Johanna K Distefano

List of Publications by Year
in descending order

95	4,143	94381	123376
papers	citations	37 h-index	61 g-index

96	96	96	6462
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	Long Noncoding RNAs and Human Liver Disease. Annual Review of Pathology: Mechanisms of Disease, 2022, 17, 1-21.	9.6	25
2	NAFLD in normal weight individuals. Diabetology and Metabolic Syndrome, 2022, 14, 45.	1.2	20
3	A Quantitative Systems Pharmacology Platform Reveals NAFLD Pathophysiological States and Targeting Strategies. Metabolites, 2022, 12, 528.	1.3	3
4	The relationship between excessive dietary fructose consumption and paediatric fatty liver disease. Pediatric Obesity, 2021, 16, e12759.	1.4	23
5	rs641738C>T near MBOAT7 is associated with liver fat, ALT and fibrosis in NAFLD: A meta-analysis. Journal of Hepatology, 2021, 74, 20-30.	1.8	77
6	Differential DNA methylation and changing cell-type proportions as fibrotic stage progresses in NAFLD. Clinical Epigenetics, 2021, 13, 152.	1.8	25
7	Emerging Role of Long Noncoding RNAs in Perioperative Neurocognitive Disorders and Anesthetic-Induced Developmental Neurotoxicity. Anesthesia and Analgesia, 2021, 132, 1614-1625.	1.1	5
8	Fructose-mediated effects on gene expression and epigenetic mechanisms associated with NAFLD pathogenesis. Cellular and Molecular Life Sciences, 2020, 77, 2079-2090.	2.4	52
9	NAFLD and NASH in Postmenopausal Women: Implications for Diagnosis and Treatment. Endocrinology, 2020, 161, .	1.4	94
10	Higher circulating levels of ANGPTL8 are associated with body mass index, triglycerides, and endothelial dysfunction in patients with coronary artery disease. Molecular and Cellular Biochemistry, 2020, 469, 29-39.	1.4	13
11	Differentially expressed mRNAs and lncRNAs shared between activated human hepatic stellate cells and nash fibrosis. Biochemistry and Biophysics Reports, 2020, 22, 100753.	0.7	9
12	Long Noncoding RNAs as Drivers of Acquired Chemoresistance in Hepatocellular Carcinoma. RNA Technologies, 2020, , 199-227.	0.2	0
13	Palmitate and Fructose Interact to Induce Human Hepatocytes to Produce Pro-Fibrotic Transcriptional Responses in Hepatic Stellate Cells Exposed to Conditioned Media. Cellular Physiology and Biochemistry, 2020, 54, 1068-1082.	1.1	0
14	AEBP1 expression increases with severity of fibrosis in NASH and is regulated by glucose, palmitate, and miR-372-3p. PLoS ONE, 2019, 14, e0219764.	1.1	29
15	Chemokine ligand 20 (CCL20) expression increases with NAFLD stage and hepatic stellate cell activation and is regulated by miR-590-5p. Cytokine, 2019, 123, 154789.	1.4	13
16	Pharmacoepigenetics in Type 2 Diabetes Mellitus. , 2019, , 563-571.		0
17	Diagnostic and Prognostic Potential of AKR1B10 in Human Hepatocellular Carcinoma. Cancers, 2019, 11, 486.	1.7	82
18	CXCL4L1 Promoter Polymorphisms Are Associated with Improved Renal Function in Type 1 Diabetes. Journal of Immunology, 2019, 202, 912-919.	0.4	1

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19	Angiopoietin-like 8 (ANGPTL8) expression is regulated by miR-143-3p in human hepatocytes. Gene, 2019, 681, 1-6.	1.0	16
20	Methods for CpG Methylation Array Profiling Via Bisulfite Conversion. Methods in Molecular Biology, 2018, 1706, 233-254.	0.4	7
21	miRNA Quantification Method Using Quantitative Polymerase Chain Reaction in Conjunction with C q Method. Methods in Molecular Biology, 2018, 1706, 257-265.	0.4	8
22	Identification of Genes for Hereditary Hemochromatosis. Methods in Molecular Biology, 2018, 1706, 353-365.	0.4	12
23	Development of Targeted Therapies Based on Gene Modification. Methods in Molecular Biology, 2018, 1706, 39-51.	0.4	1
24	The Emerging Role of Long Noncoding RNAs in Human Disease. Methods in Molecular Biology, 2018, 1706, 91-110.	0.4	154
25	Identification of Disease Susceptibility Alleles in the Next Generation Sequencing Era. Methods in Molecular Biology, 2018, 1706, 3-16.	0.4	4
26	CCL20 is up-regulated in non-alcoholic fatty liver disease fibrosis and is produced by hepatic stellate cells in response to fatty acid loading. Journal of Translational Medicine, 2018, 16, 108.	1.8	50
27	Differentially methylated loci in NAFLD cirrhosis are associated with key signaling pathways. Clinical Epigenetics, 2018, 10, 93.	1.8	22
28	Transcriptomic Profiling of Obesity-Related Nonalcoholic Steatohepatitis Reveals a Core Set of Fibrosis-Specific Genes. Journal of the Endocrine Society, 2018, 2, 710-726.	0.1	55
29	The Role of Long Non-Coding RNAs (lncRNAs) in the Development and Progression of Fibrosis Associated with Nonalcoholic Fatty Liver Disease (NAFLD). Non-coding RNA, 2018, 4, 18.	1.3	42
30	miRNA profiling for the early detection and clinical monitoring of diabetic kidney disease. Biomarkers in Medicine, 2017, 11, 99-102.	0.6	3
31	A multi-component classifier for nonalcoholic fatty liver disease (NAFLD) based on genomic, proteomic, and phenomic data domains. Scientific Reports, 2017, 7, 43238.	1.6	41
32	Long noncoding RNAs in the pathogenesis of diabetic kidney disease: implications for novel therapeutic strategies. Personalized Medicine, 2017, 14, 271-278.	0.8	34
33	Altered expression of MALAT1 lncRNA in nonalcoholic steatohepatitis fibrosis regulates CXCL5 in hepatic stellate cells. Translational Research, 2017, 190, 25-39.e21.	2.2	91
34	Long noncoding RNAs in the initiation, progression, and metastasis of hepatocellular carcinoma. Non-coding RNA Research, 2017, 2, 129-136.	2.4	57
35	Long Noncoding RNAs as Diagnostic and Therapeutic Targets in Type 2 Diabetes and Related Complications. Genes, 2017, 8, 207.	1.0	69
36	The Arg59Trp variant in ANGPTL8 (betatrophin) is associated with total and HDL-cholesterol in American Indians and Mexican Americans and differentially affects cleavage of ANGPTL3. Molecular Genetics and Metabolism, 2016, 118, 128-137.	0.5	33

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37	Circulating microRNAs in nonalcoholic fatty liver disease. Expert Review of Gastroenterology and Hepatology, 2016, 10, 161-163.	1.4	26
38	High False-Negative Rate for Nonalcoholic Steatohepatitis in Extreme Obesity. Gastroenterology, 2016, 150, 283-284.	0.6	2
39	A Modified Precipitation Method to Isolate Urinary Exosomes. Journal of Visualized Experiments, 2015, , 51158.	0.2	13
40	The Human Genome Project: Where Are We Now and Where Are We Going?. , 2015, , 7-31.		0
41	High-throughput sequencing reveals altered expression of hepatic microRNAs in nonalcoholic fatty liver diseaseâ€“related fibrosis. Translational Research, 2015, 166, 304-314.	2.2	69
42	Genome-wide analysis of hepatic lipid content in extreme obesity. Acta Diabetologica, 2015, 52, 373-382.	1.2	47
43	Beyond the Protein-Coding Sequence: Noncoding RNAs in the Pathogenesis of Type 2 Diabetes. Review of Diabetic Studies, 2015, 12, 260-276.	0.5	9
44	Urinary Exosomes as Potential Source for Identification of Biomarkers for Kidney Damage: Comparing Methodologies. Biomarkers in Disease, 2015, , 939-954.	0.0	0
45	Identification of Novel Clinical Factors Associated with Hepatic Fat Accumulation in Extreme Obesity. Journal of Obesity, 2014, 2014, 1-8.	1.1	13
46	Urinary Exosomes as a Potential Source for the Identification of Biomarkers for Kidney Damage: Comparing Methodologies. , 2014, , 1-14.		0
47	Micro RNAs in the development of non-alcoholic fatty liver disease. World Journal of Hepatology, 2014, 7, 226.	0.8	40
48	Towards microRNA-based therapeutics for diabetic nephropathy. Diabetologia, 2013, 56, 444-456.	2.9	29
49	The role of non-coding RNAs in diabetic nephropathy: Potential applications as biomarkers for disease development and progression. Diabetes Research and Clinical Practice, 2013, 99, 1-11.	1.1	96
50	Emerging Roles for miRNAs in the Development, Diagnosis, and Treatment of Diabetic Nephropathy. Current Diabetes Reports, 2013, 13, 582-591.	1.7	20
51	Comparison of protein, microRNA, and mRNA yields using different methods of urinary exosome isolation for the discovery of kidney disease biomarkers. Kidney International, 2012, 82, 1024-1032.	2.6	486
52	Technological Issues and Experimental Design of Gene Association Studies. Methods in Molecular Biology, 2011, 700, 3-16.	0.4	18
53	Targeted SNP Genotyping Using the TaqManÂ® Assay. Methods in Molecular Biology, 2011, 700, 77-87.	0.4	55
54	Association of variants in the carnosine peptidase 1 gene (CNDP1) with diabetic nephropathy in American Indians. Molecular Genetics and Metabolism, 2011, 103, 185-190.	0.5	17

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55	Functional Characterization of the Plasmacytoma Variant Translocation 1 Gene (PVT1) in Diabetic Nephropathy. PLoS ONE, 2011, 6, e18671.	1.1	146
56	Differential Effects of Multiplicity of Infection on Helicobacter pylori-Induced Signaling Pathways and Interleukin-8 Gene Transcription. Journal of Clinical Immunology, 2011, 31, 60-68.	2.0	17
57	Identification of novel genetic markers and improved treatment options for diabetic kidney disease. Biomarkers in Medicine, 2010, 4, 739-741.	0.6	2
58	Perimenopausal Obesity. Journal of Women's Health, 2010, 19, 987-996.	1.5	44
59	ELMO1 variants and susceptibility to diabetic nephropathy in American Indians. Molecular Genetics and Metabolism, 2010, 101, 383-390.	0.5	44
60	Pharmacogenetics of Anti-Diabetes Drugs. Pharmaceuticals, 2010, 3, 2610-2646.	1.7	80
61	Genomeâ€wide SNP genotyping study using pooled DNA to identify candidate markers mediating susceptibility to endâ€stage renal disease attributed to Type 1 diabetes. Diabetic Medicine, 2009, 26, 1090-1098.	1.2	61
62	Pilot Study: Association of Traditional and Genetic Risk Factors and New-Onset Diabetes Mellitus Following Kidney Transplantation. Transplantation Proceedings, 2009, 41, 4172-4177.	0.3	30
63	Variants in the Plasmacytoma Variant Translocation Gene (PVT1) Are Associated With End-Stage Renal Disease Attributed to Type 1 Diabetes. Diabetes, 2007, 56, 3027-3032.	0.3	89
64	Meta-Analysis of Genome-Wide Linkage Studies of Quantitative Lipid Traits in Families Ascertained for Type 2 Diabetes. Diabetes, 2007, 56, 890-896.	0.3	33
65	Identification of PVT1 as a Candidate Gene for End-Stage Renal Disease in Type 2 Diabetes Using a Pooling-Based Genome-Wide Single Nucleotide Polymorphism Association Study. Diabetes, 2007, 56, 975-983.	0.3	184
66	Variants in the gene encoding aldose reductase (AKR1B1) and diabetic nephropathy in American Indians. Diabetic Medicine, 2006, 23, 367-376.	1.2	26
67	IL6 Gene Promoter Polymorphisms and Type 2 Diabetes: Joint Analysis of Individual Participants' Data From 21 Studies. Diabetes, 2006, 55, 2915-2921.	0.3	99
68	Sequence Variation in PPARG May Underlie Differential Response to Troglitazone. Diabetes, 2005, 54, 3319-3325.	0.3	65
69	Analysis of Quantitative Lipid Traits in the Genetics of NIDDM (GENNID) Study. Diabetes, 2005, 54, 3007-3014.	0.3	45
70	Common Polymorphisms in the Adiponectin Gene ACDC Are Not Associated With Diabetes in Pima Indians. Diabetes, 2005, 54, 284-289.	0.3	84
71	Meta-analysis of genome-wide linkage studies for quantitative lipid traits in African Americans. Human Molecular Genetics, 2005, 14, 3955-3962.	1.4	12
72	The interleukin-6 (â^'174) G/C promoter polymorphism is associated with type-2 diabetes mellitus in Native Americans and Caucasians. Human Genetics, 2003, 112, 409-413.	1.8	157

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73	Evaluation of the microsomal glutathione S-transferase 3 (MGST3) locus on 1q23 as a Type 2 diabetes susceptibility gene in Pima Indians. Human Genetics, 2003, 113, 353-358.	1.8	21
74	Association of a promoter variant in the inducible cyclooxygenase-2 gene (PTGS2) with typeï¿½2 diabetes mellitus in Pima Indians. Human Genetics, 2003, 113, 377-381.	1.8	71
75	Variants in the interleukin 6 receptor gene are associated with obesity in Pima Indians. Molecular Genetics and Metabolism, 2003, 80, 338-343.	0.5	65
76	A C-reactive protein promoter polymorphism is associated with type 2 diabetes mellitus in Pima Indians. Molecular Genetics and Metabolism, 2003, 78, 136-144.	0.5	84
77	Association of a F479L variant in the cytosolic phospholipase A2 gene (PLA2G4A) with decreased glucose turnover and oxidation rates in Pima Indians. Molecular Genetics and Metabolism, 2003, 79, 61-66.	0.5	15
78	Variant screening of PRKAB2, a type 2 diabetes mellitus susceptibility candidate gene on 1q in Pima Indians. Molecular and Cellular Probes, 2002, 16, 421-427.	0.9	4
79	Cloning, expression and genomic structure of human LMX1A, and variant screening in Pima Indians. Gene, 2002, 290, 217-225.	1.0	13
80	Estimation of single nucleotide polymorphism allele frequency in DNA pools by using Pyrosequencing. Human Genetics, 2002, 110, 395-401.	1.8	107
81	Identification of Susceptibility Genes for Complex Metabolic Diseases. Annals of the New York Academy of Sciences, 2002, 967, 1-6.	1.8	14
82	Molecular Analysis of KCNJ10 on 1q as a Candidate Gene for Type 2 Diabetes in Pima Indians. Diabetes, 2002, 51, 3342-3346.	0.3	16
83	Polymorphism screening of the insulin receptor-related receptor gene (INSRR) on 1q in Pima Indians. Molecular and Cellular Probes, 2001, 15, 223-227.	0.9	6
84	Subcutaneous Abdominal Adipocyte Size, a Predictor of Type 2 Diabetes, Is Linked to Chromosome 1q21â€“q23 and Is Associated with a Common Polymorphism in LMNA in Pima Indians. Molecular Genetics and Metabolism, 2001, 72, 231-238.	0.5	65
85	Analysis of SLC19A2, on 1q23.3 Encoding a Thiamine Transporter as a Candidate Gene for Type 2 Diabetes Mellitus in Pima Indians. Molecular Genetics and Metabolism, 2001, 72, 360-363.	0.5	16
86	Analysis of Linkage Disequilibrium between Polymorphisms in the KCNJ9 Gene with Type 2 Diabetes Mellitus in Pima Indians. Molecular Genetics and Metabolism, 2001, 73, 97-103.	0.5	23
87	Analysis of the Lamin A/C gene as a candidate for Type II diabetes susceptibility in Pima Indians. Diabetologia, 2001, 44, 779-782.	2.9	27
88	High-throughput SNP detection by using DNA pooling and denaturing high performance liquid chromatography (DHPLC). Human Genetics, 2000, 107, 483-487.	1.8	114
89	Genomic Structure and Expression of Human KCNJ9 (Kir3.3/GIRK3). Biochemical and Biophysical Research Communications, 2000, 274, 302-309.	1.0	19
90	Molecular characterization of the human PEA15 gene on 1q21â€“q22 and association with type 2 diabetes mellitus in Pima Indians. Gene, 2000, 241, 143-148.	1.0	23

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91	Genome-Wide Scan for CAG/CTG Repeat Expansions in Pimas with Early Onset of Type 2 Diabetes Mellitus. Molecular Genetics and Metabolism, 1999, 66, 62-67.	0.5	2
92	Structure and expression of the human MTG8/ETO gene. Gene, 1998, 212, 103-109.	1.0	71
93	Polymorphism in the 3â€² Untranslated Region ofMTG8Is Associated with Obesity in Pima Indian Males. Biochemical and Biophysical Research Communications, 1998, 246, 624-626.	1.0	17
94	Binding of Sequence-Specific Proteins to the 3â€²-Untranslated Region of Vasoactive Intestinal Peptide mRNA. Biochemical and Biophysical Research Communications, 1995, 211, 819-825.	1.0	4
95	Serotonergic involvement in the regulation of prolactin and vasoactive intestinal peptide mRNA expression in the rat anterior pituitary. Molecular and Cellular Endocrinology, 1994, 105, 183-191.	1.6	8