

# Mikhail Shugay

## List of Publications by Year in descending order

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Version: 2024-02-01

57  
papers

6,450  
citations

136950

32  
h-index

161849

54  
g-index

70  
all docs

70  
docs citations

70  
times ranked

10130  
citing authors

#	ARTICLE	IF	CITATIONS
1	Accounting for B-cell Behavior and Sampling Bias Predicts Anti-PD-L1 Response in Bladder Cancer. <i>Cancer Immunology Research</i> , 2022, 10, 343-353.	3.4	9
2	Subsequent malaria enhances virus-specific T cell immunity in SIV-infected Chinese rhesus macaques. <i>Cell Communication and Signaling</i> , 2022, 20, .	6.5	2
3	T-cell tracking, safety, and effect of low-dose donor memory T-cell infusions after T cell-depleted hematopoietic stem cell transplantation. <i>Bone Marrow Transplantation</i> , 2021, 56, 900-908.	2.4	8
4	Benchmarking of T cell receptor repertoire profiling methods reveals large systematic biases. <i>Nature Biotechnology</i> , 2021, 39, 236-245.	17.5	78
5	A T cell repertoire timestamp is at the core of responsiveness to CTLA-4 blockade. <i>IScience</i> , 2021, 24, 102100.	4.1	8
6	Distinct organization of adaptive immunity in the long-lived rodent <i>Spalax galili</i> . <i>Nature Aging</i> , 2021, 1, 179-189.	11.6	5
7	Diversity in immunogenomics: the value and the challenge. <i>Nature Methods</i> , 2021, 18, 588-591.	19.0	40
8	New Regions With Molecular Alterations in a Rare Case of Insulinomatosis: Case Report With Literature Review. <i>Frontiers in Endocrinology</i> , 2021, 12, 760154.	3.5	1
9	Ancestral diversity is limited in published T cell receptor sequencing studies. <i>Immunity</i> , 2021, 54, 2177-2179.	14.3	3
10	VDJdb in 2019: database extension, new analysis infrastructure and a T-cell receptor motif compendium. <i>Nucleic Acids Research</i> , 2020, 48, D1057-D1062.	14.5	268
11	Benchmarking immunoinformatic tools for the analysis of antibody repertoire sequences. <i>Bioinformatics</i> , 2020, 36, 1731-1739.	4.1	39
12	An overview of immunoinformatics approaches and databases linking T cell receptor repertoires to their antigen specificity. <i>Immunogenetics</i> , 2020, 72, 77-84.	2.4	25
13	CD4+ T Cells Recognize Conserved Influenza A Epitopes through Shared Patterns of V-Gene Usage and Complementary Biochemical Features. <i>Cell Reports</i> , 2020, 32, 107885.	6.4	11
14	SARS-CoV-2 Epitopes Are Recognized by a Public and Diverse Repertoire of Human T Cell Receptors. <i>Immunity</i> , 2020, 53, 1245-1257.e5.	14.3	194
15	MHC-II alleles shape the CDR3 repertoires of conventional and regulatory na <sup>ï</sup> ve CD4 <sup>+</sup> T cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 13659-13669.	7.1	28
16	The Interplay between CD27 <sup>dull</sup> and CD27 <sup>bright</sup> B Cells Ensures the Flexibility, Stability, and Resilience of Human B Cell Memory. <i>Cell Reports</i> , 2020, 30, 2963-2977.e6.	6.4	76
17	Comprehensive analysis of structural and sequencing data reveals almost unconstrained chain pairing in TCR $\alpha$ complex. <i>PLoS Computational Biology</i> , 2020, 16, e1007714.	3.2	13
18	Intratumoral immunoglobulin isotypes predict survival in lung adenocarcinoma subtypes. , 2019, 7, 279.		64

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19	A Framework for Annotation of Antigen Specificities in High-Throughput T-Cell Repertoire Sequencing Studies. <i>Frontiers in Immunology</i> , 2019, 10, 2159.	4.8	36
20	Detecting T cell receptors involved in immune responses from single repertoire snapshots. <i>PLoS Biology</i> , 2019, 17, e3000314.	5.6	116
21	sumrep: A Summary Statistic Framework for Immune Receptor Repertoire Comparison and Model Validation. <i>Frontiers in Immunology</i> , 2019, 10, 2533.	4.8	22
22	CD8+ T cells with characteristic T cell receptor beta motif are detected in blood and expanded in synovial fluid of ankylosing spondylitis patients. <i>Rheumatology</i> , 2018, 57, 1097-1104.	1.9	41
23	VDJdb: a curated database of T-cell receptor sequences with known antigen specificity. <i>Nucleic Acids Research</i> , 2018, 46, D419-D427.	14.5	391
24	Comparative analysis of murine T cell receptor repertoires. <i>Immunology</i> , 2018, 153, 133-144.	4.4	72
25	Comparative Analysis of B-Cell Receptor Repertoires Induced by Live Yellow Fever Vaccine in Young and Middle-Age Donors. <i>Frontiers in Immunology</i> , 2018, 9, 2309.	4.8	25
26	High-resolution repertoire analysis reveals a major bystander activation of Tfh and Tfr cells. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 9604-9609.	7.1	62
27	The Changing Landscape of Naive T Cell Receptor Repertoire With Human Aging. <i>Frontiers in Immunology</i> , 2018, 9, 1618.	4.8	87
28	Exploring the pre-immune landscape of antigen-specific T cells. <i>Genome Medicine</i> , 2018, 10, 68.	8.2	60
29	Antigen receptor repertoire profiling from RNA-seq data. <i>Nature Biotechnology</i> , 2017, 35, 908-911.	17.5	243
30	A high-throughput assay for quantitative measurement of PCR errors. <i>Scientific Reports</i> , 2017, 7, 2718.	3.3	27
31	Application of nonsense-mediated primer exclusion (NOPE) for preparation of unique molecular barcoded libraries. <i>BMC Genomics</i> , 2017, 18, 440.	2.8	2
32	Tracking T-cell immune reconstitution after TCR $\alpha^{\pm}\beta^2$ /CD19-depleted hematopoietic cells transplantation in children. <i>Leukemia</i> , 2017, 31, 1145-1153.	7.2	44
33	MAGERI: Computational pipeline for molecular-barcoded targeted resequencing. <i>PLoS Computational Biology</i> , 2017, 13, e1005480.	3.2	37
34	Estimating the number of HIV-specific T-cells in healthy donors using high-throughput sequencing profiles of T-cell receptor repertoires. <i>Bulletin of Russian State Medical University</i> , 2017, , 75-80.	0.2	0
35	Single-cell analysis of glandular T cell receptors in Sjögren's syndrome. <i>JCI Insight</i> , 2016, 1, .	5.0	54
36	Dynamics of Individual T Cell Repertoires: From Cord Blood to Centenarians. <i>Journal of Immunology</i> , 2016, 196, 5005-5013.	0.8	160

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37	High-quality full-length immunoglobulin profiling with unique molecular barcoding. <i>Nature Protocols</i> , 2016, 11, 1599-1616.	12.0	179
38	VDJviz: a versatile browser for immunogenomics data. <i>BMC Genomics</i> , 2016, 17, 453.	2.8	35
39	TCR usage, gene expression and function of two distinct FOXP3 <sup>+</sup> Treg subsets within CD4 <sup>+</sup> CD25 <sup>hi</sup> T cells identified by expression of CD39 and CD45RO. <i>Immunology and Cell Biology</i> , 2016, 94, 293-305.	2.3	19
40	The Evidence for Increased L1 Activity in the Site of Human Adult Brain Neurogenesis. <i>PLoS ONE</i> , 2015, 10, e0117854.	2.5	41
41	P2RX7 Purinoceptor: A Therapeutic Target for Ameliorating the Symptoms of Duchenne Muscular Dystrophy. <i>PLoS Medicine</i> , 2015, 12, e1001888.	8.4	51
42	VDJtools: Unifying Post-analysis of T Cell Receptor Repertoires. <i>PLoS Computational Biology</i> , 2015, 11, e1004503.	3.2	528
43	MiXCR: software for comprehensive adaptive immunity profiling. <i>Nature Methods</i> , 2015, 12, 380-381.	19.0	1,323
44	Quantitative Profiling of Immune Repertoires for Minor Lymphocyte Counts Using Unique Molecular Identifiers. <i>Journal of Immunology</i> , 2015, 194, 6155-6163.	0.8	90
45	A mechanism for expansion of regulatory T-cell repertoire and its role in self-tolerance. <i>Nature</i> , 2015, 528, 132-136.	27.8	123
46	tcR: an R package for T cell receptor repertoire advanced data analysis. <i>BMC Bioinformatics</i> , 2015, 16, 175.	2.6	240
47	Sequencing rare T-cell populations. <i>Oncotarget</i> , 2015, 6, 39393-39394.	1.8	2
48	Age-Related Decrease in TCR Repertoire Diversity Measured with Deep and Normalized Sequence Profiling. <i>Journal of Immunology</i> , 2014, 192, 2689-2698.	0.8	396
49	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, 5980-5985.	7.1	106
50	Towards error-free profiling of immune repertoires. <i>Nature Methods</i> , 2014, 11, 653-655.	19.0	411
51	MiTCR: software for T-cell receptor sequencing data analysis. <i>Nature Methods</i> , 2013, 10, 813-814.	19.0	176
52	Oncofuse: a computational framework for the prediction of the oncogenic potential of gene fusions. <i>Bioinformatics</i> , 2013, 29, 2539-2546.	4.1	87
53	Pairing of T cell receptor chains via emulsion PCR. <i>European Journal of Immunology</i> , 2013, 43, 2507-2515.	2.9	126
54	Huge Overlap of Individual TCR Beta Repertoires. <i>Frontiers in Immunology</i> , 2013, 4, 466.	4.8	56

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55	Mother and Child's T Cell Receptor Repertoires: Deep Profiling Study. <i>Frontiers in Immunology</i> , 2013, 4, 463.	4.8	41
56	Genomic Hallmarks of Genes Involved in Chromosomal Translocations in Hematological Cancer. <i>PLoS Computational Biology</i> , 2012, 8, e1002797.	3.2	27
57	LIF, a Novel STAT5-Regulated Gene, Is Aberrantly Expressed in Myeloproliferative Neoplasms. <i>Genes and Cancer</i> , 2011, 2, 593-596.	1.9	8