Carmen A Argmann

List of Publications by Year
in descending order

47	2,744	218677	233421
papers	citations	26 h-index	45 g-index

54	54	54	6193
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Systems proteomics of liver mitochondria function. Science, 2016, 352, aad0189.	12.6	257
2	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. Nature Genetics, 2017, 49, 1437-1449.	21.4	199
3	Human Pancreatic Î² Cell lncRNAs Control Cell-Specific Regulatory Networks. Cell Metabolism, 2017, 25, 400-411.	16.2	195
4	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. Scientific Reports, 2015, 5, 15145.	3.3	180
5	Peroxisomal L-bifunctional enzyme (Ehhadh) is essential for the production of medium-chain dicarboxylic acids. Journal of Lipid Research, 2012, 53, 1296-1303.	4.2	127
6	Gut microbiota density influences host physiology and is shaped by host and microbial factors. ELife, 2019, 8, .	6.0	118
7	Intestinal Host Response to SARS-CoV-2 Infection and COVID-19 Outcomes in Patients With Gastrointestinal Symptoms. Gastroenterology, 2021, 160, 2435-2450.e34.	1.3	118
8	Combined Inhibition of DYRK1A, SMAD, and Trithorax Pathways Synergizes to Induce Robust Replication in Adult Human Beta Cells. Cell Metabolism, 2019, 29, 638-652.e5.	16.2	113
9	Very Early Onset Inflammatory Bowel Disease: A Clinical Approach With a Focus on the Role of Genetics and Underlying Immune Deficiencies. Inflammatory Bowel Diseases, 2020, 26, 820-842.	1.9	100
10	Intestinal Inflammation Modulates the Expression of ACE2 and TMPRSS2 and Potentially Overlaps With the Pathogenesis of SARS-CoV-2â€“related Disease. Gastroenterology, 2021, 160, 287-301.e20.	1.3	98
11	Integrative Analysis of DNA Methylation and Gene Expression Data Identifies EPAS1 as a Key Regulator of COPD. PLoS Genetics, 2015, 11, e1004898.	3.5	82
12	Peroxisomes can oxidize mediumâ€•and longâ€•chain fatty acids through a pathway involving ABCD3 and HSD17B4. FASEB Journal, 2019, 33, 4355-4364.	0.5	82
13	A Next Generation Multiscale View of Inborn Errors of Metabolism. Cell Metabolism, 2016, 23, 13-26.	16.2	79
14	Ulcerative colitis is characterized by a plasmablast-skewed humoral response associated with disease activity. Nature Medicine, 2022, 28, 766-779.	30.7	70
15	Insights into beta cell regeneration for diabetes via integration of molecular landscapes in human insulinomas. Nature Communications, 2017, 8, 767.	12.8	67
16	Impaired amino acid metabolism contributes to fasting-induced hypoglycemia in fatty acid oxidation defects. Human Molecular Genetics, 2013, 22, 5249-5261.	2.9	61
17	Plasma acylcarnitines inadequately reflect tissue acylcarnitine metabolism. Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids, 2014, 1841, 987-994.	2.4	60
18	Integrating siRNA and proteinâ€“protein interaction data to identify an expanded insulin signaling network. Genome Research, 2009, 19, 1057-1067.	5.5	53

#	Article	IF	Citations
19	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
20	Lysosomal Stress in Obese Adipose Tissue Macrophages Contributes to MITF-Dependent Gpnmb Induction. Diabetes, 2014, 63, 3310-3323.	0.6	49
21	A PPARÎ³-Bnip3 Axis Couples Adipose Mitochondrial Fusion-Fission Balance to Systemic Insulin Sensitivity. Diabetes, 2016, 65, 2591-2605.	0.6	45
22	Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. Nature Communications, 2021, 12, 4854.	12.8	42
23	High-Throughput Characterization of Blood Serum Proteomics of IBD Patients with Respect to Aging and Genetic Factors. PLoS Genetics, 2017, 13, e1006565.	3.5	41
24	Blood and Intestine eQTLs from an Anti-TNF-Resistant Crohn's Disease Cohort Inform IBD Genetic Association Loci. Clinical and Translational Gastroenterology, 2016, 7, e177.	2.5	40
25	Increased cardiac fatty acid oxidation in a mouse model with decreased malonyl-CoA sensitivity of CPT1B. Cardiovascular Research, 2018, 114, 1324-1334.	3.8	37
26	An Integrated Taxonomy for Monogenic Inflammatory Bowel Disease. Gastroenterology, 2022, 162, 859-876.	1.3	37
27	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. Nature Communications, 2021, 12, 547.	12.8	35
28	DNA methylation alters transcriptional rates of differentially expressed genes and contributes to pathophysiology in mice fed a high fat diet. Molecular Metabolism, 2017, 6, 327-339.	6.5	27
29	Integrative Analysis of the Inflammatory Bowel Disease Serum Metabolome Improves Our Understanding of Genetic Etiology and Points to Novel Putative Therapeutic Targets. Gastroenterology, 2022, 162, 828-843.e11.	1.3	26
30	Inter-tissue coexpression network analysis reveals DPP4 as an important gene in heart to blood communication. Genome Medicine, 2016, 8, 15.	8.2	24
31	Label-Free LC-MSe in Tissue and Serum Reveals Protein Networks Underlying Differences between Benign and Malignant Serous Ovarian Tumors. PLoS ONE, 2014, 9, e108046.	2.5	19
32	A next generation sequencing based approach to identify extracellular vesicle mediated mRNA transfers between cells. BMC Genomics, 2017, 18, 987.	2.8	19
33	High-Throughput Identification of the Plasma Proteomic Signature of Inflammatory Bowel Disease. Journal of Crohn's and Colitis, 2019, 13, 462-471.	1.3	18
34	Deep Analysis of the Peripheral Immune System in IBD Reveals New Insight in Disease Subtyping and Response to Monotherapy or Combination Therapy. Cellular and Molecular Gastroenterology and Hepatology, 2021, 12, 599-632.	4.5	17
35	Acute detachment of hexokinase II from mitochondria modestly increases oxygen consumption of the intact mouse heart. Metabolism: Clinical and Experimental, 2017, 72, 66-74.	3.4	15
36	Germline deletion of KrÃ¼ppel-like factor 14 does not increase risk of diet induced metabolic syndrome in male C57BL/6 mice. Biochimica Et Biophysica Acta - Molecular Basis of Disease, 2017, 1863, 3277-3285.	3.8	15

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37	Murine deficiency of peroxisomal l-bifunctional protein (EHHADH) causes medium-chain 3-hydroxydicarboxylic aciduria and perturbs hepatic cholesterol homeostasis. Cellular and Molecular Life Sciences, 2021, 78, 5631-5646.	5.4	15
38	Mild inborn errors of metabolism in commonly used inbred mouse strains. Molecular Genetics and Metabolism, 2019, 126, 388-396.	1.1	14
39	Molecular Characterization of Limited Ulcerative Colitis Reveals Novel Biology and Predictors of Disease Extension. Gastroenterology, 2021, 161, 1953-1968.e15.	1.3	14
40	Peroxisomal L-bifunctional Protein Deficiency Causes Male-specific Kidney Hypertrophy and Proximal Tubular Injury in Mice. Kidney360, 2021, 2, 1441-1454.	2.1	10
41	Aberrant methylation underlies insulin gene expression in human insulinoma. Nature Communications, 2020, 11, 5210.	12.8	9
42	A mitochondrial long-chain fatty acid oxidation defect leads to transfer RNA uncharging and activation of the integrated stress response in the mouse heart. Cardiovascular Research, 2022, 118, 3198-3210.	3.8	9
43	Stratification of risk of progression to colectomy in ulcerative colitis via measured and predicted gene expression. American Journal of Human Genetics, 2021, 108, 1765-1779.	6.2	6
44	Glutaric aciduria type 3 is a naturally occurring biochemical trait in inbred mice of 129 substrains. Molecular Genetics and Metabolism, 2021, 132, 139-145.	1.1	4
45	Meta-analysis of sample-level dbGaP data reveals novel shared genetic link between body height and Crohnâ€™s disease. Human Genetics, 2021, 140, 865-877.	3.8	3
46	Polygenic risk score for alcohol drinking behavior improves prediction of inflammatory bowel disease risk. Human Molecular Genetics, 2021, 30, 514-523.	2.9	2
47	Dietary restriction in the long-chain acyl-CoA dehydrogenase knockout mouse. Molecular Genetics and Metabolism Reports, 2021, 27, 100749.	1.1	0