Ilgar Z Mamedov

List of Publications by Citations

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	MiXCR: software for comprehensive adaptive immunity profiling. *Nature Methods*, **2015**, 12, 380-1	21.6	696
60	Towards error-free profiling of immune repertoires. *Nature Methods*, **2014**, 11, 653-5	21.6	267
59	Age-related decrease in TCR repertoire diversity measured with deep and normalized sequence profiling. *Journal of Immunology*, **2014**, 192, 2689-98	5.3	249
58	Local fitness landscape of the green fluorescent protein. *Nature*, **2016**, 533, 397-401	50.4	232
57	tcR: an R package for T cell receptor repertoire advanced data analysis. *BMC Bioinformatics*, **2015**, 16, 175	3.6	156
56	MiTCR: software for T-cell receptor sequencing data analysis. *Nature Methods*, **2013**, 10, 813-4	21.6	138
55	High-throughput identification of antigen-specific TCRs by TCR gene capture. *Nature Medicine*, **2013**, 19, 1534-41	50.5	127
54	Next generation sequencing for TCR repertoire profiling: platform-specific features and correction algorithms. *European Journal of Immunology*, **2012**, 42, 3073-83	6.1	121
53	High-quality full-length immunoglobulin profiling with unique molecular barcoding. *Nature Protocols*, **2016**, 11, 1599-616	18.8	109
52	Preparing unbiased T-cell receptor and antibody cDNA libraries for the deep next generation sequencing profiling. *Frontiers in Immunology*, **2013**, 4, 456	8.4	104
51	Pairing of T-cell receptor chains via emulsion PCR. *European Journal of Immunology*, **2013**, 43, 2507-15	6.1	95
50	Dynamics of Individual T Cell Repertoires: From Cord Blood to Centenarians. *Journal of Immunology* , **2016**, 196, 5005-13	5.3	94
49	Distinctive properties of identical twinsSTCR repertoires revealed by high-throughput sequencing. *Proceedings of the National Academy of Sciences of the United States of America*, **2014**, 111, 5980-5	11.5	86
48	Optogenetic in vivo cell manipulation in KillerRed-expressing zebrafish transgenics. *BMC Developmental Biology*, **2010**, 10, 110	3.1	75
47	Human-specific subfamilies of HERV-K (HML-2) long terminal repeats: three master genes were active simultaneously during branching of hominoid lineages. *Genomics*, **2003**, 81, 149-56	4.3	70
46	The Changing Landscape of Naive T Cell Receptor Repertoire With Human Aging. *Frontiers in Immunology*, **2018**, 9, 1618	8.4	58
45	Precise tracking of vaccine-responding T cell clones reveals convergent and personalized response in identical twins. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, 12704-12709	11.5	58

44	Persisting fetal clonotypes influence the structure and overlap of adult human T cell receptor repertoires. *PLoS Computational Biology*, **2017**, 13, e1005572	5	56
43	Quantitative tracking of T cell clones after haematopoietic stem cell transplantation. *EMBO Molecular Medicine*, **2011**, 3, 201-7	12	53
42	Longitudinal high-throughput TCR repertoire profiling reveals the dynamics of T-cell memory formation after mild COVID-19 infection. *ELife*, **2021**, 10,	8.9	44
41	Mother and child T cell receptor repertoires: deep profiling study. *Frontiers in Immunology*, **2013**, 4, 463	8.4	36
40	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. *Genomics*, **2002**, 79, 413-22	4.3	35
39	Phosphorus starvation and luxury uptake in green microalgae revisited. *Algal Research*, **2019**, 43, 101651	5	34
38	Tracking T-cell immune reconstitution after TCRαβ/CD19-depleted hematopoietic cells transplantation in children. *Leukemia*, **2017**, 31, 1145-1153	10.7	34
37	Method for identification of condition-associated public antigen receptor sequences. *ELife*, **2018**, 7,	8.9	33
36	The evidence for increased L1 activity in the site of human adult brain neurogenesis. *PLoS ONE*, **2015**, 10, e0117854	3.7	33
35	Normalization of genomic DNA using duplex-specific nuclease. *BioTechniques*, **2010**, 48, 455-9	2.5	33
34	Huge Overlap of Individual TCR Beta Repertoires. *Frontiers in Immunology*, **2013**, 4, 466	8.4	32
33	Whole-genome experimental identification of insertion/deletion polymorphisms of interspersed repeats by a new general approach. *Nucleic Acids Research*, **2005**, 33, e16	20.1	31
32	Contribution of functional KIR3DL1 to ankylosing spondylitis. *Cellular and Molecular Immunology*, **2010**, 7, 471-6	15.4	30
31	Comparative analysis of murine T-cell receptor repertoires. *Immunology*, **2018**, 153, 133-144	7.8	29
30	A rare event of insertion polymorphism of a HERV-K LTR in the human genome. *Genomics*, **2004**, 84, 596-8	4.3	25
29	Genome-wide comparison of differences in the integration sites of interspersed repeats between closely related genomes. *Nucleic Acids Research*, **2002**, 30, e71	20.1	25
28	Primary and secondary anti-viral response captured by the dynamics and phenotype of individual T cell clones. *ELife*, **2020**, 9,	8.9	25
27	CD8+ T cells with characteristic T cell receptor beta motif are detected in blood and expanded in synovial fluid of ankylosing spondylitis patients. *Rheumatology*, **2018**, 57, 1097-1104	3.9	22

26	First autologous hematopoietic SCT for ankylosing spondylitis: a case report and clues to understanding the therapy. *Bone Marrow Transplantation*, **2012**, 47, 1479-81	4.4	20
25	T-cell receptor and B-cell receptor repertoire profiling in adaptive immunity. *Transplant International*, **2019**, 32, 1111-1123	3	17
24	A new set of markers for human identification based on 32 polymorphic Alu insertions. *European Journal of Human Genetics*, **2010**, 18, 808-14	5.3	17
23	Full-sized HERV-K (HML-2) human endogenous retroviral LTR sequences on human chromosome 21: map locations and evolutionary history. *Gene*, **2001**, 273, 51-61	3.8	16
22	Individual characterization of stably expanded T cell clones in ankylosing spondylitis patients. *Autoimmunity*, **2009**, 42, 525-36	3	13
21	Most recent AluY insertions in human gene introns reduce the content of the primary transcripts in a cell type specific manner. *Gene*, **2007**, 390, 122-9	3.8	12
20	Aberrant Methylation of LINE-1 Transposable Elements: A Search for Cancer Biomarkers. *Cells*, **2020**, 9,	7.9	12
19	Resuscitation of Dormant "Non-culturable" Is Characterized by Immediate Transcriptional Burst. *Frontiers in Cellular and Infection Microbiology*, **2019**, 9, 272	5.9	11
18	Quantitative profiling reveals minor changes of T cell receptor repertoire in response to subunit inactivated influenza vaccine. *Vaccine*, **2018**, 36, 1599-1605	4.1	8
17	Longitudinal high-throughput TCR repertoire profiling reveals the dynamics of T cell memory formation after mild COVID-19 infection		6
16	Reliability of immune receptor rearrangements as genetic markers for minimal residual disease monitoring. *Bone Marrow Transplantation*, **2016**, 51, 1408-1410	4.4	5
15	Identification of Disease-associated Traits and Clonotypes in the T Cell Receptor Repertoire of Monozygotic Twins Affected by Inflammatory Bowel Diseases. *Journal of Crohn's and Colitis*, **2020**, 14, 778-790	1.5	5
14	High-throughput sequencing of T-cell receptor alpha chain clonal rearrangements at the DNA level in lymphoid malignancies. *British Journal of Haematology*, **2020**, 188, 723-731	4.5	5
13	Unusually long target site duplications flanking some of the long terminal repeats of human endogenous retrovirus K in the human genome. *Journal of General Virology*, **2004**, 85, 1485-1488	4.9	4
12	A new polymorphic retroelement database (PRED) for the human genome. *Molecular Biology*, **2008**, 42, 641-646	1.2	3
11	Functionally specialized human CD4 T-cell subsets express physicochemically distinct TCRs. *ELife*, **2020**, 9,	8.9	3
10	The Dynamics of the Bacterial Community of the Photobioreactor-Cultivated Green Microalga during Stress-Induced Astaxanthin Accumulation. *Biology*, **2021**, 10,	4.9	3
9	An advanced enrichment method for rare somatic retroelement insertions sequencing. *Mobile DNA*, **2018**, 9, 31	4.4	3

8	Deep cfDNA fragment end profiling enables cancer detection.. *Molecular Cancer*, **2022**, 21, 26	42.1	2
7	Comprehensive analysis of antiviral adaptive immunity formation and reactivation down to single-cell level		2
6	The energy sensor AMPK orchestrates metabolic and translational adaptation in expanding T helper cells. *FASEB Journal*, **2021**, 35, e21217	0.9	2
5	A Pipeline for the Error-Free Identification of Somatic Alu Insertions in High-Throughput Sequencing Data. *Molecular Biology*, **2019**, 53, 138-146	1.2	1
4	Precise tracking of vaccine-responding T-cell clones reveals convergent and personalized response in identical twins		1
3	SeqURE - a new copy-capture based method for sequencing of unknown Retroposition events. *Mobile DNA*, **2020**, 11, 33	4.4	0
2	T Cell Repertoire after Alpha/Beta-T Cell Depleted Allogeneic Hematopoietic Stem Cell Transplantation in Pediatric Patients. *Blood*, **2016**, 128, 4582-4582	2.2	
1	Advanced lymphoblastic clones detection in T-cell leukemia. *Doklady Biochemistry and Biophysics*, **2016**, 467, 85-8	0.8	