

# Philip A Ewels

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/9144723/publications.pdf>

Version: 2024-02-01

26  
papers

8,648  
citations

516561

16  
h-index

552653

26  
g-index

33  
all docs

33  
docs citations

33  
times ranked

17606  
citing authors

#	ARTICLE	IF	CITATIONS
1	MultiQC: summarize analysis results for multiple tools and samples in a single report. <i>Bioinformatics</i> , 2016, 32, 3047-3048.	1.8	4,633
2	The nf-core framework for community-curated bioinformatics pipelines. <i>Nature Biotechnology</i> , 2020, 38, 276-278.	9.4	963
3	Mapping long-range promoter contacts in human cells with high-resolution capture Hi-C. <i>Nature Genetics</i> , 2015, 47, 598-606.	9.4	857
4	HiCUP: pipeline for mapping and processing Hi-C data. <i>F1000Research</i> , 2015, 4, 1310.	0.8	485
5	Genetic determinants of ulcerative colitis include the ECM1 locus and five loci implicated in Crohn's disease. <i>Nature Genetics</i> , 2008, 40, 710-712.	9.4	403
6	Global Reorganization of the Nuclear Landscape in Senescent Cells. <i>Cell Reports</i> , 2015, 10, 471-483.	2.9	282
7	Molecular signatures of plastic phenotypes in two eusocial insect species with simple societies. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 13970-13975.	3.3	192
8	Large Scale Association Analysis of Novel Genetic Loci for Coronary Artery Disease. <i>Arteriosclerosis, Thrombosis, and Vascular Biology</i> , 2009, 29, 774-780.	1.1	140
9	Sorting nexin-1 defines an early phase of <i>Salmonella</i> -containing vacuole-remodeling during <i>Salmonella</i> infection. <i>Journal of Cell Science</i> , 2008, 121, 2027-2036.	1.2	92
10	Sarek: A portable workflow for whole-genome sequencing analysis of germline and somatic variants. <i>F1000Research</i> , 2020, 9, 63.	0.8	89
11	Understanding functional miRNA-target interactions in vivo by site-specific genome engineering. <i>Nature Communications</i> , 2014, 5, 4640.	5.8	86
12	A Complete Overhaul of the Electron Energy-Loss Spectroscopy and X-Ray Absorption Spectroscopy Database: eelsdb.eu. <i>Microscopy and Microanalysis</i> , 2016, 22, 717-724.	0.2	83
13	High-Throughput Genotyping of <i>Salmonella enterica</i> Serovar Typhi Allowing Geographical Assignment of Haplotypes and Pathotypes within an Urban District of Jakarta, Indonesia. <i>Journal of Clinical Microbiology</i> , 2008, 46, 1741-1746.	1.8	69
14	Transcriptomics and methylomics of CD4-positive T cells in arsenic-exposed women. <i>Archives of Toxicology</i> , 2017, 91, 2067-2078.	1.9	26
15	Building an international consortium for tracking coronavirus health status. <i>Nature Medicine</i> , 2020, 26, 1161-1165.	15.2	23
16	Sarek: A portable workflow for whole-genome sequencing analysis of germline and somatic variants. <i>F1000Research</i> , 2020, 9, 63.	0.8	21
17	Linked-read sequencing enables haplotype-resolved resequencing at population scale. <i>Molecular Ecology Resources</i> , 2020, 20, 1311-1322.	2.2	18
18	Cluster Flow: A user-friendly bioinformatics workflow tool. <i>F1000Research</i> , 2016, 5, 2824.	0.8	18

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19	DIAProteomics: A Multifunctional Data Analysis Pipeline for Data-Independent Acquisition Proteomics and Peptidomics. <i>Journal of Proteome Research</i> , 2021, 20, 3758-3766.	1.8	17
20	Cluster Flow: A user-friendly bioinformatics workflow tool. <i>F1000Research</i> , 2016, 5, 2824.	0.8	16
21	Single base resolution analysis of 5-hydroxymethylcytosine in 188 human genes: implications for hepatic gene expression. <i>Nucleic Acids Research</i> , 2016, 44, 6756-6769.	6.5	15
22	Meet the neighbours: tools to dissect nuclear structure and function. <i>Briefings in Functional Genomics</i> , 2011, 10, 11-17.	1.3	9
23	Genome-wide evidence supports mitochondrial relationships and pervasive parallel phenotypic evolution in open-habitat chats. <i>Molecular Phylogenetics and Evolution</i> , 2019, 139, 106568.	1.2	7
24	Ten simple rules for making a software tool workflow-ready. <i>PLoS Computational Biology</i> , 2022, 18, e1009823.	1.5	7
25	Local selection signals in the genome of blue tits emphasize regulatory and neuronal evolution. <i>Molecular Ecology</i> , 2022, , .	2.0	1
26	Ultralow amounts of DNA from long-term archived serum samples produce high-quality methylomes. <i>Clinical Epigenetics</i> , 2021, 13, 107.	1.8	0