Lorna Harries

List of Publications by Year
in descending order

91 papers	6,021 citations	117625 34 h-index	74163 75 g-index
95 all docs	95 docs citations	95 times ranked	11182 citing authors

#	Article	IF	Citations
1	Replication of Genome-Wide Association Signals in UK Samples Reveals Risk Loci for Type 2 Diabetes. Science, 2007, 316, 1336-1341.	12.6	2,040
2	Methylomic profiling implicates cortical deregulation of ANK1 in Alzheimer's disease. Nature Neuroscience, 2014, 17, 1164-1170.	14.8	488
3	Long non-coding RNAs and human disease. Biochemical Society Transactions, 2012, 40, 902-906.	3.4	242
4	Human aging is characterized by focused changes in gene expression and deregulation of alternative splicing. Aging Cell, 2011, 10, 868-878.	6.7	230
5	Circular RNAs (circRNAs) in Health and Disease. Genes, 2017, 8, 353.	2.4	211
6	Human longevity: 25 genetic loci associated in 389,166 UK biobank participants. Aging, 2017, 9, 2504-2520.	3.1	145
7	Associations between PFOA, PFOS and changes in the expression of genes involved in cholesterol metabolism in humans. Environment International, 2013, 57-58, 2-10.	10.0	141
8	Isomers of the TCF1 gene encoding hepatocyte nuclear factor-1 alpha show differential expression in the pancreas and define the relationship between mutation position and clinical phenotype in monogenic diabetes. Human Molecular Genetics, 2006, 15, 2216-2224.	2.9	115
9	Human longevity is influenced by many genetic variants: evidence from 75,000 UK Biobank participants. Aging, 2016, 8, 547-560.	3.1	113
10	Increased expression of miR-187 in human islets from individuals with type 2 diabetes is associated with reduced glucose-stimulated insulin secretion. Diabetologia, 2014, 57, 122-128.	6.3	102
11	The DDX6â€“4E-T interaction mediates translational repression and P-body assembly. Nucleic Acids Research, 2016, 44, 6318-6334.	14.5	97
12	MicroRNAs as Mediators of the Ageing Process. Genes, 2014, 5, 656-670.	2.4	89
13	Changes in splicing factor expression are associated with advancing age in man. Mechanisms of Ageing and Development, 2013, 134, 356-366.	4.6	88
14	Changes in the expression of splicing factor transcripts and variations in alternative splicing are associated with lifespan in mice and humans. Aging Cell, 2016, 15, 903-913.	6.7	79
15	Small molecule modulation of splicing factor expression is associated with rescue from cellular senescence. BMC Cell Biology, 2017, 18, 31.	3.0	71
16	Alterations in LMTK2, MSMB and HNF1B gene expression are associated with the development of prostate cancer. BMC Cancer, 2010, 10, 315.	2.6	69
17	Species-Specific Differences in the Expression of the HNF1A, HNF1B and HNF4A Genes. PLoS ONE, 2009, 4, e7855.	2.5	67
18	The Diabetic Phenotype in HNF4A Mutation Carriers Is Moderated By the Expression of HNF4A Isoforms From the P1 Promoter During Fetal Development. Diabetes, 2008, 57, 1745-1752.	0.6	64

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19	Partial and whole gene deletion mutations of the GCK and HNF1A genes in maturity-onset diabetes of the young. Diabetologia, 2007, 50, 2313-2317.	6.3	59
20	Investigating the Targets of MIR-15a and MIR-16-1 in Patients with Chronic Lymphocytic Leukemia (CLL). PLoS ONE, 2009, 4, e7169.	2.5	58
21	Androgen-regulated transcription of ESRP2 drives alternative splicing patterns in prostate cancer. ELife, 2019, 8, .	6.0	56
22	Advancing age is associated with gene expression changes resembling mTOR inhibition: Evidence from two human populations. Mechanisms of Ageing and Development, 2012, 133, 556-562.	4.6	54
23	Mitochondria-targeted hydrogen sulfide attenuates endothelial senescence by selective induction of splicing factors HNRNPD and SRSF2. Aging, 2018, 10, 1666-1681.	3.1	54
24	Messenger RNA Transcripts of the Hepatocyte Nuclear Factor-1Â Gene Containing Premature Termination Codons Are Subject to Nonsense-Mediated Decay. Diabetes, 2004, 53, 500-504.	0.6	50
25	Red blood cell distribution width: Genetic evidence for aging pathways in 116,666 volunteers. PLoS ONE, 2017, 12, e0185083.	2.5	49
26	Splicing regulatory factors, ageing and age-related disease. Ageing Research Reviews, 2017, 36, 165-170.	10.9	48
27	The position of premature termination codons in the hepatocyte nuclear factor â˜1 beta gene determines susceptibility to nonsense-mediated decay. Human Genetics, 2005, 118, 214-224.	3.8	45
28	Human genetic variation and its effect on miRNA biogenesis, activity and function. Biochemical Society Transactions, 2014, 42, 1184-1189.	3.4	45
29	Role of microRNAs in the age-associated decline of pancreatic beta cell function in rat islets. Diabetologia, 2016, 59, 161-169.	6.3	44
30	RNA Biology Provides New Therapeutic Targets for Human Disease. Frontiers in Genetics, 2019, 10, 205.	2.3	42
31	Astrocyte senescence may drive alterations in GFAPÎ±, CDKN2A p14ARF, and TAU3 transcript expression and contribute to cognitive decline. GeroScience, 2019, 41, 561-573.	4.6	41
32	circRNAs expressed in human peripheral blood are associated with human aging phenotypes, cellular senescence and mouse lifespan. GeroScience, 2020, 42, 183-199.	4.6	40
33	Abnormal splicing of hepatocyte nuclear factor-1 beta in the renal cysts and diabetes syndrome. Diabetologia, 2004, 47, 937-942.	6.3	37
34	An alternative polyadenylation signal in TCF7L2 generates isoforms that inhibit T cell factor/lymphoid-enhancer factor (TCF/LEF)-dependent target genes. Diabetologia, 2011, 54, 3078-3082.	6.3	35
35	LeukocyteCCR2Expression Is Associated with Mini-Mental State Examination Score in Older Adults. Rejuvenation Research, 2012, 15, 395-404.	1.8	34
36	Negligible senescence in naked mole rats may be a consequence of well-maintained splicing regulation. GeroScience, 2020, 42, 633-651.	4.6	34

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37	A Role for SPARC in the Moderation of Human Insulin Secretion. PLoS ONE, 2013, 8, e68253.	2.5	34
38	Targeted Allelic Expression Profiling in Human Islets Identifies cis-Regulatory Effects for Multiple Variants Identified by Type 2 Diabetes Genome-Wide Association Studies. Diabetes, 2015, 64, 1484-1491.	0.6	31
39	A rare SNP in pre-miR-34a is associated with increased levels of miR-34a in pancreatic beta cells. Acta Diabetologica, 2014, 51, 325-329.	2.5	30
40	Islet-expressed circular RNAs are associated with type 2 diabetes status in human primary islets and in peripheral blood. BMC Medical Genomics, 2020, 13, 64.	1.5	30
41	The splice site variant rs11078928 may be associated with a genotype-dependent alteration in expression of GSDMB transcripts. BMC Genomics, 2013, 14, 627.	2.8	29
42	FOXO1 and ETV6 genes may represent novel regulators of splicing factor expression in cellular senescence. FASEB Journal, 2019, 33, 1086-1097.	0.5	27
43	Diabetes Susceptibility in the Canadian Oji-Cree Population Is Moderated by Abnormal mRNA Processing of HNF1A G319S Transcripts. Diabetes, 2008, 57, 1978-1982.	0.6	26
44	An engaged research study to assess the effect of a â€˜real-worldâ€™ dietary intervention on urinary bisphenol A (BPA) levels in teenagers. BMJ Open, 2018, 8, e018742.	1.9	26
45	Î²â€cell differentiation status in type 2 diabetes. Diabetes, Obesity and Metabolism, 2016, 18, 1167-1175.	4.4	25
46	Obesity impacts the regulation of miR-10b and its targets in primary breast tumors. BMC Cancer, 2019, 19, 86.	2.6	24
47	Abnormal splicing of hepatocyte nuclear factor 1 alpha in maturity-onset diabetes of the young. Diabetologia, 2002, 45, 1463-1467.	6.3	23
48	CCAATâ€enhancerâ€binding proteinâ€beta expression in vivo is associated with muscle strength. Aging Cell, 2012, 11, 262-268.	6.7	23
49	Gene expression markers of age-related inflammation in two human cohorts. Experimental Gerontology, 2015, 70, 37-45.	2.8	23
50	Peripheral Blood Transcriptomic Signatures of Fasting Glucose and Insulin Concentrations. Diabetes, 2016, 65, 3794-3804.	0.6	22
51	Altered cellular redox homeostasis and redox responses under standard oxygen cell culture conditions versus physioxia. Free Radical Biology and Medicine, 2018, 126, 322-333.	2.9	22
52	The VEGFA156b isoform is dysregulated in senescent endothelial cells and may be associated with prevalent and incident coronary heart disease. Clinical Science, 2018, 132, 313-325.	4.3	19
53	Conditional expression of hepatocyte nuclear factor-1Î², the maturity-onset diabetes of the young-5 gene product, influences the viability and functional competence of pancreatic Î²-cells. Journal of Endocrinology, 2006, 190, 171-181.	2.6	18
54	MicroRNAs miR-203-3p, miR-664-3p and miR-708-5p are associated with median strain lifespan in mice. Scientific Reports, 2017, 7, 44620.	3.3	17

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55	The transcript expression levels of HNRNPM, HNRNPA0 and AKAP17A splicing factors may be predictively associated with ageing phenotypes in human peripheral blood. Biogerontology, 2019, 20, 649-663.	3.9	17
56	Analysis of haematopoietic chimaerism by quantitative real-time polymerase chain reaction. Bone Marrow Transplantation, 2005, 35, 283-290.	2.4	16
57	A cautionary tale: the non-causal association between type 2 diabetes risk SNP, rs7756992, and levels of non-coding RNA, CDKAL1-v1. Diabetologia, 2015, 58, 745-748.	6.3	16
58	Cellular stressors may alter islet hormone cell proportions by moderation of alternative splicing patterns. Human Molecular Genetics, 2019, 28, 2763-2774.	2.9	16
59	Transcriptomic metaâ€analysis of disuse muscle atrophy vs. resistance exerciseâ€induced hypertrophy in young and older humans. Journal of Cachexia, Sarcopenia and Muscle, 2021, 12, 629-645.	7.3	15
60	Dysregulated RNA processing and metabolism: a new hallmark of ageing and provocation for cellular senescence. FEBS Journal, 2023, 290, 1221-1234.	4.7	15
61	Comparison of senescence-associated miRNAs in primary skin and lung fibroblasts. Biogerontology, 2015, 16, 423-434.	3.9	14
62	PFOA and PFOS are associated with reduced expression of the parathyroid hormone 2 receptor (PTH2R) gene in women. Chemosphere, 2015, 120, 555-562.	8.2	14
63	Functional characterisation of ADIPOQ variants using individuals recruited by genotype. Molecular and Cellular Endocrinology, 2016, 428, 49-57.	3.2	12
64	The Common HNF1A Variant I27L Is a Modifier of Age at Diabetes Diagnosis in Individuals With HNF1A-MODY. Diabetes, 2018, 67, 1903-1907.	0.6	12
65	A dynamical systems model for the measurement of cellular senescence. Journal of the Royal Society Interface, 2019, 16, 20190311.	3.4	12
66	Alternative splicing in serotonergic system: Implications in neuropsychiatric disorders. Journal of Psychopharmacology, 2019, 33, 1352-1363.	4.0	12
67	Persistence of clinically relevant levels of SARS-CoV2 envelope gene subgenomic RNAs in non-immunocompromised individuals. International Journal of Infectious Diseases, 2022, 116, 418-425.	3.3	12
68	Gene transcripts associated with muscle strength: a CHARGE meta-analysis of 7,781 persons. Physiological Genomics, 2016, 48, 1-11.	2.3	11
69	MicroRNA expression profiling of human islets from individuals with and without TypeÂ2 diabetes: promises and pitfalls. Biochemical Society Transactions, 2012, 40, 800-803.	3.4	10
70	Novel monogenic diabetes mutations in the P2 promoter of the HNF4A gene are associated with impaired function in vitro. Diabetic Medicine, 2010, 27, 631-635.	2.3	9
71	The Longevity-Associated SH2B3 (LNK) Genetic Variant: Selected Aging Phenotypes in 379,758 Subjects. Journals of Gerontology - Series A Biological Sciences and Medical Sciences, 2020, 75, 1656-1662.	3.6	9
72	Dietary restriction in ILSXISS mice is associated with widespread changes in splicing regulatory factor expression levels. Experimental Gerontology, 2019, 128, 110736.	2.8	8

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73	Splicing factor 3B1 hypomethylation is associated with altered SF3B1 transcript expression in older humans. Mechanisms of Ageing and Development, 2014, 135, 50-56.	4.6	7
74	A biallelic SNIP1 Amish founder variant causes a recognizable neurodevelopmental disorder. PLoS Genetics, 2021, 17, e1009803.	3.5	7
75	The species origin of the cellular microenvironment influences markers of beta cell fate and function in EndoC-Î²H1 cells. Experimental Cell Research, 2017, 361, 284-291.	2.6	6
76	Dysregulation of Hnf1b gene expression in cultured beta-cells in response to cytotoxic fatty acid. JOP: Journal of the Pancreas, 2011, 12, 6-10.	1.5	6
77	Alternate mRNA processing of the hepatocyte nuclear factor genes and its role in monogenic diabetes. Expert Review of Endocrinology and Metabolism, 2006, 1, 715-726.	2.4	5
78	Oxidative Metabolism Genes Are Not Responsive to Oxidative Stress in Rodent Beta Cell Lines. Experimental Diabetes Research, 2012, 2012, 1-5.	3.8	4
79	Comment on Dubois-Laforgue et al. Diabetes, Associated Clinical Spectrum, Long-term Prognosis, and Genotype/Phenotype Correlations in 201 Adult Patients With Hepatocyte Nuclear Factor 1B (HNF1B) Molecular Defects. Diabetes Care 2017;40:1436â€“1443. Diabetes Care, 2018, 41, e7-e7.	8.6	4
80	Targeting Alternative Splicing for Reversal of Cellular Senescence in the Context of Aesthetic Aging. Plastic and Reconstructive Surgery, 2021, 147, 25S-32S.	1.4	4
81	Senotherapeutic Drugs: A New Avenue for Skincare?. Plastic and Reconstructive Surgery, 2021, 148, 21S-26S.	1.4	4
82	Expression Profiling of Type 2 Diabetes Susceptibility Genes in the Pancreatic Islets, Adipose Tissue and Liver of Obese Mice. Experimental and Clinical Endocrinology and Diabetes, 2013, 121, 413-419.	1.2	3
83	miRNAs responsive to the diabetic microenvironment in the human beta cell line EndoC-Î²H1 may target genes in the FOXO, HIPPO and Lysine degradation pathways. Experimental Cell Research, 2019, 384, 111559.	2.6	3
84	RNA Processing and mRNA Surveillance in Monogenic Diabetes. Gene Regulation and Systems Biology, 2008, 2, GRSB.S782.	2.3	1
85	Variants in the isoformâ€specific coding regions of the HNF1A, HNF4A and HNF1B genes are not a common cause of familial, youngâ€onset diabetes or renal cysts and diabetes (RCAD). Diabetic Medicine, 2009, 26, 569-570.	2.3	1
86	Messenger RNA processing and its role in diabetes. Diabetic Medicine, 2011, 28, 1010-1017.	2.3	1
87	The biology of ageing and the omics revolution. Biogerontology, 2018, 19, 435-436.	3.9	1
88	Extreme longevity variants at the FOXO3 locus may moderate FOXO3 isoform levels. GeroScience, 2021, , 1.	4.6	1
89	An unusual case of cyclin-D1-positive peripheral T cell lymphoma with a 11:14 translocation. Journal of Hematopathology, 2010, 3, 77-81.	0.4	0
90	Physiological effects of Type 2 diabetes on mRNA processing and gene expression. Expert Review of Endocrinology and Metabolism, 2011, 6, 255-267.	2.4	0

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91	Changes to the identity of EndoC-Î²H1 beta cells may be mediated by stress-induced depletion of HNRNPD. Cell and Bioscience, 2021, 11, 144.	4.8	0