

Colm E Nestor

List of Publications by Year in descending order

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Version: 2024-02-01

33
papers

2,422
citations

331259

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395343

33
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docs citations

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times ranked

4712
citing authors

#	ARTICLE	IF	CITATIONS
1	CD4 ⁺ T-cell DNA methylation changes during pregnancy significantly correlate with disease-associated methylation changes in autoimmune diseases. <i>Epigenetics</i> , 2022, 17, 1040-1055.	1.3	4
2	Progesterone Inhibits the Establishment of Activation-Associated Chromatin During TH1 Differentiation. <i>Frontiers in Immunology</i> , 2022, 13, 835625.	2.2	7
3	TET2 as a tumor suppressor and therapeutic target in T-cell acute lymphoblastic leukemia. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	3.3	29
4	Mapping DNA Methylation in Mammals: The State of the Art. <i>Methods in Molecular Biology</i> , 2021, 2198, 37-50.	0.4	3
5	Analyzing DNA-Immunoprecipitation Sequencing Data. <i>Methods in Molecular Biology</i> , 2021, 2198, 431-439.	0.4	0
6	DNA methylation in infants with low and high body fatness. <i>BMC Genomics</i> , 2020, 21, 769.	1.2	1
7	No evidence for DNA N ⁶ -methyladenine in mammals. <i>Science Advances</i> , 2020, 6, eaay3335.	4.7	102
8	A validated single-cell-based strategy to identify diagnostic and therapeutic targets in complex diseases. <i>Genome Medicine</i> , 2019, 11, 47.	3.6	68
9	TCF / LEF dependent and independent transcriptional regulation of Wnt/β-catenin target genes. <i>EMBO Journal</i> , 2019, 38, .	3.5	142
10	DNA methylation as a genomic marker of exposure to chemical and environmental agents. <i>Current Opinion in Chemical Biology</i> , 2018, 45, 48-56.	2.8	55
11	A reassessment of DNA-immunoprecipitation-based genomic profiling. <i>Nature Methods</i> , 2018, 15, 499-504.	9.0	92
12	GAB2 regulates type 2 T helper cell differentiation in humans. <i>Cytokine</i> , 2017, 96, 234-237.	1.4	3
13	LASSI—A network inference toolbox for genome-wide mechanistic modeling. <i>PLoS Computational Biology</i> , 2017, 13, e1005608.	1.5	6
14	Potential Involvement of Type I Interferon Signaling in Immunotherapy in Seasonal Allergic Rhinitis. <i>Journal of Immunology Research</i> , 2016, 2016, 1-6.	0.9	4
15	5-Hydroxymethylcytosine Remodeling Precedes Lineage Specification during Differentiation of Human CD4 ⁺ T Cells. <i>Cell Reports</i> , 2016, 16, 559-570.	2.9	56
16	Dynamic Response Genes in CD4 ⁺ T Cells Reveal a Network of Interactive Proteins that Classifies Disease Activity in Multiple Sclerosis. <i>Cell Reports</i> , 2016, 16, 2928-2939.	2.9	38
17	Rapid reprogramming of epigenetic and transcriptional profiles in mammalian culture systems. <i>Genome Biology</i> , 2015, 16, 11.	3.8	137
18	5-Hydroxymethylcytosine Profiling in Human DNA. <i>Methods in Molecular Biology</i> , 2015, 1589, 89-98.	0.4	4

#	ARTICLE	IF	CITATIONS
19	A validated gene regulatory network and GWAS identifies early regulators of T cell-associated diseases. <i>Science Translational Medicine</i> , 2015, 7, 313ra178.	5.8	66
20	Modules, networks and systems medicine for understanding disease and aiding diagnosis. <i>Genome Medicine</i> , 2014, 6, 82.	3.6	169
21	DNA Methylation Changes Separate Allergic Patients from Healthy Controls and May Reflect Altered CD4+ T-Cell Population Structure. <i>PLoS Genetics</i> , 2014, 10, e1004059.	1.5	70
22	Integrated genomic and prospective clinical studies show the importance of modular pleiotropy for disease susceptibility, diagnosis and treatment. <i>Genome Medicine</i> , 2014, 6, 17.	3.6	27
23	Investigating 5-Hydroxymethylcytosine (5hmC): The State of the Art. <i>Methods in Molecular Biology</i> , 2014, 1094, 243-258.	0.4	16
24	Hydroxymethylated DNA Immunoprecipitation (hmeDIP). <i>Methods in Molecular Biology</i> , 2014, 1094, 259-267.	0.4	27
25	Targeted omics and systems medicine: personalising care. <i>Lancet Respiratory Medicine</i> , 2014, 2, 785-787.	5.2	20
26	Redistribution of H3K27me3 upon DNA hypomethylation results in de-repression of Polycomb target genes. <i>Genome Biology</i> , 2013, 14, R25.	13.9	200
27	Comparative analysis of affinity-based 5-hydroxymethylation enrichment techniques. <i>Nucleic Acids Research</i> , 2013, 41, e206-e206.	6.5	44
28	Promoter DNA methylation couples genome-defence mechanisms to epigenetic reprogramming in the mouse germline. <i>Development (Cambridge)</i> , 2012, 139, 3623-3632.	1.2	130
29	Tissue of origin determines cancer-associated CpG island promoter hypermethylation patterns. <i>Genome Biology</i> , 2012, 13, R84.	13.9	140
30	Non-genotoxic carcinogen exposure induces defined changes in the 5-hydroxymethylome. <i>Genome Biology</i> , 2012, 13, R93.	13.9	74
31	Tissue type is a major modifier of the 5-hydroxymethylcytosine content of human genes. <i>Genome Research</i> , 2012, 22, 467-477.	2.4	348
32	Transcriptionally repressed genes become aberrantly methylated and distinguish tumors of different lineages in breast cancer. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 4364-4369.	3.3	144
33	Enzymatic approaches and bisulfite sequencing cannot distinguish between 5-methylcytosine and 5-hydroxymethylcytosine in DNA. <i>BioTechniques</i> , 2010, 48, 317-319.	0.8	193