based probe for rapid, multi-platform detection of bacteria. Analyst, The, 2015, 140, 7629-7636.	1.7	36
39	Milk bioactives may manipulate microbes to mediate parent-offspring conflict. Evolution, Medicine and Public Health, 2015, 2015, 106-121.	1.1	42
40	The marriage of nutrigenomics with the microbiome: the case of infant-associated bifidobacteria and milk. American Journal of Clinical Nutrition, 2014, 99, 697S-703S.	2.2	36
41	Infant Gut Microbiota: Developmental Influences and Health Outcomes. , 2013, , 233-256.		13
42	Bifidobacterium longum subsp. infantis ATCC 15697 Î±-Fucosidases Are Active on Fucosylated Human Milk Oligosaccharides. Applied and Environmental Microbiology, 2012, 78, 795-803.	1.4	204
43	Bifidobacterial utilization of human milk oligosaccharides. International Journal of Food Microbiology, 2011, 149, 58-64.	2.1	88
44	An infant-associated bacterial commensal utilizes breast milk sialyloligosaccharides.. Journal of Biological Chemistry, 2011, 286, 23620.	1.6	3
45	An Infant-associated Bacterial Commensal Utilizes Breast Milk Sialyloligosaccharides. Journal of Biological Chemistry, 2011, 286, 11909-11918.	1.6	164
46	Broad Conservation of Milk Utilization Genes in Bifidobacterium longum subsp. infantis as Revealed by Comparative Genomic Hybridization. Applied and Environmental Microbiology, 2010, 76, 7373-7381.	1.4	193
47	Nursing our microbiota: molecular linkages between bifidobacteria and milk oligosaccharides. Trends in Microbiology, 2010, 18, 298-307.	3.5	402
48	Glycoprofiling Bifidobacterial Consumption of Galacto-Oligosaccharides by Mass Spectrometry Reveals Strain-Specific, Preferential Consumption of Glycans. Applied and Environmental Microbiology, 2009, 75, 7319-7325.	1.4	78
49	Comparative Analyses of Prophage-Like Elements Present in Bifidobacterial Genomes. Applied and Environmental Microbiology, 2009, 75, 6929-6936.	1.4	45
50	Role of Hypermutability in the Evolution of the GenusOenococcus. Journal of Bacteriology, 2008, 190, 564-570.	1.0	70
51	The genome sequence of Bifidobacterium longum subsp. infantis reveals adaptations for milk utilization within the infant microbiome. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 18964-18969.	3.3	748
52	Glycoprofiling of Bifidobacterial Consumption of Human Milk Oligosaccharides Demonstrates Strain Specific, Preferential Consumption of Small Chain Glycans Secreted in Early Human Lactation. Journal of Agricultural and Food Chemistry, 2007, 55, 8914-8919.	2.4	313
53	Characterization of the lactococcal group II intron target site in its native host. Plasmid, 2007, 58, 127-139.	0.4	1