Colm E Nestor

List of Publications by Year
in descending order

33 papers	2,422 citations	304743 22 h-index	395702 33 g-index
34 all docs	34 docs citations	34 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. Epigenetics, 2022, 17, 1040-1055.	2.7	4
2	Progesterone Inhibits the Establishment of Activation-Associated Chromatin During TH1 Differentiation. Frontiers in Immunology, 2022, 13, 835625.	4.8	7
3	TET2 as a tumor suppressor and therapeutic target in T-cell acute lymphoblastic leukemia. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	29
4	Mapping DNA Methylation in Mammals: The State of the Art. Methods in Molecular Biology, 2021, 2198, 37-50.	0.9	3
5	Analyzing DNA-Immunoprecipitation Sequencing Data. Methods in Molecular Biology, 2021, 2198, 431-439.	0.9	0
6	DNA methylation in infants with low and high body fatness. BMC Genomics, 2020, 21, 769.	2.8	1
7	No evidence for DNA N ⁶-methyladenine in mammals. Science Advances, 2020, 6, eaay3335.	10.3	102
8	A validated single-cell-based strategy to identify diagnostic and therapeutic targets in complex diseases. Genome Medicine, 2019, 11, 47.	8.2	68
9	TCF / LEF dependent and independent transcriptional regulation of Wnt/Î²â€atenin target genes. EMBO Journal, 2019, 38, .	7.8	142
10	DNA methylation as a genomic marker of exposure to chemical and environmental agents. Current Opinion in Chemical Biology, 2018, 45, 48-56.	6.1	55
11	A reassessment of DNA-immunoprecipitation-based genomic profiling. Nature Methods, 2018, 15, 499-504.	19.0	92
12	GAB2 regulates type 2 T helper cell differentiation in humans. Cytokine, 2017, 96, 234-237.	3.2	3
13	LASSIMâ€"A network inference toolbox for genome-wide mechanistic modeling. PLoS Computational Biology, 2017, 13, e1005608.	3.2	6
14	Potential Involvement of Type I Interferon Signaling in Immunotherapy in Seasonal Allergic Rhinitis. Journal of Immunology Research, 2016, 2016, 1-6.	2.2	4
15	5-Hydroxymethylcytosine Remodeling Precedes Lineage Specification during Differentiation of Human CD4+ T Cells. Cell Reports, 2016, 16, 559-570.	6.4	56
16	Dynamic Response Genes in CD4+ T Cells Reveal a Network of Interactive Proteins that Classifies Disease Activity in Multiple Sclerosis. Cell Reports, 2016, 16, 2928-2939.	6.4	38
17	Rapid reprogramming of epigenetic and transcriptional profiles in mammalian culture systems. Genome Biology, 2015, 16, 11.	8.8	137
18	5-Hydroxymethylcytosine Profiling in Human DNA. Methods in Molecular Biology, 2015, 1589, 89-98.	0.9	4

#	Article	IF	Citations
19	A validated gene regulatory network and GWAS identifies early regulators of T cell–associated diseases. Science Translational Medicine, 2015, 7, 313ra178.	12.4	66
20	Modules, networks and systems medicine for understanding disease and aiding diagnosis. Genome Medicine, 2014, 6, 82.	8.2	169
21	DNA Methylation Changes Separate Allergic Patients from Healthy Controls and May Reflect Altered CD4+ T-Cell Population Structure. PLoS Genetics, 2014, 10, e1004059.	3.5	70
22	Integrated genomic and prospective clinical studies show the importance of modular pleiotropy for disease susceptibility, diagnosis and treatment. Genome Medicine, 2014, 6, 17.	8.2	27
23	Investigating 5-Hydroxymethylcytosine (5hmC): The State of the Art. Methods in Molecular Biology, 2014, 1094, 243-258.	0.9	16
24	Hydroxymethylated DNA Immunoprecipitation (hmeDIP). Methods in Molecular Biology, 2014, 1094, 259-267.	0.9	27
25	Targeted omics and systems medicine: personalising care. Lancet Respiratory Medicine,the, 2014, 2, 785-787.	10.7	20
26	Redistribution of H3K27me3 upon DNA hypomethylation results in de-repression of Polycomb target genes. Genome Biology, 2013, 14, R25.	9.6	200
27	Comparative analysis of affinity-based 5-hydroxymethylation enrichment techniques. Nucleic Acids Research, 2013, 41, e206-e206.	14.5	44
28	Promoter DNA methylation couples genome-defence mechanisms to epigenetic reprogramming in the mouse germline. Development (Cambridge), 2012, 139, 3623-3632.	2.5	130
29	Tissue of origin determines cancer-associated CpG island promoter hypermethylation patterns. Genome Biology, 2012, 13, R84.	9.6	140
30	Non-genotoxic carcinogen exposure induces defined changes in the 5-hydroxymethylome. Genome Biology, 2012, 13, R93.	9.6	74
31	Tissue type is a major modifier of the 5-hydroxymethylcytosine content of human genes. Genome Research, 2012, 22, 467-477.	5.5	348
32	Transcriptionally repressed genes become aberrantly methylated and distinguish tumors of different lineages in breast cancer. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 4364-4369.	7.1	144
33	Enzymatic approaches and bisulfite sequencing cannot distinguish between 5-methylcytosine and 5-hydroxymethylcytosine in DNA. BioTechniques, 2010, 48, 317-319.	1.8	193