

Dmitriy A Bolotin

List of Publications by Year in Descending Order

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Version: 2024-04-25

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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.

27
papers

3,148
citations

20
h-index

28
g-index

28
ext. papers

4,580
ext. citations

13.9
avg, IF

4.69
L-index

| # | Paper | IF | Citations |
|----|---|------|-----------|
| 27 | Distinct organization of adaptive immunity in the long-lived rodent <i>Spalax galili</i> . <i>Nature Aging</i> , 2021 , 1, 179-189 | | 1 |
| 26 | Comparative analysis of murine T-cell receptor repertoires. <i>Immunology</i> , 2018 , 153, 133-144 | 7.8 | 29 |
| 25 | Reply to "Evaluation of immune repertoire inference methods from RNA-seq data". <i>Nature Biotechnology</i> , 2018 , 36, 1035-1036 | 44.5 | 4 |
| 24 | Antigen receptor repertoire profiling from RNA-seq data. <i>Nature Biotechnology</i> , 2017 , 35, 908-911 | 44.5 | 125 |
| 23 | Application of nonsense-mediated primer exclusion (NOPE) for preparation of unique molecular barcoded libraries. <i>BMC Genomics</i> , 2017 , 18, 440 | 4.5 | 2 |
| 22 | Local fitness landscape of the green fluorescent protein. <i>Nature</i> , 2016 , 533, 397-401 | 50.4 | 232 |
| 21 | Dynamics of Individual T Cell Repertoires: From Cord Blood to Centenarians. <i>Journal of Immunology</i> , 2016 , 196, 5005-13 | 5.3 | 94 |
| 20 | High-quality full-length immunoglobulin profiling with unique molecular barcoding. <i>Nature Protocols</i> , 2016 , 11, 1599-616 | 18.8 | 109 |
| 19 | MiXCR: software for comprehensive adaptive immunity profiling. <i>Nature Methods</i> , 2015 , 12, 380-1 | 21.6 | 696 |
| 18 | Quantitative profiling of immune repertoires for minor lymphocyte counts using unique molecular identifiers. <i>Journal of Immunology</i> , 2015 , 194, 6155-63 | 5.3 | 58 |
| 17 | tcR: an R package for T cell receptor repertoire advanced data analysis. <i>BMC Bioinformatics</i> , 2015 , 16, 175 | 3.6 | 156 |
| 16 | Redberry: a computer algebra system designed for tensor manipulation. <i>Journal of Physics: Conference Series</i> , 2015 , 608, 012060 | 0.3 | 7 |
| 15 | VDJtools: Unifying Post-analysis of T Cell Receptor Repertoires. <i>PLoS Computational Biology</i> , 2015 , 11, e1004503 | 5 | 282 |
| 14 | Age-related decrease in TCR repertoire diversity measured with deep and normalized sequence profiling. <i>Journal of Immunology</i> , 2014 , 192, 2689-98 | 5.3 | 249 |
| 13 | Distinctive properties of identical twins' TCR repertoires revealed by high-throughput sequencing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014 , 111, 5980-5 | 11.5 | 86 |
| 12 | Towards error-free profiling of immune repertoires. <i>Nature Methods</i> , 2014 , 11, 653-5 | 21.6 | 267 |
| 11 | MiTCR: software for T-cell receptor sequencing data analysis. <i>Nature Methods</i> , 2013 , 10, 813-4 | 21.6 | 138 |

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|----|---|------|-----|
| 10 | High-throughput identification of antigen-specific TCRs by TCR gene capture. <i>Nature Medicine</i> , 2013 , 19, 1534-41 | 50.5 | 127 |
| 9 | Pairing of T-cell receptor chains via emulsion PCR. <i>European Journal of Immunology</i> , 2013 , 43, 2507-15 | 6.1 | 95 |
| 8 | Preparing unbiased T-cell receptor and antibody cDNA libraries for the deep next generation sequencing profiling. <i>Frontiers in Immunology</i> , 2013 , 4, 456 | 8.4 | 104 |
| 7 | Huge Overlap of Individual TCR Beta Repertoires. <i>Frontiers in Immunology</i> , 2013 , 4, 466 | 8.4 | 32 |
| 6 | Mother and child T cell receptor repertoires: deep profiling study. <i>Frontiers in Immunology</i> , 2013 , 4, 463 | 8.4 | 36 |
| 5 | First autologous hematopoietic SCT for ankylosing spondylitis: a case report and clues to understanding the therapy. <i>Bone Marrow Transplantation</i> , 2012 , 47, 1479-81 | 4.4 | 20 |
| 4 | Next generation sequencing for TCR repertoire profiling: platform-specific features and correction algorithms. <i>European Journal of Immunology</i> , 2012 , 42, 3073-83 | 6.1 | 121 |
| 3 | Can we see PIP(3) and hydrogen peroxide with a single probe?. <i>Antioxidants and Redox Signaling</i> , 2012 , 17, 505-12 | 8.4 | 18 |
| 2 | Quantitative tracking of T cell clones after haematopoietic stem cell transplantation. <i>EMBO Molecular Medicine</i> , 2011 , 3, 201-7 | 12 | 53 |
| 1 | Rhodobase, a meta-analytical tool for reconstructing gene regulatory networks in a model photosynthetic bacterium. <i>BioSystems</i> , 2011 , 103, 125-31 | 1.9 | 5 |