

# Belinda Phipson

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3214932/publications.pdf>

Version: 2024-02-01

40  
papers

31,762  
citations

201674

27  
h-index

330143

37  
g-index

50  
all docs

50  
docs citations

50  
times ranked

59059  
citing authors

#	ARTICLE	IF	CITATIONS
1	Sex-Specific Control of Human Heart Maturation by the Progesterone Receptor. <i>Circulation</i> , 2021, 143, 1614-1628.	1.6	42
2	Gene set enrichment analysis for genome-wide DNA methylation data. <i>Genome Biology</i> , 2021, 22, 173.	8.8	68
3	Single cell analysis of the developing mouse kidney provides deeper insight into marker gene expression and ligand-receptor crosstalk. <i>Development (Cambridge)</i> , 2019, 146, .	2.5	123
4	Evaluation of variability in human kidney organoids. <i>Nature Methods</i> , 2019, 16, 79-87.	19.0	176
5	Patient-iPSC-Derived Kidney Organoids Show Functional Validation of a Ciliopathic Renal Phenotype and Reveal Underlying Pathogenetic Mechanisms. <i>American Journal of Human Genetics</i> , 2018, 102, 816-831.	6.2	157
6	Haploinsufficiency for the Six2 gene increases nephron progenitor proliferation promoting branching and nephron number. <i>Kidney International</i> , 2018, 93, 589-598.	5.2	27
7	3D organoid-derived human glomeruli for personalised podocyte disease modelling and drug screening. <i>Nature Communications</i> , 2018, 9, 5167.	12.8	175
8	Shifts in ovine cardiopulmonary microRNA expression in late gestation and the perinatal period. <i>PLoS ONE</i> , 2018, 13, e0204038.	2.5	3
9	Exploring the single-cell RNA-seq analysis landscape with the scRNA-tools database. <i>PLoS Computational Biology</i> , 2018, 14, e1006245.	3.2	222
10	STRetch: detecting and discovering pathogenic short tandem repeat expansions. <i>Genome Biology</i> , 2018, 19, 121.	8.8	117
11	Modeling human hematopoiesis in pluripotent stem cells. <i>Experimental Hematology</i> , 2017, 53, S30.	0.4	0
12	Functionally distinct roles for different miR-155 expression levels through contrasting effects on gene expression, in acute myeloid leukaemia. <i>Leukemia</i> , 2017, 31, 808-820.	7.2	46
13	Splatter: simulation of single-cell RNA sequencing data. <i>Genome Biology</i> , 2017, 18, 174.	8.8	626
14	Gene length and detection bias in single cell RNA sequencing protocols. <i>F1000Research</i> , 2017, 6, 595.	1.6	76
15	Robust hyperparameter estimation protects against hypervariable genes and improves power to detect differential expression. <i>Annals of Applied Statistics</i> , 2016, 10, 946-963.	1.1	764
16	Differentiation of human embryonic stem cells to HOXA+ hemogenic vasculature that resembles the aorta-gonad-mesonephros. <i>Nature Biotechnology</i> , 2016, 34, 1168-1179.	17.5	150
17	missMethyl: an R package for analyzing data from Illumina's HumanMethylation450 platform. <i>Bioinformatics</i> , 2016, 32, 286-288.	4.1	573
18	A cross-package Bioconductor workflow for analysing methylation array data. <i>F1000Research</i> , 2016, 5, 1281.	1.6	93

#	ARTICLE	IF	CITATIONS
19	A cross-package Bioconductor workflow for analysing methylation array data. <i>F1000Research</i> , 2016, 5, 1281.	1.6	103
20	The Dose-Dependent Effects of MicroRNA-155 in Acute Myeloid Leukemia. <i>Blood</i> , 2016, 128, 2841-2841.	1.4	0
21	limma powers differential expression analyses for RNA-sequencing and microarray studies. <i>Nucleic Acids Research</i> , 2015, 43, e47-e47.	14.5	26,032
22	MOZ (MYST3, KAT6A) inhibits senescence via the INK4A-ARF pathway. <i>Oncogene</i> , 2015, 34, 5807-5820.	5.9	61
23	Early Lineage Priming by Trisomy of Erg Leads to Myeloproliferation in a Down Syndrome Model. <i>PLoS Genetics</i> , 2015, 11, e1005211.	3.5	16
24	MOZ and BMI1 play opposing roles during <i>Hox</i> gene activation in ES cells and in body segment identity specification in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5437-5442.	7.1	28
25	DiffVar: a new method for detecting differential variability with application to methylation in cancer and aging. <i>Genome Biology</i> , 2014, 15, 465.	8.8	84
26	The monocytic leukaemia zinc finger (MOZ) protein is a repressor of cellular senescence, and haploinsufficiency for MOZ increases survival 3-fold in the E $\mu$ 1/4-Myc lymphoma model. <i>Experimental Hematology</i> , 2013, 41, S54.	0.4	0
27	Polycomb repressive complex 2 (PRC2) suppresses E $\mu$ 1/4-myc lymphoma. <i>Blood</i> , 2013, 122, 2654-2663.	1.4	26
28	Neither loss of Bik alone, nor combined loss of Bik and Noxa, accelerate murine lymphoma development or render lymphoma cells resistant to DNA damaging drugs. <i>Cell Death and Disease</i> , 2012, 3, e306-e306.	6.3	9
29	Proteomic and Metabolomic Analyses of Mitochondrial Complex I-deficient Mouse Model Generated by Spontaneous B2 Short Interspersed Nuclear Element (SINE) Insertion into NADH Dehydrogenase (Ubiquinone) Fe-S Protein 4 (Ndufs4) Gene. <i>Journal of Biological Chemistry</i> , 2012, 287, 20652-20663.	3.4	58
30	Bcl-2, Bcl-xL, and Bcl-w are not equivalent targets of ABT-737 and navitoclax (ABT-263) in lymphoid and leukemic cells. <i>Blood</i> , 2012, 119, 5807-5816.	1.4	168
31	Aire regulates the transfer of antigen from mTECs to dendritic cells for induction of thymic tolerance. <i>Blood</i> , 2011, 118, 2462-2472.	1.4	174
32	Targeting Antigen to Mouse Dendritic Cells via Clec9A Induces Potent CD4 T Cell Responses Biased toward a Follicular Helper Phenotype. <i>Journal of Immunology</i> , 2011, 187, 842-850.	0.8	208
33	Opposing roles of polycomb repressive complexes in hematopoietic stem and progenitor cells. <i>Blood</i> , 2010, 116, 731-739.	1.4	117
34	Maximal killing of lymphoma cells by DNA damage-inducing therapy requires not only the p53 targets Puma and Noxa, but also Bim. <i>Blood</i> , 2010, 116, 5256-5267.	1.4	87
35	A recombination hotspot leads to sequence variability within a novel gene (AK005651) and contributes to type 1 diabetes susceptibility. <i>Genome Research</i> , 2010, 20, 1629-1638.	5.5	14
36	Permutation P-values Should Never Be Zero: Calculating Exact P-values When Permutations Are Randomly Drawn. <i>Statistical Applications in Genetics and Molecular Biology</i> , 2010, 9, Article39.	0.6	413

#	ARTICLE	IF	CITATIONS
37	Pro-Inflammatory CD11c+CD206+ Adipose Tissue Macrophages Are Associated With Insulin Resistance in Human Obesity. <i>Diabetes</i> , 2010, 59, 1648-1656.	0.6	521
38	Murine hematopoietic blast colony-forming cells and their progeny have distinctive membrane marker profiles. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 19102-19107.	7.1	9
39	Molecular dissection of the pea shoot apical meristem*. <i>Journal of Experimental Botany</i> , 2009, 60, 4201-4213.	4.8	13
40	A cross-package Bioconductor workflow for analysing methylation array data. <i>F1000Research</i> , 0, 5, 1281.	1.6	97