

# Eugene Andres Houseman

## List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

8

papers

2,405

citations

8

h-index

9

g-index

9

ext. papers

3,078

ext. citations

5.4

avg, IF

4.71

L-index

| # | Paper  | IF   | Citations |
|---|--|------|-----------|
| 8 | Guidelines for cell-type heterogeneity quantification based on a comparative analysis of reference-free DNA methylation deconvolution software. <i>BMC Bioinformatics</i> , <b>2020</b> , 21, 16       | 3.6  | 11        |
| 7 | A Pan-Cancer Analysis Reveals High-Frequency Genetic Alterations in Mediators of Signaling by the TGF- $\beta$ Superfamily. <i>Cell Systems</i> , <b>2018</b> , 7, 422-437.e7                          | 10.6 | 85        |
| 6 | Maternal serum PFOA concentration and DNA methylation in cord blood: A pilot study. <i>Environmental Research</i> , <b>2017</b> , 158, 174-178   | 7.9  | 17        |
| 5 | Nightshift work, chronotype, and genome-wide DNA methylation in blood. <i>Epigenetics</i> , <b>2017</b> , 12, 833-840.   | 9.7  | 15        |
| 4 | Reference-free deconvolution of DNA methylation data and mediation by cell composition effects. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 259  | 3.6  | 134       |
| 3 | Normal cell-type epigenetics and breast cancer classification: a case study of cell mixture-adjusted analysis of DNA methylation data from tumors. <i>Cancer Informatics</i> , <b>2014</b> , 13, 53-64 | 2.4  | 12        |
| 2 | Reference-free cell mixture adjustments in analysis of DNA methylation data. <i>Bioinformatics</i> , <b>2014</b> , 30, 1431-9  | 7.2  | 316       |
| 1 | DNA methylation arrays as surrogate measures of cell mixture distribution. <i>BMC Bioinformatics</i> , <b>2012</b> , 13, 86  | 3.6  | 1815      |