

# Michael D Morgan

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7543183/publications.pdf>

Version: 2024-02-01

19  
papers

3,539  
citations

566801

15  
h-index

752256

20  
g-index

26  
all docs

26  
docs citations

26  
times ranked

7301  
citing authors

#	ARTICLE	IF	CITATIONS
1	Differential abundance testing on single-cell data using k-nearest neighbor graphs. <i>Nature Biotechnology</i> , 2022, 40, 245-253.	9.4	229
2	Coagulation factor V is a T-cell inhibitor expressed by leukocytes in COVID-19. <i>Science</i> , 2022, 25, 103971.	1.9	7
3	The impact of hypoxia on B cells in COVID-19. <i>EBioMedicine</i> , 2022, 77, 103878.	2.7	15
4	Single-cell multi-omics analysis of the immune response in COVID-19. <i>Nature Medicine</i> , 2021, 27, 904-916.	15.2	452
5	Longitudinal analysis reveals that delayed bystander CD8+ T cell activation and early immune pathology distinguish severe COVID-19 from mild disease. <i>Immunity</i> , 2021, 54, 1257-1275.e8.	6.6	230
6	Cells of the human intestinal tract mapped across space and time. <i>Nature</i> , 2021, 597, 250-255.	13.7	266
7	Tracing the emergence of primordial germ cells from bilaminar disc rabbit embryos and pluripotent stem cells. <i>Cell Reports</i> , 2021, 37, 109812.	2.9	37
8	Quantitative genetic analysis deciphers the impact of cis and trans regulation on cell-to-cell variability in protein expression levels. <i>PLoS Genetics</i> , 2020, 16, e1008686.	1.5	8
9	Ageing compromises mouse thymus function and remodels epithelial cell differentiation. <i>ELife</i> , 2020, 9, .	2.8	92
10	Challenges in measuring and understanding biological noise. <i>Nature Reviews Genetics</i> , 2019, 20, 536-548.	7.7	154
11	Batch effects in single-cell RNA-sequencing data are corrected by matching mutual nearest neighbors. <i>Nature Biotechnology</i> , 2018, 36, 421-427.	9.4	1,595
12	Genome-wide study of hair colour in UK Biobank explains most of the SNP heritability. <i>Nature Communications</i> , 2018, 9, 5271.	5.8	96
13	Genome-wide association study of response to methotrexate in early rheumatoid arthritis patients. <i>Pharmacogenomics Journal</i> , 2018, 18, 528-538.	0.9	42
14	CpG island composition differences are a source of gene expression noise indicative of promoter responsiveness. <i>Genome Biology</i> , 2018, 19, 81.	3.8	25
15	Blood Eosinophils and Outcomes in Severe Hospitalized Exacerbations of COPD. <i>Chest</i> , 2016, 150, 320-328.	0.4	125
16	Comprehensive respiratory assessment in advanced COPD: a "campus to clinic" translational framework. <i>Thorax</i> , 2015, 70, 805-808.	2.7	19
17	MTHFR functional genetic variation and methotrexate treatment response in rheumatoid arthritis: a meta-analysis. <i>Pharmacogenomics</i> , 2014, 15, 467-475.	0.6	16
18	Allele dose association of the C5orf30rs26232 variant with joint damage in rheumatoid arthritis. <i>Arthritis and Rheumatism</i> , 2013, 65, n/a-n/a.	6.7	20

#	ARTICLE	IF	CITATIONS
19	Evaluation of the rheumatoid arthritis susceptibility loci HLA-DRB1, PTPN22, OLIG3/TNFAIP3, STAT4 and TRAF1/C5 in an inception cohort. <i>Arthritis Research and Therapy</i> , 2010, 12, R57.	1.6	37