

# Michael Morley

## List of Publications by Year in descending order

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Version: 2024-02-01

26  
papers

5,164  
citations

361413

20  
h-index

552781

26  
g-index

26  
all docs

26  
docs citations

26  
times ranked

7862  
citing authors

#	ARTICLE	IF	CITATIONS
1	Differential expression of members of SOX family of transcription factors in failing human hearts. <i>Translational Research</i> , 2022, 242, 66-78.	5.0	6
2	Whole-Transcriptome Profiling of Human Heart Tissues Reveals the Potential Novel Players and Regulatory Networks in Different Cardiomyopathy Subtypes of Heart Failure. <i>Circulation Genomic and Precision Medicine</i> , 2021, 14, e003142.	3.6	7
3	Truncated titin proteins in dilated cardiomyopathy. <i>Science Translational Medicine</i> , 2021, 13, eabd7287.	12.4	39
4	Global analysis of histone modifications and long-range chromatin interactions revealed the differential cistrome changes and novel transcriptional players in human dilated cardiomyopathy. <i>Journal of Molecular and Cellular Cardiology</i> , 2020, 145, 30-42.	1.9	11
5	Genomics-First Evaluation of Heart Disease Associated With Titin-Truncating Variants. <i>Circulation</i> , 2019, 140, 42-54.	1.6	97
6	Antisense regulation of atrial natriuretic peptide expression. <i>JCI Insight</i> , 2019, 4, .	5.0	14
7	Single-Cell Transcriptomic Profiling of Pluripotent Stem Cell-Derived SCGB3A2+ Airway Epithelium. <i>Stem Cell Reports</i> , 2018, 10, 1579-1595.	4.8	78
8	A common variant alters SCN5A-miR-24 interaction and associates with heart failure mortality. <i>Journal of Clinical Investigation</i> , 2018, 128, 1154-1163.	8.2	34
9	Differentiation of Human Pluripotent Stem Cells into Functional Lung Alveolar Epithelial Cells. <i>Cell Stem Cell</i> , 2017, 21, 472-488.e10.	11.1	406
10	Discovery of Genetic Variation on Chromosome 5q22 Associated with Mortality in Heart Failure. <i>PLoS Genetics</i> , 2016, 12, e1006034.	3.5	34
11	RNA-Seq identifies novel myocardial gene expression signatures of heart failure. <i>Genomics</i> , 2015, 105, 83-89.	2.9	220
12	Genetic association study of QT interval highlights role for calcium signaling pathways in myocardial repolarization. <i>Nature Genetics</i> , 2014, 46, 826-836.	21.4	281
13	Genetic variation in radiation-induced cell death. <i>Genome Research</i> , 2012, 22, 332-339.	5.5	33
14	RNA-sequence analysis of human B-cells. <i>Genome Research</i> , 2011, 21, 991-998.	5.5	126
15	Polymorphic Cis- and Trans-Regulation of Human Gene Expression. <i>PLoS Biology</i> , 2010, 8, e1000480.	5.6	142
16	Genetic analysis of radiation-induced changes in human gene expression. <i>Nature</i> , 2009, 459, 587-591.	27.8	192
17	Monozygotic Twins Reveal Germline Contribution to Allelic Expression Differences. <i>American Journal of Human Genetics</i> , 2008, 82, 1357-1360.	6.2	55
18	Common genetic variants account for differences in gene expression among ethnic groups. <i>Nature Genetics</i> , 2007, 39, 226-231.	21.4	466

#	ARTICLE	IF	CITATIONS
19	Mapping determinants of human gene expression by regional and genome-wide association. Nature, 2005, 437, 1365-1369.	27.8	550
20	Genetic analysis of genome-wide variation in human gene expression. Nature, 2004, 430, 743-747.	27.8	1,146
21	Method for manufacturing whole-genome microarrays by rolling circle amplification. Genes Chromosomes and Cancer, 2004, 40, 72-77.	2.8	20
22	Direct IBD mapping: identical-by-descent mapping without genotyping. Genomics, 2004, 83, 335-345.	2.9	6
23	Natural variation in human gene expression assessed in lymphoblastoid cells. Nature Genetics, 2003, 33, 422-425.	21.4	533
24	Gene Expression Phenotype in Heterozygous Carriers of Ataxia Telangiectasia. American Journal of Human Genetics, 2002, 71, 791-800.	6.2	50
25	A Resource of Mapped Human Bacterial Artificial Chromosome Clones. Genome Research, 1999, 9, 989-993.	5.5	12
26	Making and reading microarrays. Nature Genetics, 1999, 21, 15-19.	21.4	606