

# Olivier Delaneau

## List of Publications by Citations

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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.

41  
papers

8,453  
citations

26  
h-index

51  
g-index

51  
ext. papers

12,482  
ext. citations

18.7  
avg, IF

6.06  
L-index

#	Paper	IF	Citations
41	The UK Biobank resource with deep phenotyping and genomic data. <i>Nature</i> , <b>2018</b> , 562, 203-209	50.4	2108
40	A reference panel of 64,976 haplotypes for genotype imputation. <i>Nature Genetics</i> , <b>2016</b> , 48, 1279-83	36.3	1447
39	A linear complexity phasing method for thousands of genomes. <i>Nature Methods</i> , <b>2011</b> , 9, 179-81	21.6	1228
38	Improved whole-chromosome phasing for disease and population genetic studies. <i>Nature Methods</i> , <b>2013</b> , 10, 5-6	21.6	868
37	A general approach for haplotype phasing across the full spectrum of relatedness. <i>PLoS Genetics</i> , <b>2014</b> , 10, e1004234	6	377
36	Haplotype estimation using sequencing reads. <i>American Journal of Human Genetics</i> , <b>2013</b> , 93, 687-96	11	254
35	Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. <i>Nature Communications</i> , <b>2014</b> , 5, 3934	17.4	253
34	Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank. <i>Lancet Respiratory Medicine</i> , <b>2015</b> , 3, 769-81	35.1	245
33	Fast and efficient QTL mapper for thousands of molecular phenotypes. <i>Bioinformatics</i> , <b>2016</b> , 32, 1479-85	7.2	241
32	Population Variation and Genetic Control of Modular Chromatin Architecture in Humans. <i>Cell</i> , <b>2015</b> , 162, 1039-50	56.2	156
31	CD39/adenosine pathway is involved in AIDS progression. <i>PLoS Pathogens</i> , <b>2011</b> , 7, e1002110	7.6	128
30	Haplotype estimation for biobank-scale data sets. <i>Nature Genetics</i> , <b>2016</b> , 48, 817-20	36.3	121
29	Estimating the causal tissues for complex traits and diseases. <i>Nature Genetics</i> , <b>2017</b> , 49, 1676-1683	36.3	106
28	A complete tool set for molecular QTL discovery and analysis. <i>Nature Communications</i> , <b>2017</b> , 8, 15452	17.4	103
27	A genome-wide association study of shared risk across psychiatric disorders implicates gene regulation during fetal neurodevelopment. <i>Nature Neuroscience</i> , <b>2019</b> , 22, 353-361	25.5	93
26	Accurate, scalable and integrative haplotype estimation. <i>Nature Communications</i> , <b>2019</b> , 10, 5436	17.4	89
25	Biased allelic expression in human primary fibroblast single cells. <i>American Journal of Human Genetics</i> , <b>2015</b> , 96, 70-80	11	88

24	Association study of common genetic variants and HIV-1 acquisition in 6,300 infected cases and 7,200 controls. <i>PLoS Pathogens</i> , <b>2013</b> , 9, e1003515	7.6	86
23	Chromatin three-dimensional interactions mediate genetic effects on gene expression. <i>Science</i> , <b>2019</b> , 364,	33.3	85
22	Predicting causal variants affecting expression by using whole-genome sequencing and RNA-seq from multiple human tissues. <i>Nature Genetics</i> , <b>2017</b> , 49, 1747-1751	36.3	55
21	Genome-wide association study implicates PARD3B-based AIDS restriction. <i>Journal of Infectious Diseases</i> , <b>2011</b> , 203, 1491-502	7	45
20	Expression estimation and eQTL mapping for HLA genes with a personalized pipeline. <i>PLoS Genetics</i> , <b>2019</b> , 15, e1008091	6	34
19	Efficient phasing and imputation of low-coverage sequencing data using large reference panels. <i>Nature Genetics</i> , <b>2021</b> , 53, 120-126	36.3	33
18	A genome-wide association study in Caucasian women points out a putative role of the STXBP5L gene in facial photoaging. <i>Journal of Investigative Dermatology</i> , <b>2013</b> , 133, 929-35	4.3	32
17	Genome-wide association scan in HIV-1-infected individuals identifying variants influencing disease course. <i>PLoS ONE</i> , <b>2011</b> , 6, e22208	3.7	32
16	The effect of genetic variation on promoter usage and enhancer activity. <i>Nature Communications</i> , <b>2017</b> , 8, 1358	17.4	26
15	Multicohort genomewide association study reveals a new signal of protection against HIV-1 acquisition. <i>Journal of Infectious Diseases</i> , <b>2012</b> , 205, 1155-62	7	21
14	Genotype imputation using the Positional Burrows Wheeler Transform. <i>PLoS Genetics</i> , <b>2020</b> , 16, e1009049	4.9	18
13	MBV: a method to solve sample mislabeling and detect technical bias in large combined genotype and sequencing assay datasets. <i>Bioinformatics</i> , <b>2017</b> , 33, 1895-1897	7.2	15
12	Phasing for medical sequencing using rare variants and large haplotype reference panels. <i>Bioinformatics</i> , <b>2016</b> , 32, 1974-80	7.2	15
11	Identification of Genes Whose Expression Profile Is Associated with Non-Progression towards AIDS Using eQTLs. <i>PLoS ONE</i> , <b>2015</b> , 10, e0136989	3.7	7
10	Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome. <i>Nature Communications</i> , <b>2021</b> , 12, 5647	17.4	7
9	The genomic history of the Aegean palatial civilizations. <i>Cell</i> , <b>2021</b> , 184, 2565-2586.e21	56.2	7
8	Genotype imputation using the Positional Burrows Wheeler Transform		6
7	Gene regulation contributes to explain the impact of early life socioeconomic disadvantage on adult inflammatory levels in two cohort studies. <i>Scientific Reports</i> , <b>2021</b> , 11, 3100	4.9	6

6	High-throughput SARS-CoV-2 and host genome sequencing from single nasopharyngeal swabs <b>2020,</b>	4
5	Integrative haplotype estimation with sub-linear complexity	4
4	Efficient phasing and imputation of low-coverage sequencing data using large reference panels	3
3	Parent-of-origin effects in the UK Biobank	2
2	Improved whole-chromosome phasing for disease and population genetic studies	1
1	The molecular basis, genetic control and pleiotropic effects of local gene co-expression. <i>Nature Communications</i> , <b>2021</b> , 12, 4842	17.4 1