

# Urszula Czerwinska

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4906249/publications.pdf>

Version: 2024-02-01

16  
papers

434  
citations

1040056

9  
h-index

1199594

12  
g-index

18  
all docs

18  
docs citations

18  
times ranked

1056  
citing authors

| #  | ARTICLE   | IF   | CITATIONS |
|----|---|------|-----------|
| 1  | Adjustment of dendritic cells to the breast-cancer microenvironment is subset specific. <i>Nature Immunology</i> , 2018, 19, 885-897.   | 14.5 | 152       |
| 2  | Independent Component Analysis for Unraveling the Complexity of Cancer Omics Datasets. <i>International Journal of Molecular Sciences</i> , 2019, 20, 4414.   | 4.1  | 62        |
| 3  | Determining the optimal number of independent components for reproducible transcriptomic data analysis. <i>BMC Genomics</i> , 2017, 18, 712.  | 2.8  | 50        |
| 4  | A multiscale signalling network map of innate immune response in cancer reveals cell heterogeneity signatures. <i>Nature Communications</i> , 2019, 10, 4808.   | 12.8 | 44        |
| 5  | Reproducibility of Fluorescent Expression from Engineered Biological Constructs in <i>E. coli</i> . <i>PLoS ONE</i> , 2016, 11, e0150182.   | 2.5  | 33        |
| 6  | A Blood RNA Signature Detecting Severe Disease in Young Dengue Patients at Hospital Arrival. <i>Journal of Infectious Diseases</i> , 2018, 217, 1690-1698.  | 4.0  | 27        |
| 7  | Deconvolution of transcriptomes and miRNomes by independent component analysis provides insights into biological processes and clinical outcomes of melanoma patients. <i>BMC Medical Genomics</i> , 2019, 12, 132. | 1.5  | 22        |
| 8  | DeDaL: Cytoscape 3 app for producing and morphing data-driven and structure-driven network layouts. <i>BMC Systems Biology</i> , 2015, 9, 46.   | 3.0  | 17        |
| 9  | Reconstruction and signal propagation analysis of the Syk signaling network in breast cancer cells. <i>PLoS Computational Biology</i> , 2017, 13, e1005432.   | 3.2  | 11        |
| 10 | The inconvenience of data of convenience: computational research beyond post-mortem analyses. <i>Nature Methods</i> , 2017, 14, 937-938.  | 19.0 | 9         |
| 11 | Application of Independent Component Analysis to Tumor Transcriptomes Reveals Specific and Reproducible Immune-Related Signals. <i>Lecture Notes in Computer Science</i> , 2018, , 501-513.                         | 1.3  | 2         |
| 12 | Collective intelligence defines biological functions in Wikipedia as communities in the hidden protein connection network. <i>PLoS Computational Biology</i> , 2020, 16, e1007652.                                  | 3.2  | 2         |
| 13 | Title is missing!. , 2020, 16, e1007652.  |      | 0         |
| 14 | Title is missing!. , 2020, 16, e1007652.  |      | 0         |
| 15 | Title is missing!. , 2020, 16, e1007652.  |      | 0         |
| 16 | Title is missing!. , 2020, 16, e1007652.  |      | 0         |