

Carmen A Argmann

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2926956/publications.pdf>

Version: 2024-02-01

47
papers

2,744
citations

218677

26
h-index

233421

45
g-index

54
all docs

54
docs citations

54
times ranked

6193
citing authors

#	ARTICLE	IF	CITATIONS
1	An Integrated Taxonomy for Monogenic Inflammatory Bowel Disease. <i>Gastroenterology</i> , 2022, 162, 859-876.	1.3	37
2	Integrative Analysis of the Inflammatory Bowel Disease Serum Metabolome Improves Our Understanding of Genetic Etiology and Points to Novel Putative Therapeutic Targets. <i>Gastroenterology</i> , 2022, 162, 828-843.e11.	1.3	26
3	A mechanistic framework for cardiometabolic and coronary artery diseases. , 2022, 1, 85-100.		51
4	Ulcerative colitis is characterized by a plasmablast-skewed humoral response associated with disease activity. <i>Nature Medicine</i> , 2022, 28, 766-779.	30.7	70
5	A mitochondrial long-chain fatty acid oxidation defect leads to transfer RNA uncharging and activation of the integrated stress response in the mouse heart. <i>Cardiovascular Research</i> , 2022, 118, 3198-3210.	3.8	9
6	Intestinal Inflammation Modulates the Expression of ACE2 and TMPRSS2 and Potentially Overlaps With the Pathogenesis of SARS-CoV-2â€related Disease. <i>Gastroenterology</i> , 2021, 160, 287-301.e20.	1.3	98
7	An integrative multiomic network model links lipid metabolism to glucose regulation in coronary artery disease. <i>Nature Communications</i> , 2021, 12, 547.	12.8	35
8	Meta-analysis of sample-level dbGaP data reveals novel shared genetic link between body height and Crohnâ€™s disease. <i>Human Genetics</i> , 2021, 140, 865-877.	3.8	3
9	Polygenic risk score for alcohol drinking behavior improves prediction of inflammatory bowel disease risk. <i>Human Molecular Genetics</i> , 2021, 30, 514-523.	2.9	2
10	Glutaric aciduria type 3 is a naturally occurring biochemical trait in inbred mice of 129 substrains. <i>Molecular Genetics and Metabolism</i> , 2021, 132, 139-145.	1.1	4
11	Dietary restriction in the long-chain acyl-CoA dehydrogenase knockout mouse. <i>Molecular Genetics and Metabolism Reports</i> , 2021, 27, 100749.	1.1	0
12	Peroxisomal L-bifunctional Protein Deficiency Causes Male-specific Kidney Hypertrophy and Proximal Tubular Injury in Mice. <i>Kidney360</i> , 2021, 2, 1441-1454.	2.1	10
13	Intestinal Host Response to SARS-CoV-2 Infection and COVID-19 Outcomes in Patients With Gastrointestinal Symptoms. <i>Gastroenterology</i> , 2021, 160, 2435-2450.e34.	1.3	118
14	Murine deficiency of peroxisomal l-bifunctional protein (EHHADH) causes medium-chain 3-hydroxydicarboxylic aciduria and perturbs hepatic cholesterol homeostasis. <i>Cellular and Molecular Life Sciences</i> , 2021, 78, 5631-5646.	5.4	15
15	Downregulation of exhausted cytotoxic T cells in gene expression networks of multisystem inflammatory syndrome in children. <i>Nature Communications</i> , 2021, 12, 4854.	12.8	42
16	Stratification of risk of progression to colectomy in ulcerative colitis via measured and predicted gene expression. <i>American Journal of Human Genetics</i> , 2021, 108, 1765-1779.	6.2	6
17	Molecular Characterization of Limited Ulcerative Colitis Reveals Novel Biology and Predictors of Disease Extension. <i>Gastroenterology</i> , 2021, 161, 1953-1968.e15.	1.3	14
18	Deep Analysis of the Peripheral Immune System in IBD Reveals New Insight in Disease Subtyping and Response to Monotherapy or Combination Therapy. <i>Cellular and Molecular Gastroenterology and Hepatology</i> , 2021, 12, 599-632.	4.5	17

#	ARTICLE	IF	CITATIONS
19	Very Early Onset Inflammatory Bowel Disease: A Clinical Approach With a Focus on the Role of Genetics and Underlying Immune Deficiencies. <i>Inflammatory Bowel Diseases</i> , 2020, 26, 820-842.	1.9	100
20	Aberrant methylation underlies insulin gene expression in human insulinoma. <i>Nature Communications</i> , 2020, 11, 5210.	12.8	9
21	Gut microbiota density influences host physiology and is shaped by host and microbial factors. <i>ELife</i> , 2019, 8, .	6.0	118
22	Mild inborn errors of metabolism in commonly used inbred mouse strains. <i>Molecular Genetics and Metabolism</i> , 2019, 126, 388-396.	1.1	14
23	Combined Inhibition of DYRK1A, SMAD, and Trithorax Pathways Synergizes to Induce Robust Replication in Adult Human Beta Cells. <i>Cell Metabolism</i> , 2019, 29, 638-652.e5.	16.2	113
24	High-Throughput Identification of the Plasma Proteomic Signature of Inflammatory Bowel Disease. <i>Journal of Crohn's and Colitis</i> , 2019, 13, 462-471.	1.3	18
25	Peroxisomes can oxidize medium- and long-chain fatty acids through a pathway involving ABCD3 and HSD17B4. <i>FASEB Journal</i> , 2019, 33, 4355-4364.	0.5	82
26	Increased cardiac fatty acid oxidation in a mouse model with decreased malonyl-CoA sensitivity of CPT1B. <i>Cardiovascular Research</i> , 2018, 114, 1324-1334.	3.8	37
27	Acute detachment of hexokinase II from mitochondria modestly increases oxygen consumption of the intact mouse heart. <i>Metabolism: Clinical and Experimental</i> , 2017, 72, 66-74.	3.4	15
28	DNA methylation alters transcriptional rates of differentially expressed genes and contributes to pathophysiology in mice fed a high fat diet. <i>Molecular Metabolism</i> , 2017, 6, 327-339.	6.5	27
29	Human Pancreatic β Cell lncRNAs Control Cell-Specific Regulatory Networks. <i>Cell Metabolism</i> , 2017, 25, 400-411.	16.2	195
30	Insights into beta cell regeneration for diabetes via integration of molecular landscapes in human insulinomas. <i>Nature Communications</i> , 2017, 8, 767.	12.8	67
31	Germline deletion of KrÄppel-like factor 14 does not increase risk of diet induced metabolic syndrome in male C57BL/6 mice. <i>Biochimica Et Biophysica Acta - Molecular Basis of Disease</i> , 2017, 1863, 3277-3285.	3.8	15
32	A functional genomics predictive network model identifies regulators of inflammatory bowel disease. <i>Nature Genetics</i> , 2017, 49, 1437-1449.	21.4	199
33	A next generation sequencing based approach to identify extracellular vesicle mediated mRNA transfers between cells. <i>BMC Genomics</i> , 2017, 18, 987.	2.8	19
34	High-Throughput Characterization of Blood Serum Proteomics of IBD Patients with Respect to Aging and Genetic Factors. <i>PLoS Genetics</i> , 2017, 13, e1006565.	3.5	41
35	Systems proteomics of liver mitochondria function. <i>Science</i> , 2016, 352, aad0189.	12.6	257
36	Inter-tissue coexpression network analysis reveals DPP4 as an important gene in heart to blood communication. <i>Genome Medicine</i> , 2016, 8, 15.	8.2	24

#	ARTICLE	IF	CITATIONS
37	A PPAR β -Bnip3 Axis Couples Adipose Mitochondrial Fusion-Fission Balance to Systemic Insulin Sensitivity. <i>Diabetes</i> , 2016, 65, 2591-2605.	0.6	45
38	Blood and Intestine eQTLs from an Anti-TNF-Resistant Crohn's Disease Cohort Inform IBD Genetic Association Loci. <i>Clinical and Translational Gastroenterology</i> , 2016, 7, e177.	2.5	40
39	A Next Generation Multiscale View of Inborn Errors of Metabolism. <i>Cell Metabolism</i> , 2016, 23, 13-26.	16.2	79
40	Synchronized age-related gene expression changes across multiple tissues in human and the link to complex diseases. <i>Scientific Reports</i> , 2015, 5, 15145.	3.3	180
41	Integrative Analysis of DNA Methylation and Gene Expression Data Identifies EPAS1 as a Key Regulator of COPD. <i>PLoS Genetics</i> , 2015, 11, e1004898.	3.5	82
42	Label-Free LC-MSE in Tissue and Serum Reveals Protein Networks Underlying Differences between Benign and Malignant Serous Ovarian Tumors. <i>PLoS ONE</i> , 2014, 9, e108046.	2.5	19
43	Lysosomal Stress in Obese Adipose Tissue Macrophages Contributes to MITF-Dependent Gpnmb Induction. <i>Diabetes</i> , 2014, 63, 3310-3323.	0.6	49
44	Plasma acylcarnitines inadequately reflect tissue acylcarnitine metabolism. <i>Biochimica Et Biophysica Acta - Molecular and Cell Biology of Lipids</i> , 2014, 1841, 987-994.	2.4	60
45	Impaired amino acid metabolism contributes to fasting-induced hypoglycemia in fatty acid oxidation defects. <i>Human Molecular Genetics</i> , 2013, 22, 5249-5261.	2.9	61
46	Peroxisomal L-bifunctional enzyme (Ehhadh) is essential for the production of medium-chain dicarboxylic acids. <i>Journal of Lipid Research</i> , 2012, 53, 1296-1303.	4.2	127
47	Integrating siRNA and protein-protein interaction data to identify an expanded insulin signaling network. <i>Genome Research</i> , 2009, 19, 1057-1067.	5.5	53