# Colm E Nestor

List of Publications by Year
in descending order

| 33 papers | 2,422 citations | 331259<br>21<br>h-index | 395343<br>33<br>g-index |
|---|---|---|---|
| 34<br>all docs | 34<br>docs citations | 34<br>times ranked | 4712<br>citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | Tissue type is a major modifier of the 5-hydroxymethylcytosine content of human genes. Genome Research, 2012, 22, 467-477. | 2.4 | 348 |
| 2 | Redistribution of H3K27me3 upon DNA hypomethylation results in de-repression of Polycomb target genes. Genome Biology, 2013, 14, R25. | 13.9 | 200 |
| 3 | Enzymatic approaches and bisulfite sequencing cannot distinguish between 5-methylcytosine and 5-hydroxymethylcytosine in DNA. BioTechniques, 2010, 48, 317-319. | 0.8 | 193 |
| 4 | Modules, networks and systems medicine for understanding disease and aiding diagnosis. Genome Medicine, 2014, 6, 82. | 3.6 | 169 |
| 5 | 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. | 3.3 | 144 |
| 6 | <scp>TCF</scp> / <scp>LEF</scp> dependent and independent transcriptional regulation of Wnt/β‐catenin target genes. EMBO Journal, 2019, 38, . | 3.5 | 142 |
| 7 | Tissue of origin determines cancer-associated CpG island promoter hypermethylation patterns. Genome Biology, 2012, 13, R84. | 13.9 | 140 |
| 8 | Rapid reprogramming of epigenetic and transcriptional profiles in mammalian culture systems. Genome Biology, 2015, 16, 11. | 3.8 | 137 |
| 9 | Promoter DNA methylation couples genome-defence mechanisms to epigenetic reprogramming in the mouse germline. Development (Cambridge), 2012, 139, 3623-3632. | 1.2 | 130 |
| 10 | No evidence for DNA $N^6$-methyladenine in mammals. Science Advances, 2020, 6, eaay3335. | 4.7 | 102 |
| 11 | A reassessment of DNA-immunoprecipitation-based genomic profiling. Nature Methods, 2018, 15, 499-504. | 9.0 | 92 |
| 12 | Non-genotoxic carcinogen exposure induces defined changes in the 5-hydroxymethylome. Genome Biology, 2012, 13, R93. | 13.9 | 74 |
| 13 | DNA Methylation Changes Separate Allergic Patients from Healthy Controls and May Reflect Altered CD4+ T-Cell Population Structure. PLoS Genetics, 2014, 10, e1004059. | 1.5 | 70 |
| 14 | A validated single-cell-based strategy to identify diagnostic and therapeutic targets in complex diseases. Genome Medicine, 2019, 11, 47. | 3.6 | 68 |
| 15 | A validated gene regulatory network and GWAS identifies early regulators of T cell‐associated diseases. Science Translational Medicine, 2015, 7, 313ra178. | 5.8 | 66 |
| 16 | 5-Hydroxymethylcytosine Remodeling Precedes Lineage Specification during Differentiation of Human CD4+ T Cells. Cell Reports, 2016, 16, 559-570. | 2.9 | 56 |
| 17 | DNA methylation as a genomic marker of exposure to chemical and environmental agents. Current Opinion in Chemical Biology, 2018, 45, 48-56. | 2.8 | 55 |
| 18 | Comparative analysis of affinity-based 5-hydroxymethylation enrichment techniques. Nucleic Acids Research, 2013, 41, e206-e206. | 6.5 | 44 |

| # | Article | IF | Citations |
|---|---------|-----|-----------|
| 19 | 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. | 2.9 | 38 |
| 20 | 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, . | 3.3 | 29 |
| 21 | Integrated genomic and prospective clinical studies show the importance of modular pleiotropy for disease susceptibility, diagnosis and treatment. Genome Medicine, 2014, 6, 17. | 3.6 | 27 |
| 22 | Hydroxymethylated DNA Immunoprecipitation (hmeDIP). Methods in Molecular Biology, 2014, 1094, 259-267. | 0.4 | 27 |
| 23 | Targeted omics and systems medicine: personalising care. Lancet Respiratory Medicine,the, 2014, 2, 785-787. | 5.2 | 20 |
| 24 | Investigating 5-Hydroxymethylcytosine (5hmC): The State of the Art. Methods in Molecular Biology, 2014, 1094, 243-258. | 0.4 | 16 |
| 25 | Progesterone Inhibits the Establishment of Activation-Associated Chromatin During TH1 Differentiation. Frontiers in Immunology, 2022, 13, 835625. | 2.2 | 7 |
| 26 | LASSIMâ€"A network inference toolbox for genome-wide mechanistic modeling. PLoS Computational Biology, 2017, 13, e1005608. | 1.5 | 6 |
| 27 | 5-Hydroxymethylcytosine Profiling in Human DNA. Methods in Molecular Biology, 2015, 1589, 89-98. | 0.4 | 4 |
| 28 | Potential Involvement of Type I Interferon Signaling in Immunotherapy in Seasonal Allergic Rhinitis. Journal of Immunology Research, 2016, 2016, 1-6. | 0.9 | 4 |
| 29 | CD4+T-cell DNA methylation changes during pregnancy significantly correlate with disease-associated methylation changes in autoimmune diseases. Epigenetics, 2022, 17, 1040-1055. | 1.3 | 4 |
| 30 | GAB2 regulates type 2 T helper cell differentiation in humans. Cytokine, 2017, 96, 234-237. | 1.4 | 3 |
| 31 | Mapping DNA Methylation in Mammals: The State of the Art. Methods in Molecular Biology, 2021, 2198, 37-50. | 0.4 | 3 |
| 32 | DNA methylation in infants with low and high body fatness. BMC Genomics, 2020, 21, 769. | 1.2 | 1 |
| 33 | Analyzing DNA-Immunoprecipitation Sequencing Data. Methods in Molecular Biology, 2021, 2198, 431-439. | 0.4 | 0 |