

# Halit Ongen

## 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.

15  
papers

6,203  
citations

12  
h-index

21  
g-index

21  
ext. papers

7,949  
ext. citations

19.4  
avg, IF

4.37  
L-index

| #  | Paper  | IF   | Citations |
|----|--|------|-----------|
| 15 | MethCORR modelling of methylomes from formalin-fixed paraffin-embedded tissue enables characterization and prognostication of colorectal cancer. <i>Nature Communications</i> , <b>2020</b> , 11, 2025   | 17.4 | 2         |
| 14 | Combined genetic and transcriptome analysis of patients with SLE: distinct, targetable signatures for susceptibility and severity. <i>Annals of the Rheumatic Diseases</i> , <b>2019</b> , 78, 1079-1089 | 2.4  | 45        |
| 13 | Comprehensive evaluation of coding region point mutations in microsatellite-unstable colorectal cancer. <i>EMBO Molecular Medicine</i> , <b>2018</b> , 10,   | 12   | 6         |
| 12 | Contribution of allelic imbalance to colorectal cancer. <i>Nature Communications</i> , <b>2018</b> , 9, 3664   | 17.4 | 11        |
| 11 | Using an atlas of gene regulation across 44 human tissues to inform complex disease- and trait-associated variation. <i>Nature Genetics</i> , <b>2018</b> , 50, 956-967                                  | 36.3 | 239       |
| 10 | Molecular-Subtype-Specific Biomarkers Improve Prediction of Prognosis in Colorectal Cancer. <i>Cell Reports</i> , <b>2017</b> , 19, 1268-1280  | 10.6 | 55        |
| 9  | A complete tool set for molecular QTL discovery and analysis. <i>Nature Communications</i> , <b>2017</b> , 8, 15452  | 17.4 | 103       |
| 8  | Estimating the causal tissues for complex traits and diseases. <i>Nature Genetics</i> , <b>2017</b> , 49, 1676-1683  | 36.3 | 106       |
| 7  | Fast and efficient QTL mapper for thousands of molecular phenotypes. <i>Bioinformatics</i> , <b>2016</b> , 32, 1479-85   | 7.2  | 241       |
| 6  | Tissue-specific effects of genetic and epigenetic variation on gene regulation and splicing. <i>PLoS Genetics</i> , <b>2015</b> , 11, e1004958   | 6    | 140       |
| 5  | Human genomics. The Genotype-Tissue Expression (GTEx) pilot analysis: multitissue gene regulation in humans. <i>Science</i> , <b>2015</b> , 348, 648-60  | 33.3 | 3242      |
| 4  | Alternative Splicing QTLs in European and African Populations. <i>American Journal of Human Genetics</i> , <b>2015</b> , 97, 567-75  | 11   | 39        |
| 3  | Putative cis-regulatory drivers in colorectal cancer. <i>Nature</i> , <b>2014</b> , 512, 87-90   | 50.4 | 115       |
| 2  | Passive and active DNA methylation and the interplay with genetic variation in gene regulation. <i>ELife</i> , <b>2013</b> , 2, e00523   | 8.9  | 295       |
| 1  | Genetic variants in novel pathways influence blood pressure and cardiovascular disease risk. <i>Nature</i> , <b>2011</b> , 478, 103-9  | 50.4 | 1564      |