

David Humphreys

List of Publications by Citations

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Version: 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

43
papers

4,321
citations

25
h-index

44
g-index

44
ext. papers

5,073
ext. citations

9.7
avg, IF

4.95
L-index

#	Paper	IF	Citations
43	Insights into RNA biology from an atlas of mammalian mRNA-binding proteins. <i>Cell</i> , 2012 , 149, 1393-406	56.2	1328
42	Widespread occurrence of 5-methylcytosine in human coding and non-coding RNA. <i>Nucleic Acids Research</i> , 2012 , 40, 5023-33	20.1	605
41	MicroRNAs control translation initiation by inhibiting eukaryotic initiation factor 4E/cap and poly(A) tail function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 16961-6	11.5	486
40	Clusterin has chaperone-like activity similar to that of small heat shock proteins. <i>Journal of Biological Chemistry</i> , 1999 , 274, 6875-81	5.4	323
39	Glioma microvesicles carry selectively packaged coding and non-coding RNAs which alter gene expression in recipient cells. <i>RNA Biology</i> , 2013 , 10, 1333-44	4.8	181
38	Neuronal microRNA deregulation in response to Alzheimer's disease amyloid-beta. <i>PLoS ONE</i> , 2010 , 5, e11070	3.7	152
37	Target gene repression mediated by miRNAs miR-181c and miR-9 both of which are down-regulated by amyloid- β . <i>Journal of Molecular Neuroscience</i> , 2012 , 46, 324-35	3.3	121
36	NAD Deficiency, Congenital Malformations, and Niacin Supplementation. <i>New England Journal of Medicine</i> , 2017 , 377, 544-552	59.2	114
35	Male-lineage transmission of an acquired metabolic phenotype induced by grand-paternal obesity. <i>Molecular Metabolism</i> , 2016 , 5, 699-708	8.8	104
34	The human Piwi protein Hiwi2 associates with tRNA-derived piRNAs in somatic cells. <i>Nucleic Acids Research</i> , 2014 , 42, 8984-95	20.1	102
33	microRNA-mediated messenger RNA deadenylation contributes to translational repression in mammalian cells. <i>PLoS ONE</i> , 2009 , 4, e6783	3.7	78
32	Effects of clusterin overexpression on TNFalpha- and TGFbeta-mediated death of L929 cells. <i>Biochemistry</i> , 1997 , 36, 15233-43	3.2	76
31	Complexity of murine cardiomyocyte miRNA biogenesis, sequence variant expression and function. <i>PLoS ONE</i> , 2012 , 7, e30933	3.7	65
30	Genetic variation in the two-pore domain potassium channel, TASK-1, may contribute to an atrial substrate for arrhythmogenesis. <i>Journal of Molecular and Cellular Cardiology</i> , 2014 , 67, 69-76	5.8	51
29	Methods to analyze microRNA-mediated control of mRNA translation. <i>Methods in Enzymology</i> , 2007 , 431, 83-111	1.7	41
28	Modes of L929 cell death induced by TNF-alpha and other cytotoxic agents. <i>Cytokine</i> , 1999 , 11, 773-82	4	39
27	A Screening Approach to Identify Clinically Actionable Variants Causing Congenital Heart Disease in Exome Data. <i>Circulation Genomic and Precision Medicine</i> , 2018 , 11, e001978	5.2	37

26	A reexamination of the role of clusterin as a complement regulator. <i>Experimental Cell Research</i> , 1999 , 249, 13-21	4.2	37
25	Periconceptional undernutrition programs changes in insulin-signaling molecules and microRNAs in skeletal muscle in singleton and twin fetal sheep. <i>Biology of Reproduction</i> , 2014 , 90, 5	3.9	36
24	A heterozygous variant in the human cardiac miR-133 gene, MIR133A2, alters miRNA duplex processing and strand abundance. <i>BMC Genetics</i> , 2013 , 14, 18	2.6	34
23	Global phosphoproteomics identifies a major role for AKT and 14-3-3 in regulating EDC3. <i>Molecular and Cellular Proteomics</i> , 2010 , 9, 682-94	7.6	34
22	Impact of embryo number and maternal undernutrition around the time of conception on insulin signaling and gluconeogenic factors and microRNAs in the liver of fetal sheep. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2014 , 306, E1013-24	6	31
21	miRspring: a compact standalone research tool for analyzing miRNA-seq data. <i>Nucleic Acids Research</i> , 2013 , 41, e147	20.1	30
20	Impact of next-generation sequencing error on analysis of barcoded plasmid libraries of known complexity and sequence. <i>Nucleic Acids Research</i> , 2014 , 42, e129	20.1	28
19	Identification of clinically actionable variants from genome sequencing of families with congenital heart disease. <i>Genetics in Medicine</i> , 2019 , 21, 1111-1120	8.1	25
18	mRNA isoform diversity can obscure detection of miRNA-mediated control of translation. <i>Rna</i> , 2011 , 17, 1025-31	5.8	22
17	Sierra: discovery of differential transcript usage from polyA-captured single-cell RNA-seq data. <i>Genome Biology</i> , 2020 , 21, 167	18.3	21
16	PCR-based expression analysis and identification of microRNAs. <i>Journal of Rnai and Gene Silencing</i> , 2005 , 1, 44-9		17
15	Longitudinal structural, functional, and cellular myocardial alterations with chronic centrifugal continuous-flow left ventricular assist device support. <i>Journal of Heart and Lung Transplantation</i> , 2017 , 36, 722-731	5.8	14
14	Role of miRNAs and alternative mRNA 3'end cleavage and polyadenylation of their mRNA targets in cardiomyocyte hypertrophy. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2016 , 1859, 744-56	6	14
13	miRNA Effects on mRNA closed-loop formation during translation initiation. <i>Progress in Molecular and Subcellular Biology</i> , 2010 , 50, 99-112	3	13
12	Impact of periconceptional and preimplantation undernutrition on factors regulating myogenesis and protein synthesis in muscle of singleton and twin fetal sheep. <i>Physiological Reports</i> , 2015 , 3, e12495	2.6	11
11	Hif-1a suppresses ROS-induced proliferation of cardiac fibroblasts following myocardial infarction. <i>Cell Stem Cell</i> , 2021 ,	18	11
10	Impact of maternal undernutrition around the time of conception on factors regulating hepatic lipid metabolism and microRNAs in singleton and twin fetuses. <i>American Journal of Physiology - Endocrinology and Metabolism</i> , 2016 , 310, E148-59	6	9
9	Krüppel-like factor 1 is a core cardiomyogenic trigger in zebrafish. <i>Science</i> , 2021 , 372, 201-205	33.3	9

8	The promises and challenges of exome sequencing in familial, non-syndromic congenital heart disease. <i>International Journal of Cardiology</i> , 2017 , 230, 155-163	3.2	8
7	Computational analysis, biochemical purification, and detection of tRNA-derived small RNA fragments. <i>Methods in Molecular Biology</i> , 2014 , 1173, 157-67	1.4	6
6	Modeling and analysis of repeat RNA toxicity in Drosophila. <i>Methods in Molecular Biology</i> , 2013 , 1017, 173-92	1.4	3
5	Heterozygous loss of WBP11 function causes multiple congenital defects in humans and mice. <i>Human Molecular Genetics</i> , 2020 , 29, 3662-3678	5.6	3
4	Inhibition of translation initiation by a microRNA85-101		1
3	Exploring the Genetic Architecture of Spontaneous Coronary Artery Dissection Using Whole-Genome Sequencing.. <i>Circulation Genomic and Precision Medicine</i> , 2022 , 101161CIRCGEN121003527	5.2	1
2	Decoding the complex genetic causes of heart diseases using systems biology. <i>Biophysical Reviews</i> , 2015 , 7, 141-159	3.7	
1	Congenital Heart Disease Gene: a Curated Database for Congenital Heart Disease Genes.. <i>Circulation Genomic and Precision Medicine</i> , 2022 , 101161CIRCGEN121003539	5.2	