

# Charles Plessy

## List of Publications by Year in descending order

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Version: 2024-02-01

57  
papers

9,700  
citations

201658

27  
h-index

144002

57  
g-index

71  
all docs

71  
docs citations

71  
times ranked

15880  
citing authors

#	ARTICLE	IF	CITATIONS
1	Automated phenol-chloroform extraction of high molecular weight genomic DNA for use in long-read single-molecule sequencing. <i>F1000Research</i> , 2022, 11, 240.	1.6	4
2	Multi-omics analysis of hiPSCs-derived HLCs matured on a chip revealed patterns typical of liver regeneration. <i>Biotechnology and Bioengineering</i> , 2021, 118, 3716-3732.	3.3	7
3	Telomere-to-telomere assembly of the genome of an individual <i>Oikopleura dioica</i> from Okinawa using Nanopore-based sequencing. <i>BMC Genomics</i> , 2021, 22, 222.	2.8	18
4	Decoding Neuronal Diversification by Multiplexed Single-cell RNA-Seq. <i>Stem Cell Reports</i> , 2021, 16, 810-824.	4.8	8
5	Investigation of the hepatic development in the coculture of hiPSCs-derived LSECs and HLCs in a fluidic microenvironment. <i>APL Bioengineering</i> , 2021, 5, 026104.	6.2	8
6	A genome database for a Japanese population of the larvacean <i>Oikopleura dioica</i> . <i>Development Growth and Differentiation</i> , 2020, 62, 450-461.	1.5	13
7	Use of Cap Analysis Gene Expression to detect human papillomavirus promoter activity patterns at different disease stages. <i>Scientific Reports</i> , 2020, 10, 17991.	3.3	1
8	Characterization of liver zonation-like transcriptomic patterns in HLCs derived from hiPSCs in a microfluidic biochip environment. <i>Biotechnology Progress</i> , 2020, 36, e3013.	2.6	13
9	Analysis of hiPSCs differentiation toward hepatocyte-like cells upon extended exposition to oncostatin. <i>Differentiation</i> , 2020, 114, 36-48.	1.9	11
10	Machine-driven parameter screen of biochemical reactions. <i>Nucleic Acids Research</i> , 2020, 48, e37-e37.	14.5	0
11	RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions. <i>Nature Communications</i> , 2020, 11, 1018.	12.8	98
12	Integration of metabolomic and transcriptomic profiles of hiPSCs-derived hepatocytes in a microfluidic environment. <i>Biochemical Engineering Journal</i> , 2020, 155, 107490.	3.6	5
13	Transcriptome profiling of hiPSC-derived LSECs with nanoCAGE. <i>Molecular Omics</i> , 2020, 16, 138-146.	2.8	11
14	H3S28P Antibody Staining of Okinawan <i>Oikopleura dioica</i> Suggests the Presence of Three Chromosomes. <i>F1000Research</i> , 2020, 9, 780.	1.6	2
15	Centromere-specific antibody-mediated karyotyping of Okinawan <i>Oikopleura dioica</i> suggests the presence of three chromosomes. <i>F1000Research</i> , 2020, 9, 780.	1.6	2
16	C1 CAGE detects transcription start sites and enhancer activity at single-cell resolution. <i>Nature Communications</i> , 2019, 10, 360.	12.8	102
17	Optimized protocol for the hepatic differentiation of induced pluripotent stem cells in a fluidic microenvironment. <i>Biotechnology and Bioengineering</i> , 2019, 116, 1762-1776.	3.3	27
18	Analysis of the transcription factors and their regulatory roles during a step-by-step differentiation of induced pluripotent stem cells into hepatocyte-like cells. <i>Molecular Omics</i> , 2019, 15, 383-398.	2.8	11

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19	Profiling of derived-hepatocyte progenitors from induced pluripotent stem cells using nanoCAGE promoter analysis. <i>Biochemical Engineering Journal</i> , 2019, 142, 7-17.	3.6	9
20	Widespread use of the "œœascidian" mitochondrial genetic code in tunicates. <i>F1000Research</i> , 2019, 8, 2072.	1.6	3
21	Widespread use of the "œœascidian" mitochondrial genetic code in tunicates. <i>F1000Research</i> , 2019, 8, 2072.	1.6	2
22	SCPortalen: human and mouse single-cell centric database. <i>Nucleic Acids Research</i> , 2018, 46, D781-D787.	14.5	48
23	NanoCAGE: A Method for the Analysis of Coding and Noncoding 5' Capped Transcriptomes. <i>Methods in Molecular Biology</i> , 2017, 1543, 57-109.	0.9	29
24	Linking FANTOM5 CAGE peaks to annotations with CAGEscan. <i>Scientific Data</i> , 2017, 4, 170147.	5.3	29
25	Targeted reduction of highly abundant transcripts using pseudo-random primers. <i>BioTechniques</i> , 2016, 60, 169-174.	1.8	27
26	Characterization of Novel Transcripts of Human Papillomavirus Type 16 Using Cap Analysis Gene Expression Technology. <i>Journal of Virology</i> , 2015, 89, 2448-2452.	3.4	6
27	NanoCAGE analysis of the mouse olfactory epithelium identifies the expression of vomeronasal receptors and of proximal LINE elements. <i>Frontiers in Cellular Neuroscience</i> , 2014, 8, 41.	3.7	11
28	Digital expression profiling of the compartmentalized translome of Purkinje neurons. <i>Genome Research</i> , 2014, 24, 1396-1410.	5.5	49
29	Mesencephalic dopaminergic neurons express a repertoire of olfactory receptors and respond to odorant-like molecules. <i>BMC Genomics</i> , 2014, 15, 729.	2.8	46
30	A promoter-level mammalian expression atlas. <i>Nature</i> , 2014, 507, 462-470.	27.8	1,838
31	Two independent transcription initiation codes overlap on vertebrate core promoters. <i>Nature</i> , 2014, 507, 381-385.	27.8	182
32	Multiplicity of 5' Cap Structures Present on Short RNAs. <i>PLoS ONE</i> , 2014, 9, e102895.	2.5	29
33	Comparison of RNA- or LNA-hybrid oligonucleotides in template-switching reactions for high-speed sequencing library preparation. <i>BMC Genomics</i> , 2013, 14, 665.	2.8	23
34	Population transcriptomics with single-cell resolution: A new field made possible by microfluidics. <i>BioEssays</i> , 2013, 35, 131-140.	2.5	20
35	High-fidelity promoter profiling reveals widespread alternative promoter usage and transposon-driven developmental gene expression. <i>Genome Research</i> , 2013, 23, 169-180.	5.5	176
36	Suppression of artifacts and barcode bias in high-throughput transcriptome analyses utilizing template switching. <i>Nucleic Acids Research</i> , 2013, 41, e44-e44.	14.5	65

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37	Promoter architecture of mouse olfactory receptor genes. <i>Genome Research</i> , 2012, 22, 486-497.	5.5	52
38	NanoCAGE: A High-Resolution Technique to Discover and Interrogate Cell Transcriptomes. <i>Cold Spring Harbor Protocols</i> , 2011, 2011, pdb.prot5559-pdb.prot5559.	0.3	61
39	Community-driven computational biology with Debian Linux. <i>BMC Bioinformatics</i> , 2010, 11, S5.	2.6	42
40	Linking promoters to functional transcripts in small samples with nanoCAGE and CAGEscan. <i>Nature Methods</i> , 2010, 7, 528-534.	19.0	152
41	The genome sequence of the spontaneously hypertensive rat: Analysis and functional significance. <i>Genome Research</i> , 2010, 20, 791-803.	5.5	84
42	High-throughput verification of transcriptional starting sites by Deep-RACE. <i>BioTechniques</i> , 2009, 46, 130-132.	1.8	33
43	Tunable fractionation of nucleic acids. <i>BioTechniques</i> , 2009, 47, 1041-1043.	1.8	4
44	The regulated retrotransposon transcriptome of mammalian cells. <i>Nature Genetics</i> , 2009, 41, 563-571.	21.4	731
45	The transcriptional network that controls growth arrest and differentiation in a human myeloid leukemia cell line. <i>Nature Genetics</i> , 2009, 41, 553-562.	21.4	408
46	Unexpected expression of $\hat{1}\pm$ - and $\hat{1}^2$ -globin in mesencephalic dopaminergic neurons and glial cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 15454-15459.	7.1	240
47	A Resource for Transcriptomic Analysis in the Mouse Brain. <i>PLoS ONE</i> , 2008, 3, e3012.	2.5	11
48	Genome-wide analysis of mammalian promoter architecture and evolution. <i>Nature Genetics</i> , 2006, 38, 626-635.	21.4	1,201
49	The complexity of the mammalian transcriptome. <i>Journal of Physiology</i> , 2006, 575, 321-332.	2.9	91
50	Enhancer sequence conservation between vertebrates is favoured in developmental regulator genes. <i>Trends in Genetics</i> , 2005, 21, 207-210.	6.7	59
51	The Transcriptional Landscape of the Mammalian Genome. <i>Science</i> , 2005, 309, 1559-1563.	12.6	3,227
52	Expression Profiling and Comparative Genomics Identify a Conserved Regulatory Region Controlling Midline Expression in the Zebrafish Embryo. <i>Genome Research</i> , 2004, 14, 228-238.	5.5	34
53	Conserved and acquired features of neurogenin1 regulation. <i>Development (Cambridge)</i> , 2004, 131, 5627-5637.	2.5	59
54	Her5 acts as a prepattern factor that blocks neurogenin1 and coe2 expression upstream of Notch to inhibit neurogenesis at the midbrain-hindbrain boundary. <i>Development (Cambridge)</i> , 2004, 131, 1993-2006.	2.5	64

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55	Multiple regulatory elements with spatially and temporally distinct activities control neurogenin1 expression in primary neurons of the zebrafish embryo. <i>Mechanisms of Development</i> , 2003, 120, 211-218.	1.7	163
56	Precocious Expression of the <i>Glide/Gcm</i> Glial-Promoting Factor in <i>Drosophila</i> Induces Neurogenesis. <i>Genetics</i> , 2002, 160, 1095-1106.	2.9	9
57	Expression of brain subtype creatine kinase in the zebrafish embryo. <i>Mechanisms of Development</i> , 2001, 109, 409-412.	1.7	21