

# Ilgar Z Mamedov

## List of Publications by Year in Descending Order

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**Version:** 2024-04-10

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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.

61 papers	3,526 citations	30 h-index	59 g-index
71 ext. papers	5,025 ext. citations	8.7 avg, IF	4.94 L-index

#	Paper	IF	Citations
61	Deep cfDNA fragment end profiling enables cancer detection.. <i>Molecular Cancer</i> , <b>2022</b> , 21, 26	42.1	2
60	Longitudinal high-throughput TCR repertoire profiling reveals the dynamics of T-cell memory formation after mild COVID-19 infection. <i>ELife</i> , <b>2021</b> , 10,	8.9	44
59	The Dynamics of the Bacterial Community of the Photobioreactor-Cultivated Green Microalga during Stress-Induced Astaxanthin Accumulation. <i>Biology</i> , <b>2021</b> , 10,	4.9	3
58	The energy sensor AMPK orchestrates metabolic and translational adaptation in expanding T helper cells. <i>FASEB Journal</i> , <b>2021</b> , 35, e21217	0.9	2
57	SeqURE - a new copy-capture based method for sequencing of unknown Retroposition events. <i>Mobile DNA</i> , <b>2020</b> , 11, 33	4.4	0
56	Primary and secondary anti-viral response captured by the dynamics and phenotype of individual T cell clones. <i>ELife</i> , <b>2020</b> , 9,	8.9	25
55	Functionally specialized human CD4 T-cell subsets express physicochemically distinct TCRs. <i>ELife</i> , <b>2020</b> , 9,	8.9	3
54	Identification of Disease-associated Traits and Clonotypes in the T Cell Receptor Repertoire of Monozygotic Twins Affected by Inflammatory Bowel Diseases. <i>Journal of Crohns and Colitis</i> , <b>2020</b> , 14, 778-790	1.5	5
53	High-throughput sequencing of T-cell receptor alpha chain clonal rearrangements at the DNA level in lymphoid malignancies. <i>British Journal of Haematology</i> , <b>2020</b> , 188, 723-731	4.5	5
52	Aberrant Methylation of LINE-1 Transposable Elements: A Search for Cancer Biomarkers. <i>Cells</i> , <b>2020</b> , 9,	7.9	12
51	Resuscitation of Dormant "Non-culturable" Is Characterized by Immediate Transcriptional Burst. <i>Frontiers in Cellular and Infection Microbiology</i> , <b>2019</b> , 9, 272	5.9	11
50	Phosphorus starvation and luxury uptake in green microalgae revisited. <i>Algal Research</i> , <b>2019</b> , 43, 101651	15	34
49	A Pipeline for the Error-Free Identification of Somatic Alu Insertions in High-Throughput Sequencing Data. <i>Molecular Biology</i> , <b>2019</b> , 53, 138-146	1.2	1
48	T-cell receptor and B-cell receptor repertoire profiling in adaptive immunity. <i>Transplant International</i> , <b>2019</b> , 32, 1111-1123	3	17
47	Quantitative profiling reveals minor changes of T cell receptor repertoire in response to subunit inactivated influenza vaccine. <i>Vaccine</i> , <b>2018</b> , 36, 1599-1605	4.1	8
46	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> , <b>2018</b> , 57, 1097-1104	3.9	22
45	Comparative analysis of murine T-cell receptor repertoires. <i>Immunology</i> , <b>2018</b> , 153, 133-144	7.8	29

44	The Changing Landscape of Naive T Cell Receptor Repertoire With Human Aging. <i>Frontiers in Immunology</i> , <b>2018</b> , 9, 1618	8.4	58
43	Method for identification of condition-associated public antigen receptor sequences. <i>ELife</i> , <b>2018</b> , 7,	8.9	33
42	An advanced enrichment method for rare somatic retroelement insertions sequencing. <i>Mobile DNA</i> , <b>2018</b> , 9, 31	4.4	3
41	Precise tracking of vaccine-responding T cell clones reveals convergent and personalized response in identical twins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2018</b> , 115, 12704-12709	11.5	58
40	Tracking T-cell immune reconstitution after TCR/CD19-depleted hematopoietic cells transplantation in children. <i>Leukemia</i> , <b>2017</b> , 31, 1145-1153	10.7	34
39	Persisting fetal clonotypes influence the structure and overlap of adult human T cell receptor repertoires. <i>PLoS Computational Biology</i> , <b>2017</b> , 13, e1005572	5	56
38	Reliability of immune receptor rearrangements as genetic markers for minimal residual disease monitoring. <i>Bone Marrow Transplantation</i> , <b>2016</b> , 51, 1408-1410	4.4	5
37	T Cell Repertoire after Alpha/Beta-T Cell Depleted Allogeneic Hematopoietic Stem Cell Transplantation in Pediatric Patients. <i>Blood</i> , <b>2016</b> , 128, 4582-4582	2.2	
36	Advanced lymphoblastic clones detection in T-cell leukemia. <i>Doklady Biochemistry and Biophysics</i> , <b>2016</b> , 467, 85-8	0.8	
35	Local fitness landscape of the green fluorescent protein. <i>Nature</i> , <b>2016</b> , 533, 397-401	50.4	232
34	Dynamics of Individual T Cell Repertoires: From Cord Blood to Centenarians. <i>Journal of Immunology</i> , <b>2016</b> , 196, 5005-13	5.3	94
33	High-quality full-length immunoglobulin profiling with unique molecular barcoding. <i>Nature Protocols</i> , <b>2016</b> , 11, 1599-616	18.8	109
32	MiXCR: software for comprehensive adaptive immunity profiling. <i>Nature Methods</i> , <b>2015</b> , 12, 380-1	21.6	696
31	tcR: an R package for T cell receptor repertoire advanced data analysis. <i>BMC Bioinformatics</i> , <b>2015</b> , 16, 175	3.6	156
30	The evidence for increased L1 activity in the site of human adult brain neurogenesis. <i>PLoS ONE</i> , <b>2015</b> , 10, e0117854	3.7	33
29	Age-related decrease in TCR repertoire diversity measured with deep and normalized sequence profiling. <i>Journal of Immunology</i> , <b>2014</b> , 192, 2689-98	5.3	249
28	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> , <b>2014</b> , 111, 5980-5	11.5	86
27	Towards error-free profiling of immune repertoires. <i>Nature Methods</i> , <b>2014</b> , 11, 653-5	21.6	267

26	MiTCR: software for T-cell receptor sequencing data analysis. <i>Nature Methods</i> , <b>2013</b> , 10, 813-4	21.6	138
25	High-throughput identification of antigen-specific TCRs by TCR gene capture. <i>Nature Medicine</i> , <b>2013</b> , 19, 1534-41	50.5	127
24	Pairing of T-cell receptor chains via emulsion PCR. <i>European Journal of Immunology</i> , <b>2013</b> , 43, 2507-15	6.1	95
23	Preparing unbiased T-cell receptor and antibody cDNA libraries for the deep next generation sequencing profiling. <i>Frontiers in Immunology</i> , <b>2013</b> , 4, 456	8.4	104
22	Huge Overlap of Individual TCR Beta Repertoires. <i>Frontiers in Immunology</i> , <b>2013</b> , 4, 466	8.4	32
21	Mother and child T cell receptor repertoires: deep profiling study. <i>Frontiers in Immunology</i> , <b>2013</b> , 4, 463	8.4	36
20	First autologous hematopoietic SCT for ankylosing spondylitis: a case report and clues to understanding the therapy. <i>Bone Marrow Transplantation</i> , <b>2012</b> , 47, 1479-81	4.4	20
19	Next generation sequencing for TCR repertoire profiling: platform-specific features and correction algorithms. <i>European Journal of Immunology</i> , <b>2012</b> , 42, 3073-83	6.1	121
18	Quantitative tracking of T cell clones after haematopoietic stem cell transplantation. <i>EMBO Molecular Medicine</i> , <b>2011</b> , 3, 201-7	12	53
17	Contribution of functional KIR3DL1 to ankylosing spondylitis. <i>Cellular and Molecular Immunology</i> , <b>2010</b> , 7, 471-6	15.4	30
16	A new set of markers for human identification based on 32 polymorphic Alu insertions. <i>European Journal of Human Genetics</i> , <b>2010</b> , 18, 808-14	5.3	17
15	Normalization of genomic DNA using duplex-specific nuclease. <i>BioTechniques</i> , <b>2010</b> , 48, 455-9	2.5	33
14	Optogenetic in vivo cell manipulation in KillerRed-expressing zebrafish transgenics. <i>BMC Developmental Biology</i> , <b>2010</b> , 10, 110	3.1	75
13	Individual characterization of stably expanded T cell clones in ankylosing spondylitis patients. <i>Autoimmunity</i> , <b>2009</b> , 42, 525-36	3	13
12	A new polymorphic retroelement database (PRED) for the human genome. <i>Molecular Biology</i> , <b>2008</b> , 42, 641-646	1.2	3
11	Most recent AluY insertions in human gene introns reduce the content of the primary transcripts in a cell type specific manner. <i>Gene</i> , <b>2007</b> , 390, 122-9	3.8	12
10	Whole-genome experimental identification of insertion/deletion polymorphisms of interspersed repeats by a new general approach. <i>Nucleic Acids Research</i> , <b>2005</b> , 33, e16	20.1	31
9	A rare event of insertion polymorphism of a HERV-K LTR in the human genome. <i>Genomics</i> , <b>2004</b> , 84, 596-9	4.3	25

8	Unusually long target site duplications flanking some of the long terminal repeats of human endogenous retrovirus K in the human genome. <i>Journal of General Virology</i> , <b>2004</b> , 85, 1485-1488	4.9	4
7	Human-specific subfamilies of HERV-K (HML-2) long terminal repeats: three master genes were active simultaneously during branching of hominoid lineages. <i>Genomics</i> , <b>2003</b> , 81, 149-56	4.3	70
6	Genome-wide comparison of differences in the integration sites of interspersed repeats between closely related genomes. <i>Nucleic Acids Research</i> , <b>2002</b> , 30, e71	20.1	25
5	A technique for genome-wide identification of differences in the interspersed repeats integrations between closely related genomes and its application to detection of human-specific integrations of HERV-K LTRs. <i>Genomics</i> , <b>2002</b> , 79, 413-22	4.3	35
4	Full-sized HERV-K (HML-2) human endogenous retroviral LTR sequences on human chromosome 21: map locations and evolutionary history. <i>Gene</i> , <b>2001</b> , 273, 51-61	3.8	16
3	Precise tracking of vaccine-responding T-cell clones reveals convergent and personalized response in identical twins		1
2	Comprehensive analysis of antiviral adaptive immunity formation and reactivation down to single-cell level		2
1	Longitudinal high-throughput TCR repertoire profiling reveals the dynamics of T cell memory formation after mild COVID-19 infection		6