

Danielle G Lemay

List of Publications by Year in descending order

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Version: 2024-02-01

55
papers

4,352
citations

230014

27
h-index

169272

56
g-index

64
all docs

64
docs citations

64
times ranked

7484
citing authors

#	ARTICLE	IF	CITATIONS
1	Special report: AI Institute for next generation food systems (AIFS). Computers and Electronics in Agriculture, 2022, 196, 106819.	3.7	1
2	Dietary Fiber to Starch Ratio Affects Bovine Milk Oligosaccharide Profiles. Current Developments in Nutrition, 2022, 6, nzac033.	0.1	3
3	Tree-Based Analysis of Dietary Diversity Captures Associations Between Fiber Intake and Gut Microbiota Composition in a Healthy US Adult Cohort. Journal of Nutrition, 2022, 152, 779-788.	1.3	20
4	Unique Transcriptomic Changes Underlie Hormonal Interactions During Mammary Histomorphogenesis in Female Pigs. Endocrinology, 2022, 163, .	1.4	2
5	The Development of the Davis Food Glycopediaâ€”A Glycan Encyclopedia of Food. Nutrients, 2022, 14, 1639.	1.7	3
6	A Low-Starch and High-Fiber Diet Intervention Impacts the Microbial Community of Raw Bovine Milk. Current Developments in Nutrition, 2022, 6, nzac086.	0.1	1
7	Association of Diet and Antimicrobial Resistance in Healthy U.S. Adults. MBio, 2022, 13, e0010122.	1.8	25
8	Effect of Manual Data Cleaning on Nutrient Intakes Using the Automated Self-Administered 24-Hour Dietary Assessment Tool (ASA24). Current Developments in Nutrition, 2021, 5, nzab005.	0.1	10
9	Technician-Scored Stool Consistency Spans the Full Range of the Bristol Scale in a Healthy US Population and Differs by Diet and Chronic Stress Load. Journal of Nutrition, 2021, 151, 1443-1452.	1.3	13
10	Multimodal AI to Improve Agriculture. IT Professional, 2021, 23, 53-57.	1.4	3
11	Machine Learning Identifies Stool pH as a Predictor of Bone Mineral Density in Healthy Multiethnic US Adults. Journal of Nutrition, 2021, 151, 3379-3390.	1.3	4
12	Association of the Lactase Persistence Haplotype Block With Disease Risk in Populations of European Descent. Frontiers in Genetics, 2020, 11, 558762.	1.1	3
13	Reservoirs of antimicrobial resistance genes in retail raw milk. Microbiome, 2020, 8, 99.	4.9	47
14	Pre- and post-sequencing recommendations for functional annotation of human fecal metagenomes. BMC Bioinformatics, 2020, 21, 74.	1.2	13
15	Fecal metatranscriptomics and glycomics suggest that bovine milk oligosaccharides are fully utilized by healthy adults. Journal of Nutritional Biochemistry, 2020, 79, 108340.	1.9	8
16	Association of Lactase Persistence Genotypes (rs4988235) and Ethnicity with Dairy Intake in a Healthy U.S. Population. Nutrients, 2019, 11, 1860.	1.7	18
17	Temporal changes in postprandial blood transcriptomes reveal subject-specific pattern of expression of innate immunity genes after a high-fat meal. Journal of Nutritional Biochemistry, 2019, 72, 108209.	1.9	9
18	The fecal resistome of dairy cattle is associated with diet during nursing. Nature Communications, 2019, 10, 4406.	5.8	100

#	ARTICLE	IF	CITATIONS
19	Fecal metatranscriptomics of macaques with idiopathic chronic diarrhea reveals altered mucin degradation and fucose utilization. <i>Microbiome</i> , 2019, 7, 41.	4.9	30
20	Nutrient Estimation from 24-Hour Food Recalls Using Machine Learning and Database Mapping: A Case Study with Lactose. <i>Nutrients</i> , 2019, 11, 3045.	1.7	22
21	Pilot study of probiotic/colostrum supplementation on gut function in children with autism and gastrointestinal symptoms. <i>PLoS ONE</i> , 2019, 14, e0210064.	1.1	126
22	21st century toolkit for optimizing population health through precision nutrition. <i>Critical Reviews in Food Science and Nutrition</i> , 2018, 58, 3004-3015.	5.4	28
23	The collaborative effect of scientific meetings: A study of the International Milk Genomics Consortium. <i>PLoS ONE</i> , 2018, 13, e0201637.	1.1	7
24	SAMSA2: a standalone metatranscriptome analysis pipeline. <i>BMC Bioinformatics</i> , 2018, 19, 175.	1.2	107
25	The Fecal Microbial Community of Breast-fed Infants from Armenia and Georgia. <i>Scientific Reports</i> , 2017, 7, 40932.	1.6	28
26	Tolerability and safety of the intake of bovine milk oligosaccharides extracted from cheese whey in healthy human adults. <i>Journal of Nutritional Science</i> , 2017, 6, e6.	0.7	17
27	The Transcriptome of Estrogen-Independent Mammary Growth in Female Mice Reveals That Not All Mammary Glands Are Created Equally. <i>Endocrinology</i> , 2017, 158, 3126-3139.	1.4	6
28	SAMSA: a comprehensive metatranscriptome analysis pipeline. <i>BMC Bioinformatics</i> , 2016, 17, 399.	1.2	49
29	A novel gene cluster allows preferential utilization of fucosylated milk oligosaccharides in <i>Bifidobacterium longum</i> subsp. <i>longum</i> SC596. <i>Scientific Reports</i> , 2016, 6, 35045.	1.6	137
30	Comparative transcriptomics reveals key differences in the response to milk oligosaccharides of infant gut-associated bifidobacteria. <i>Scientific Reports</i> , 2015, 5, 13517.	1.6	144
31	Maternal fucosyltransferase 2 status affects the gut bifidobacterial communities of breastfed infants. <i>Microbiome</i> , 2015, 3, 13.	4.9	319
32	Comparative genomics reveals tissue-specific regulation of prolactin receptor gene expression. <i>Journal of Molecular Endocrinology</i> , 2015, 54, 1-15.	1.1	23
33	The Human Colostrum Whey Proteome Is Altered in Gestational Diabetes Mellitus. <i>Journal of Proteome Research</i> , 2015, 14, 512-520.	1.8	33
34	Comparative Proteomics of Human and Macaque Milk Reveals Species-Specific Nutrition during Postnatal Development. <i>Journal of Proteome Research</i> , 2015, 14, 2143-2157.	1.8	60
35	Changes in intestinal barrier function and gut microbiota in high-fat diet-fed rats are dynamic and region dependent. <i>American Journal of Physiology - Renal Physiology</i> , 2015, 308, G840-G851.	1.6	249
36	Bifidobacteria grown on human milk oligosaccharides downregulate the expression of inflammation-related genes in Caco-2 cells. <i>BMC Microbiology</i> , 2015, 15, 172.	1.3	67

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37	Human milk oligosaccharides in premature infants: absorption, excretion, and influence on the intestinal microbiota. <i>Pediatric Research</i> , 2015, 78, 670-677.	1.1	155
38	Sequencing the transcriptome of milk production: milk trumps mammary tissue. <i>BMC Genomics</i> , 2013, 14, 872.	1.2	44
39	Epigenetic Modifications Unlock the Milk Protein Gene Loci during Mouse Mammary Gland Development and Differentiation. <i>PLoS ONE</i> , 2013, 8, e53270.	1.1	50
40	RNA Sequencing of the Human Milk Fat Layer Transcriptome Reveals Distinct Gene Expression Profiles at Three Stages of Lactation. <i>PLoS ONE</i> , 2013, 8, e67531.	1.1	179
41	From Genes to Milk: Genomic Organization and Epigenetic Regulation of the Mammary Transcriptome. <i>PLoS ONE</i> , 2013, 8, e75030.	1.1	17
42	G-NEST: a gene neighborhood scoring tool to identify co-conserved, co-expressed genes. <i>BMC Bioinformatics</i> , 2012, 13, 253.	1.2	14
43	Lactosomes: Structural and Compositional Classification of Unique Nanometer-Sized Protein Lipid Particles of Human Milk. <i>Journal of Agricultural and Food Chemistry</i> , 2010, 58, 11234-11242.	2.4	46
44	Lessons from the Bovine Genome: Implications for Human Nutrition and Research. <i>Journal of Nutrition</i> , 2009, 139, 1271-1272.	1.3	2
45	Unlocking the bovine genome. <i>BMC Genomics</i> , 2009, 10, 193.	1.2	46
46	The Genome Sequence of Taurine Cattle: A Window to Ruminant Biology and Evolution. <i>Science</i> , 2009, 324, 522-528.	6.0	1,038
47	The bovine lactation genome: insights into the evolution of mammalian milk. <i>Genome Biology</i> , 2009, 10, R43.	13.9	164
48	Milk fat globule structure and function: nanoscience comes to milk production. <i>Trends in Food Science and Technology</i> , 2008, 19, 617-623.	7.8	83
49	Building the bridges to bioinformatics in nutrition research. <i>American Journal of Clinical Nutrition</i> , 2007, 86, 1261-1269.	2.2	28
50	A multi-ontology framework to guide agriculture and food towards diet and health. <i>Journal of the Science of Food and Agriculture</i> , 2007, 87, 1427-1434.	1.7	24
51	Gene regulatory networks in lactation: identification of global principles using bioinformatics. <i>BMC Systems Biology</i> , 2007, 1, 56.	3.0	114
52	Genome-wide identification of peroxisome proliferator response elements using integrated computational genomics. <i>Journal of Lipid Research</i> , 2006, 47, 1583-1587.	2.0	123
53	The regulation of the expression of inducible nitric oxide synthase by Src-family tyrosine kinases mediated through MyD88-independent signaling pathways of Toll-like receptor 4. <i>Biochemical Pharmacology</i> , 2005, 70, 1231-1240.	2.0	59
54	Saturated and Polyunsaturated Fatty Acids Reciprocally Modulate Dendritic Cell Functions Mediated through TLR4. <i>Journal of Immunology</i> , 2005, 174, 5390-5397.	0.4	274

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55	Chapter 1. Food Structure for Nutrition. , 0, , 1-15.		0