Olivier Delaneau

List of Publications by Year in Descending Order

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	Differentially expressed genes reflect disease-induced rather than disease-causing changes in the transcriptome. *Nature Communications*, **2021**, 12, 5647	17.4	7
40	The genomic history of the Aegean palatial civilizations. *Cell*, **2021**, 184, 2565-2586.e21	56.2	7
39	Efficient phasing and imputation of low-coverage sequencing data using large reference panels. *Nature Genetics*, **2021**, 53, 120-126	36.3	33
38	Gene regulation contributes to explain the impact of early life socioeconomic disadvantage on adult inflammatory levels in two cohort studies. *Scientific Reports*, **2021**, 11, 3100	4.9	6
37	The molecular basis, genetic control and pleiotropic effects of local gene co-expression. *Nature Communications*, **2021**, 12, 4842	17.4	1
36	Genotype imputation using the Positional Burrows Wheeler Transform. *PLoS Genetics*, **2020**, 16, e1009049	6	18
35	High-throughput SARS-CoV-2 and host genome sequencing from single nasopharyngeal swabs **2020**,		4
34	A genome-wide association study of shared risk across psychiatric disorders implicates gene regulation during fetal neurodevelopment. *Nature Neuroscience*, **2019**, 22, 353-361	25.5	93
33	Expression estimation and eQTL mapping for HLA genes with a personalized pipeline. *PLoS Genetics* , **2019**, 15, e1008091	6	34
32	Chromatin three-dimensional interactions mediate genetic effects on gene expression. *Science*, **2019**, 364,	33.3	85
31	Accurate, scalable and integrative haplotype estimation. *Nature Communications*, **2019**, 10, 5436	17.4	89
30	The UK Biobank resource with deep phenotyping and genomic data. *Nature*, **2018**, 562, 203-209	50.4	2108
29	MBV: a method to solve sample mislabeling and detect technical bias in large combined genotype and sequencing assay datasets. *Bioinformatics*, **2017**, 33, 1895-1897	7.2	15
28	A complete tool set for molecular QTL discovery and analysis. *Nature Communications*, **2017**, 8, 15452	17.4	103
27	Predicting causal variants affecting expression by using whole-genome sequencing and RNA-seq from multiple human tissues. *Nature Genetics*, **2017**, 49, 1747-1751	36.3	55
26	Estimating the causal tissues for complex traits and diseases. *Nature Genetics*, **2017**, 49, 1676-1683	36.3	106
25	The effect of genetic variation on promoter usage and enhancer activity. *Nature Communications*, **2017**, 8, 1358	17.4	26

24	A reference panel of 64,976 haplotypes for genotype imputation. *Nature Genetics*, **2016**, 48, 1279-83	36.3	1447
23	Haplotype estimation for biobank-scale data sets. *Nature Genetics*, **2016**, 48, 817-20	36.3	121
22	Fast and efficient QTL mapper for thousands of molecular phenotypes. *Bioinformatics*, **2016**, 32, 1479-85	7.2	241
21	Phasing for medical sequencing using rare variants and large haplotype reference panels. *Bioinformatics*, **2016**, 32, 1974-80	7.2	15
20	Novel insights into the genetics of smoking behaviour, lung function, and chronic obstructive pulmonary disease (UK BiLEVE): a genetic association study in UK Biobank. *Lancet Respiratory Medicine,the*, **2015**, 3, 769-81	35.1	245
19	Population Variation and Genetic Control of Modular Chromatin Architecture in Humans. *Cell*, **2015**, 162, 1039-50	56.2	156
18	Identification of Genes Whose Expression Profile Is Associated with Non-Progression towards AIDS Using eQTLs. *PLoS ONE*, **2015**, 10, e0136989	3.7	7
17	Biased allelic expression in human primary fibroblast single cells. *American Journal of Human Genetics*, **2015**, 96, 70-80	11	88
16	Integrating sequence and array data to create an improved 1000 Genomes Project haplotype reference panel. *Nature Communications*, **2014**, 5, 3934	17.4	253
15	A general approach for haplotype phasing across the full spectrum of relatedness. *PLoS Genetics*, **2014**, 10, e1004234	6	377
14	A genome-wide association study in Caucasian women points out a putative role of the STXBP5L gene in facial photoaging. *Journal of Investigative Dermatology*, **2013**, 133, 929-35	4.3	32
13	Haplotype estimation using sequencing reads. *American Journal of Human Genetics*, **2013**, 93, 687-96	11	254
12	Improved whole-chromosome phasing for disease and population genetic studies. *Nature Methods*, **2013**, 10, 5-6	21.6	868
11	Association study of common genetic variants and HIV-1 acquisition in 6,300 infected cases and 7,200 controls. *PLoS Pathogens*, **2013**, 9, e1003515	7.6	86
10	Multicohort genomewide association study reveals a new signal of protection against HIV-1 acquisition. *Journal of Infectious Diseases*, **2012**, 205, 1155-62	7	21
9	A linear complexity phasing method for thousands of genomes. *Nature Methods*, **2011**, 9, 179-81	21.6	1228
8	Genome-wide association study implicates PARD3B-based AIDS restriction. *Journal of Infectious Diseases*, **2011**, 203, 1491-502	7	45
7	CD39/adenosine pathway is involved in AIDS progression. *PLoS Pathogens*, **2011**, 7, e1002110	7.6	128

6	Genome-wide association scan in HIV-1-infected individuals identifying variants influencing disease course. *PLoS ONE*, **2011**, 6, e22208	3.7	32
5	Parent-of-origin effects in the UK Biobank		2
4	Improved whole-chromosome phasing for disease and population genetic studies		1
3	Efficient phasing and imputation of low-coverage sequencing data using large reference panels		3
2	Integrative haplotype estimation with sub-linear complexity		4
1	Genotype imputation using the Positional Burrows Wheeler Transform		6