## Tao Wu

## List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/11694128/publications.pdf

Version: 2024-02-01

|               |                     | 1163117           | 1474206               |  |
|---------------|---------------------|-------------------|-----------------------|--|
| 9             | 524                 | 8                 | 9                     |  |
| papers        | citations           | h-index           | g-index               |  |
|               |                     |                   |                       |  |
|               |                     |                   |                       |  |
| 0             | 0                   | 0                 | 0.49                  |  |
| 9             | 9                   | 9                 | 948                   |  |
| all docs      | docs citations      | times ranked      | citing authors        |  |
|               |                     |                   |                       |  |
| 9<br>all docs | 9<br>docs citations | 9<br>times ranked | 948<br>citing authors |  |

| # | Article  | IF   | Citations |
|---|--|------|-----------|
| 1 | The Developmental Potential of iPSCs Is Greatly Influenced by Reprogramming Factor Selection. Cell Stem Cell, 2014, 15, 295-309.   | 11.1 | 137       |
| 2 | NPInter: the noncoding RNAs and protein related biomacromolecules interaction database. Nucleic Acids Research, 2006, 34, D150-D152.   | 14.5 | 93        |
| 3 | Extensive Nuclear Reprogramming Underlies Lineage Conversion into Functional Trophoblast<br>Stem-like Cells. Cell Stem Cell, 2015, 17, 543-556.                              | 11.1 | 80        |
| 4 | Mammalian ALKBH1 serves as an N6-mA demethylase of unpairing DNA. Cell Research, 2020, 30, 197-210.  | 12.0 | 71        |
| 5 | Histone Variant H2A.X Deposition Pattern Serves as a Functional Epigenetic Mark for Distinguishing the Developmental Potentials of iPSCs. Cell Stem Cell, 2014, 15, 281-294. | 11.1 | 58        |
| 6 | Mapping the <i>C. elegans</i> noncoding transcriptome with a whole-genome tiling microarray. Genome Research, 2007, 17, 1471-1477.   | 5.5  | 53        |
| 7 | Identifying Hfq-binding small RNA targets in Escherichia coli. Biochemical and Biophysical Research<br>Communications, 2006, 343, 950-955.                                   | 2.1  | 13        |
| 8 | Genome-scale identification of Caenorhabditis elegans regulatory elements by tiling-array mapping of DNase I hypersensitive sites. BMC Genomics, 2009, 10, 92.               | 2.8  | 13        |
| 9 | Enzymatic Characterization of In Vitro Activity of RNA Methyltransferase PCIF1 on DNA. Biochemistry, 2022, 61, 1005-1013.  | 2.5  | 6         |