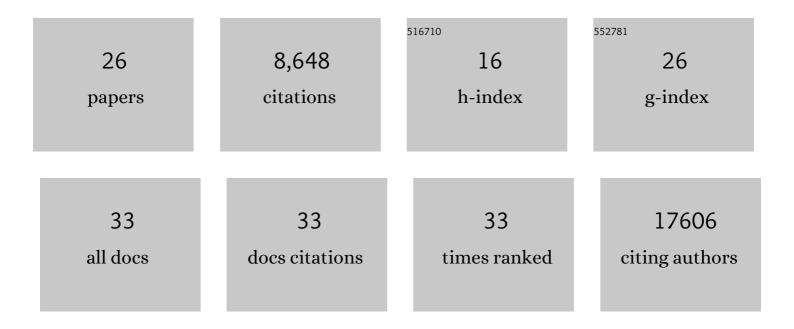
Philip A Ewels

List of Publications by Year in descending order

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DHILLD & FINELS

#	Article	IF	CITATIONS
1	Local selection signals in the genome of blue tits emphasize regulatory and neuronal evolution. Molecular Ecology, 2022, , .	3.9	1
2	Ten simple rules for making a software tool workflow-ready. PLoS Computational Biology, 2022, 18, e1009823.	3.2	7
3	Ultralow amounts of DNA from long-term archived serum samples produce high-quality methylomes. Clinical Epigenetics, 2021, 13, 107.	4.1	0
4	DIAproteomics: A Multifunctional Data Analysis Pipeline for Data-Independent Acquisition Proteomics and Peptidomics. Journal of Proteome Research, 2021, 20, 3758-3766.	3.7	17
5	Linkedâ€read sequencing enables haplotypeâ€resolved resequencing at population scale. Molecular Ecology Resources, 2020, 20, 1311-1322.	4.8	18
6	Building an international consortium for tracking coronavirus health status. Nature Medicine, 2020, 26, 1161-1165.	30.7	23
7	The nf-core framework for community-curated bioinformatics pipelines. Nature Biotechnology, 2020, 38, 276-278.	17.5	963
8	Sarek: A portable workflow for whole-genome sequencing analysis of germline and somatic variants. F1000Research, 2020, 9, 63.	1.6	21
9	Sarek: A portable workflow for whole-genome sequencing analysis of germline and somatic variants. F1000Research, 2020, 9, 63.	1.6	89
10	Genome-wide evidence supports mitochondrial relationships and pervasive parallel phenotypic evolution in open-habitat chats. Molecular Phylogenetics and Evolution, 2019, 139, 106568.	2.7	7
11	Transcriptomics and methylomics of CD4-positive T cells in arsenic-exposed women. Archives of Toxicology, 2017, 91, 2067-2078.	4.2	26
12	A Complete Overhaul of the Electron Energy-Loss Spectroscopy and X-Ray Absorption Spectroscopy Database: eelsdb.eu. Microscopy and Microanalysis, 2016, 22, 717-724.	0.4	83
13	Single base resolution analysis of 5-hydroxymethylcytosine in 188 human genes: implications for hepatic gene expression. Nucleic Acids Research, 2016, 44, 6756-6769.	14.5	15
14	MultiQC: summarize analysis results for multiple tools and samples in a single report. Bioinformatics, 2016, 32, 3047-3048.	4.1	4,633
15	Cluster Flow: A user-friendly bioinformatics workflow tool. F1000Research, 2016, 5, 2824.	1.6	18
16	Cluster Flow: A user-friendly bioinformatics workflow tool. F1000Research, 2016, 5, 2824.	1.6	16
17	HiCUP: pipeline for mapping and processing Hi-C data. F1000Research, 2015, 4, 1310.	1.6	485
18	Global Reorganization of the Nuclear Landscape in Senescent Cells. Cell Reports, 2015, 10, 471-483.	6.4	282

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#	Article	IF	CITATIONS
19	Mapping long-range promoter contacts in human cells with high-resolution capture Hi-C. Nature Genetics, 2015, 47, 598-606.	21.4	857
20	Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. Proceedings of the National Academy of Sciences of the United States of America, 2015, 112, 13970-13975.	7.1	192
21	Understanding functional miRNA–target interactions in vivo by site-specific genome engineering. Nature Communications, 2014, 5, 4640.	12.8	86
22	Meet the neighbours: tools to dissect nuclear structure and function. Briefings in Functional Genomics, 2011, 10, 11-17.	2.7	9
23	Large Scale Association Analysis of Novel Genetic Loci for Coronary Artery Disease. Arteriosclerosis, Thrombosis, and Vascular Biology, 2009, 29, 774-780.	2.4	140
24	Genetic determinants of ulcerative colitis include the ECM1 locus and five loci implicated in Crohn's disease. Nature Genetics, 2008, 40, 710-712.	21.4	403
25	High-Throughput Genotyping of <i>Salmonella enterica</i> Serovar Typhi Allowing Geographical Assignment of Haplotypes and Pathotypes within an Urban District of Jakarta, Indonesia. Journal of Clinical Microbiology, 2008, 46, 1741-1746.	3.9	69
26	Sorting nexin-1 defines an early phase of <i>Salmonella</i> -containing vacuole-remodeling during <i>Salmonella</i> infection. Journal of Cell Science, 2008, 121, 2027-2036.	2.0	92