

# Dimitry Tegunov

## List of Publications by Citations

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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.

25  
papers

1,787  
citations

14  
h-index

29  
g-index

29  
ext. papers

2,767  
ext. citations

21.9  
avg, IF

5.94  
L-index

| #  | Paper   | IF   | Citations |
|----|---|------|-----------|
| 25 | Real-time cryo-electron microscopy data preprocessing with Warp. <i>Nature Methods</i> , <b>2019</b> , 16, 1146-1152  | 21.6 | 355       |
| 24 | Structure of replicating SARS-CoV-2 polymerase. <i>Nature</i> , <b>2020</b> , 584, 154-156  | 50.4 | 351       |
| 23 | Architecture of the RNA polymerase II-Mediator core initiation complex. <i>Nature</i> , <b>2015</b> , 518, 376-80   | 50.4 | 205       |
| 22 | Mechanism of SARS-CoV-2 polymerase stalling by remdesivir. <i>Nature Communications</i> , <b>2021</b> , 12, 279   | 17.4 | 171       |
| 21 | Structures of transcription pre-initiation complex with TFIID and Mediator. <i>Nature</i> , <b>2017</b> , 551, 204-209  | 50.4 | 147       |
| 20 | Using the Volta phase plate with defocus for cryo-EM single particle analysis. <i>ELife</i> , <b>2017</b> , 6,  | 8.9  | 87        |
| 19 | In-cell architecture of an actively transcribing-translating expressome. <i>Science</i> , <b>2020</b> , 369, 554-557  | 33.3 | 82        |
| 18 | Multi-particle cryo-EM refinement with M visualizes ribosome-antibiotic complex at 3.5 Å in cells. <i>Nature Methods</i> , <b>2021</b> , 18, 186-193  | 21.6 | 78        |
| 17 | Structural basis of TFIID activation for nucleotide excision repair. <i>Nature Communications</i> , <b>2019</b> , 10, 2885  | 17.4 | 61        |
| 16 | Architecture of the RNA polymerase II-Paf1C-TFIIS transcription elongation complex. <i>Nature Communications</i> , <b>2017</b> , 8, 15741   | 17.4 | 60        |
| 15 | Structure of SWI/SNF chromatin remodeller RSC bound to a nucleosome. <i>Nature</i> , <b>2020</b> , 579, 448-451   | 50.4 | 54        |
| 14 | Charting the native architecture of thylakoid membranes with single-molecule precision. <i>ELife</i> , <b>2020</b> , 9,   | 8.9  | 41        |
| 13 | Real-time cryo-EM data pre-processing with Warp   |      | 30        |
| 12 | Liquid-crystalline phase transitions in lipid droplets are related to cellular states and specific organelle association. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2019</b> , 116, 16866-16871 | 11.5 | 28        |
| 11 | Multi-particle cryo-EM refinement with M visualizes ribosome-antibiotic complex at 3.7 Å inside cells   |      | 11        |
| 10 | In-cell architecture of an actively transcribing-translating expressome   |      | 9         |
| 9  | Dimeric form of SARS-CoV-2 polymerase   |      | 4         |

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|---|---|-----|---|
| 8 | Structure of replicating SARS-CoV-2 polymerase  |     | 3 |
| 7 | The structure of a dimeric form of SARS-CoV-2 polymerase. <i>Communications Biology</i> , <b>2021</b> , 4, 999  | 6.7 | 3 |
| 6 | Mechanism of SARS-CoV-2 polymerase inhibition by remdesivir   |     | 2 |
| 5 | Charting the native architecture of thylakoid membranes with single-molecule precision  |     | 2 |
| 4 | Using the Volta phase plate with defocus for cryo-EM single particle analysis   |     | 2 |
| 3 | Structure of SWI/SNF chromatin remodeller RSC bound to a nucleosome   |     | 1 |
| 2 | High-resolution In Situ imaging of Biological Samples with Warp and M. <i>Microscopy and Microanalysis</i> , <b>2020</b> , 26, 2998-2999                                  | 0.5 | 0 |
| 1 | Embedding Heterogeneous Cryo-EM Data with 3D Principal Component Analysis and Variational Autoencoders. <i>Microscopy and Microanalysis</i> , <b>2020</b> , 26, 1820-1821 | 0.5 |   |