

# Sharon Moshitch-Moshkovitz

## 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.

|                   |                         |                 |                 |
|-------------------|-------------------------|-----------------|-----------------|
| 13<br>papers      | 4,199<br>citations      | 9<br>h-index    | 13<br>g-index   |
| 13<br>ext. papers | 5,487<br>ext. citations | 22.9<br>avg, IF | 4.82<br>L-index |

| #  | Paper   | IF   | Citations |
|----|---|------|-----------|
| 13 | The epitranscriptome toolbox.. <i>Cell</i> , <b>2022</b> , 185, 764-776   | 56.2 | 4         |
| 12 | Dynamic regulation of N,2eO-dimethyladenosine (mAm) in obesity. <i>Nature Communications</i> , <b>2021</b> , 12, 7185   | 17.4 | 2         |
| 11 | Epigenetic loss of m1A RNA demethylase ALKBH3 in Hodgkin lymphoma targets collagen, conferring poor clinical outcome. <i>Blood</i> , <b>2021</b> , 137, 994-999 | 2.2  | 7         |
| 10 | The mA epitranscriptome: transcriptome plasticity in brain development and function. <i>Nature Reviews Neuroscience</i> , <b>2020</b> , 21, 36-51               | 13.5 | 86        |
| 9  | The Epitranscriptome in Translation Regulation. <i>Cold Spring Harbor Perspectives in Biology</i> , <b>2019</b> , 11,   | 10.2 | 23        |
| 8  | Whole-genome sequencing reveals principles of brain retrotransposition in neurodevelopmental disorders. <i>Cell Research</i> , <b>2018</b> , 28, 187-203        | 24.7 | 29        |
| 7  | Nm-seq maps 2eO-methylation sites in human mRNA with base precision. <i>Nature Methods</i> , <b>2017</b> , 14, 695-698  | 21.6 | 146       |
| 6  | The dynamic N(1)-methyladenosine methylome in eukaryotic messenger RNA. <i>Nature</i> , <b>2016</b> , 530, 441-6  | 50.4 | 523       |
| 5  | Mimp/Mtch2, an Obesity Susceptibility Gene, Induces Alteration of Fatty Acid Metabolism in Transgenic Mice. <i>PLoS ONE</i> , <b>2016</b> , 11, e0157850        | 3.7  | 6         |
| 4  | Transcriptome-Wide Mapping of NEMethyladenosine by mA-Seq. <i>Methods in Enzymology</i> , <b>2015</b> , 560, 131-47   | 1.7  | 16        |
| 3  | FTO: linking m6A demethylation to adipogenesis. <i>Cell Research</i> , <b>2015</b> , 25, 3-4  | 24.7 | 66        |
| 2  | Stem cells. m6A mRNA methylation facilitates resolution of naïve pluripotency toward differentiation. <i>Science</i> , <b>2015</b> , 347, 1002-6                | 33.3 | 904       |
| 1  | Topology of the human and mouse m6A RNA methylomes revealed by m6A-seq. <i>Nature</i> , <b>2012</b> , 485, 201-6  | 50.4 | 2387      |