

Nikos Darzentas

List of Publications by Year in descending order

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Version: 2024-02-01

90
papers

4,226
citations

186265

28
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114465

63
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all docs

92
docs citations

92
times ranked

5584
citing authors

#	ARTICLE	IF	CITATIONS
1	Gene capture by transposable elements leads to epigenetic conflict in maize. <i>Molecular Plant</i> , 2021, 14, 237-252.	8.3	17
2	Potential and pitfalls of whole transcriptome-based immunogenetic marker identification in acute lymphoblastic leukemia; a EuroMRD and EuroClonality-NGS Working Group study. <i>Leukemia</i> , 2021, 35, 924-928.	7.2	3
3	Consistent B Cell Receptor Immunoglobulin Features Between Siblings in Familial Chronic Lymphocytic Leukemia. <i>Frontiers in Oncology</i> , 2021, 11, 740083.	2.8	5
4	Multiple Immunoglobulin κ Gene Rearrangements within a Single Clone Unraveled by Next-Generation Sequencing-Based Clonality Assessment. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 1097-1104.	2.8	8
5	Next-Generation Sequencing-Based Clonality Assessment of Ig Gene Rearrangements. <i>Journal of Molecular Diagnostics</i> , 2021, 23, 1105-1115.	2.8	25
6	Validation of the EuroClonality-NGS DNA capture panel as an integrated genomic tool for lymphoproliferative disorders. <i>Blood Advances</i> , 2021, 5, 3188-3198.	5.2	2
7	Disease Kinetics Measured By Circulating Tumor DNA Correlates with Treatment Response after Tafasitamab in Combination with R-CHOP with or without Lenalidomide in First Line Treatment of DLBCL. <i>Blood</i> , 2021, 138, 3498-3498.	1.4	0
8	Karyosequencing: Integrating Genome-Wide and Targeted Sequencing for Comprehensive Diagnosis of Lymphoproliferative Disorders. <i>Blood</i> , 2021, 138, 272-272.	1.4	0
9	NGS-Based MRD Quantitation: An Alternative to qPCR Validated on a Large Consecutive Cohort of Children with ALL. <i>Blood</i> , 2021, 138, 1314-1314.	1.4	2
10	Automation of Amplicon-Based Library Preparation for Next-Generation Sequencing by Centrifugal Microfluidics. <i>Analytical Chemistry</i> , 2020, 92, 12833-12841.	6.5	15
11	Standardized next-generation sequencing of immunoglobulin and T-cell receptor gene recombinations for MRD marker identification in acute lymphoblastic leukaemia; a EuroClonality-NGS validation study. <i>Leukemia</i> , 2019, 33, 2241-2253.	7.2	177
12	The presence of CLL-associated stereotypic B cell receptors in the normal BCR repertoire from healthy individuals increases with age. <i>Immunity and Ageing</i> , 2019, 16, 22.	4.2	17
13	A review of canine B cell clonality assays and primer set optimization using large-scale repertoire data. <i>Veterinary Immunology and Immunopathology</i> , 2019, 209, 45-52.	1.2	4
14	Quality control and quantification in IG/TR next-generation sequencing marker identification: protocols and bioinformatic functionalities by EuroClonality-NGS. <i>Leukemia</i> , 2019, 33, 2254-2265.	7.2	70
15	Next-generation sequencing of immunoglobulin gene rearrangements for clonality assessment: a technical feasibility study by EuroClonality-NGS. <i>Leukemia</i> , 2019, 33, 2227-2240.	7.2	92
16	Composite lymphoma of concurrent T zone lymphoma and large cell B cell lymphoma in a dog. <i>BMC Veterinary Research</i> , 2019, 15, 413.	1.9	10
17	Euroclonality-NGS DNA Capture Panel for Integrated Analysis of IG/TR Rearrangements, Translocations, Copy Number and Sequence Variation in Lymphoproliferative Disorders. <i>Blood</i> , 2019, 134, 888-888.	1.4	4
18	Deep Immunoprofiling By Flow Cytometry and NGS Reveals Distinct T Cell Profile in Pediatric Hepatitis-Associated Aplastic Anemia. <i>Blood</i> , 2019, 134, 2508-2508.	1.4	0

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19	No improvement in long-term survival over time for chronic lymphocytic leukemia patients in stereotyped subsets #1 and #2 treated with chemo(immuno)therapy. <i>Haematologica</i> , 2018, 103, e158-e161.	3.5	16
20	Characterization of the canine immunoglobulin heavy chain repertoire by next generation sequencing. <i>Veterinary Immunology and Immunopathology</i> , 2018, 202, 181-190.	1.2	9
21	Monitoring of the Clonal Architecture of B-Cell Precursor ALL during Induction Chemoimmunotherapy. <i>Blood</i> , 2018, 132, 1555-1555.	1.4	0
22	The IG/TR Next Generation Marker Screening Developed within Euroclonality-NGS Consortium Is Successful in 94% of Acute Lymphoblastic Leukemia Samples. <i>Blood</i> , 2018, 132, 2830-2830.	1.4	2
23	High-Throughput Immunogenetics for Clinical and Research Applications in Immunohematology: Potential and Challenges. <i>Journal of Immunology</i> , 2017, 198, 3765-3774.	0.8	61
24	Chronic Lymphocytic Leukemia with Mutated IGHV4-34 Receptors: Shared and Distinct Immunogenetic Features and Clinical Outcomes. <i>Clinical Cancer Research</i> , 2017, 23, 5292-5301.	7.0	27
25	Considerations and complications of mapping small RNA high-throughput data to transposable elements. <i>Mobile DNA</i> , 2017, 8, 3.	3.6	11
26	High resolution IgH repertoire analysis reveals fetal liver as the likely origin of life-long, innate B lymphopoiesis in humans. <i>Clinical Immunology</i> , 2017, 183, 8-16.	3.2	15
27	An Immunogenetic Signature of Ongoing Antigen Interactions in Splenic Marginal Zone Lymphoma Expressing IGHV1-2*04 Receptors. <i>Clinical Cancer Research</i> , 2016, 22, 2032-2040.	7.0	17
28	A role for palindromic structures in the cis-region of maize Sirevirus LTRs in transposable element evolution and host epigenetic response. <i>Genome Research</i> , 2016, 26, 226-237.	5.5	22
29	Reappraising Immunoglobulin Repertoire Restrictions in Chronic Lymphocytic Leukemia: Focus on Major Stereotyped Subsets and Closely Related Satellites. <i>Blood</i> , 2016, 128, 4376-4376.	1.4	1
30	A Versatile DNA/RNA NGS Targeted Capture Strategy for Detection of Fusion Genes in Pediatric ALL. <i>Blood</i> , 2016, 128, 2913-2913.	1.4	0
31	Not all IGHV3-21 chronic lymphocytic leukemias are equal: prognostic considerations. <i>Blood</i> , 2015, 125, 856-859.	1.4	70
32	ARResT/AssignSubsets: a novel application for robust subclassification of chronic lymphocytic leukemia based on B cell receptor IG stereotypy. <i>Bioinformatics</i> , 2015, 31, 3844-3846.	4.1	43
33	Immunoglobulin heavy variable (IGHV) genes and alleles: new entities, new names and implications for research and prognostication in chronic lymphocytic leukaemia. <i>Immunogenetics</i> , 2015, 67, 61-66.	2.4	20
34	Library Preparation Is the Major Factor Affecting Differences in Results of Immunoglobulin Gene Rearrangements Detection on Two Major Next-Generation Sequencing Platforms. <i>Blood</i> , 2015, 126, 1411-1411.	1.4	1
35	T-Prolymphocytic Leukemia Is Sensitive to Polyclonal T Cell-Derived Graft-Versus-Leukemia Effects: Evidence from Minimal Residual Disease Kinetics and TCR Repertoire Diversity Analyses. <i>Blood</i> , 2015, 126, 3159-3159.	1.4	0
36	CLL with Mutated IGHV4-34 Antigen Receptors Is Clinically Heterogeneous: Antigen Receptor Stereotypy Makes the Difference. <i>Blood</i> , 2015, 126, 5263-5263.	1.4	0

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37	Lack of common TCRA and TCRB clonotypes in CD8+/TCR β ⁺ T-cell large granular lymphocyte leukemia: a review on the role of antigenic selection in the immunopathogenesis of CD8+ T-LGL. Blood Cancer Journal, 2014, 4, e172-e172.	6.2	17
38	Clinical effect of stereotyped B-cell receptor immunoglobulins in chronic lymphocytic leukaemia: a retrospective multicentre study. Lancet Haematology, 2014, 1, e74-e84.	4.6	93
39	IgG-Switched CLL Has a Distinct Immunogenetic Signature from the Common MD Variant: Ontogenetic Implications. Clinical Cancer Research, 2014, 20, 323-330.	7.0	27
40	Charting Unique Signatures of Somatic Hypermutation Amongst Chronic Lymphocytic Leukemia Patients Expressing IGHV4-34 Clonotypic B Cell Receptors. Blood, 2014, 124, 1969-1969.	1.4	0
41	Clinical Impact of Stereotyped Antigen Receptors in Chronic Lymphocytic Leukemia. Blood, 2014, 124, 3280-3280.	1.4	0
42	Sirevirus LTR retrotransposons: phylogenetic misconceptions in the plant world. Mobile DNA, 2013, 4, 9.	3.6	16
43	Antigen selection in B-cell lymphomas—Tracing the evidence. Seminars in Cancer Biology, 2013, 23, 399-409.	9.6	38
44	Stereotyped B Cell Receptors in B Cell Leukemias and Lymphomas. Methods in Molecular Biology, 2013, 971, 135-148.	0.9	22
45	The Significance of Stereotyped B-Cell Receptors in Chronic Lymphocytic Leukemia. Hematology/Oncology Clinics of North America, 2013, 27, 237-250.	2.2	13
46	Temporal Dynamics of Clonal Evolution in Chronic Lymphocytic Leukemia with Stereotyped IGHV4-34/IGKV2-30 Antigen Receptors: Longitudinal Immunogenetic Evidence. Molecular Medicine, 2013, 19, 230-236.	4.4	11
47	Ongoing Antigen Interactions In Splenic Marginal Zone Lymphoma: Revelations From The Analysis Of Intraclonal Diversification In Immunoglobulin Light Chain Genes. Blood, 2013, 122, 2999-2999.	1.4	0
48	Molecular Subsets of Mantle Cell Lymphoma Defined by the IGHV Mutational Status and SOX11 Expression Have Distinct Biologic and Clinical Features. Cancer Research, 2012, 72, 5307-5316.	0.9	231
49	Selection of antigen receptors in splenic marginal-zone lymphoma: further support from the analysis of the immunoglobulin light-chain gene repertoire. Leukemia, 2012, 26, 2567-2569.	7.2	16
50	Antigen receptor stereotypy across B-cell lymphoproliferations: the case of IGHV4-59/IGKV3-20 receptors with rheumatoid factor activity. Leukemia, 2012, 26, 1127-1131.	7.2	59
51	Stereotyped B-cell receptors in one-third of chronic lymphocytic leukemia: a molecular classification with implications for targeted therapies. Blood, 2012, 119, 4467-4475.	1.4	350
52	MASiVEDb: the Sirevirus Plant Retrotransposon Database. BMC Genomics, 2012, 13, 158.	2.8	24
53	The turbulent life of Sirevirus retrotransposons and the evolution of the maize genome: more than ten thousand elements tell the story. Plant Journal, 2012, 69, 475-488.	5.7	36
54	Barcode High Resolution Melting (Bar-HRM) analysis for detection and quantification of PDO (Fava Santorinis) adulterants. Food Chemistry, 2012, 133, 505-512.	8.2	76

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55	T Cell Receptor Gene Repertoire Restriction in Chronic Lymphocytic Leukemia with Stereotyped IGHV4â€“34/IGKV2â€“30 Antigen Receptors. <i>Blood</i> , 2012, 120, 3908-3908.	1.4	6
56	Distinct Profiles of in Vivo Class Switch Recombination in Chronic Lymphocytic Leukemia Subsets with Stereotyped B Cell Receptors, Suggestive of Distinct Modes of Activation by Antigen. <i>Blood</i> , 2012, 120, 1777-1777.	1.4	1
57	Skewing of the T Cell Receptor Gene Repertoire and Public Clonotypes in Cytotoxic T Cells of Patients with Chronic Idiopathic Neutropenia: A Role for Antigen Selection in Disease Development. <i>Blood</i> , 2012, 120, 831-831.	1.4	0
58	Clonal Selection in the Ontogeny and Evolution of Splenic Marginal Zone Lymphoma Confirming the Existence of Distinct Molecular Subtypes. <i>Blood</i> , 2012, 120, 1556-1556.	1.4	0
59	Is there a role for antigen selection in mantle cell lymphoma? Immunogenetic support from a series of 807 cases. <i>Blood</i> , 2011, 118, 3088-3095.	1.4	149
60	The study of the E-class SEPALLATA3-like MADS-box genes in wild-type and mutant flowers of cultivated saffron crocus (<i>Crocus sativus</i> L.) and its putative progenitors. <i>Journal of Plant Physiology</i> , 2011, 168, 1675-1684.	3.5	36
61	A restricted clonal T-cell receptor Î±Î² repertoire in SÃ©zary syndrome is indicative of superantigenic stimulation. <i>British Journal of Dermatology</i> , 2011, 165, 78-84.	1.5	11
62	Multiple evidence for the role of an Ovate-like gene in determining fruit shape in pepper. <i>BMC Plant Biology</i> , 2011, 11, 46.	3.6	92
63	The study of a SPATULA-like bHLH transcription factor expressed during peach (<i>Prunus persica</i>) fruit development. <i>Plant Physiology and Biochemistry</i> , 2011, 49, 654-663.	5.8	31
64	Distinctive Patterns of Intraclonal Diversification In IGHV1-2*04 Immunoglobulin Receptors of Patients with Splenic Marginal Zone Lymphoma: A of Ongoing Interactions with Antigen?. <i>Blood</i> , 2011, 118, 2638-2638.	1.4	0
65	The normal IGHV1-69â€“derived B-cell repertoire contains stereotypic patterns characteristic of unmutated CLL. <i>Blood</i> , 2010, 115, 71-77.	1.4	83
66	Highly conserved motifs in non-coding regions of Sirevirus retrotransposons: the key for their pattern of distribution within and across plants?. <i>BMC Genomics</i> , 2010, 11, 89.	2.8	25
67	A different ontogenesis for chronic lymphocytic leukemia cases carrying stereotyped antigen receptors: molecular and computational evidence. <i>Leukemia</i> , 2010, 24, 125-132.	7.2	109
68	Intraclonal diversification of immunoglobulin light chains in a subset of chronic lymphocytic leukemia alludes to antigen-driven clonal evolution. <i>Leukemia</i> , 2010, 24, 1317-1324.	7.2	50
69	Circoletto: visualizing sequence similarity with Circos. <i>Bioinformatics</i> , 2010, 26, 2620-2621.	4.1	293
70	famRCA-RACE: A ROLLING CIRCLE AMPLIFICATION RACE FOR ISOLATING A FAMILY OF HOMOLOGOUS cDNAs IN ONE REACTION AND ITS APPLICATION TO OBTAIN NAC GENES TRANSCRIPTION FACTORS FROM CROCUS (<i>CROCUS SATIVUS</i>) FLOWER. <i>Preparative Biochemistry and Biotechnology</i> , 2010, 40, 177-187.	1.9	2
71	Coexistence of different types of biallelic immunoglobulin heavy variable gene replacement events in a case of pediatric B precursor acute lymphoblastic leukemia. <i>Leukemia and Lymphoma</i> , 2010, 51, 1748-1750.	1.3	0
72	The Composition of the B Cell Receptor Repertoire In 7428 Cases of Chronic Lymphocytic Leukemia: One Third Stereotyped, Two Thirds Heterogeneous - What Does This Mean?. <i>Blood</i> , 2010, 116, 43-43.	1.4	2

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73	Over 30% of Patients with Splenic Marginal Zone Lymphoma Express Distinctive Antigen Receptors Utilizing a Single Immunoglobulin Variable Gene: Implications for the Origin and Selection of the Neoplastic Cells. <i>Blood</i> , 2010, 116, 634-634.	1.4	2
74	Molecular evidence for EBV and CMV persistence in a subset of patients with chronic lymphocytic leukemia expressing stereotyped IGHV4-34 B-cell receptors. <i>Leukemia</i> , 2009, 23, 919-924.	7.2	72
75	Analysis of xyloglucan endotransglycosylase/hydrolase (XTH) genes from allotetraploid (<i>Gossypium</i>) Tj ETQq1 1 0.784314 rgBT /Overl Physiology, 2009, 166, 403-416.	3.5	44
76	Evidence for the significant role of immunoglobulin light chains in antigen recognition and selection in chronic lymphocytic leukemia. <i>Blood</i> , 2009, 113, 403-411.	1.4	71
77	Extensive intraclonal diversification in a subgroup of chronic lymphocytic leukemia patients with stereotyped IGHV4-34 receptors: implications for ongoing interactions with antigen. <i>Blood</i> , 2009, 114, 4460-4468.	1.4	64
78	Evidence for Antigen-Driven Development of Molecularly Classified Burkitt Lymphomas.. <i>Blood</i> , 2009, 114, 317-317.	1.4	1
79	The Normal IGHV1-69-derived B Cell Repertoire Contains "Stereotypic" Patterns Characteristic of Unmutated CLL.. <i>Blood</i> , 2009, 114, 4370-4370.	1.4	0
80	Stereotyped patterns of somatic hypermutation in subsets of patients with chronic lymphocytic leukemia: implications for the role of antigen selection in leukemogenesis. <i>Blood</i> , 2008, 111, 1524-1533.	1.4	285
81	A Different Ontogenesis for CLL Cases Carrying Stereotyped Antigen Receptors: Molecular and Computational Evidence. <i>Blood</i> , 2008, 112, 777-777.	1.4	0
82	Science communication media for scientists and the public. <i>EMBO Reports</i> , 2007, 8, 886-887.	4.5	3
83	Stereotyped Patterns of Somatic Hypermutation (SHM) in Subsets of Patients with Chronic Lymphocytic Leukemia (CLL): Implications for the Role of Antigen Selection in Leukemogenesis.. <i>Blood</i> , 2007, 110, 744-744.	1.4	0
84	A minimal estimate for the gene content of the last universal common ancestor"exobiology from a terrestrial perspective. <i>Research in Microbiology</i> , 2006, 157, 57-68.	2.1	130
85	Genome coverage, literally speaking. <i>EMBO Reports</i> , 2005, 6, 397-399.	4.5	34
86	Sensitive detection of sequence similarity using combinatorial pattern discovery: A challenging study of two distantly related protein families. <i>Proteins: Structure, Function and Bioinformatics</i> , 2005, 61, 926-937.	2.6	7
87	Expansion of the BioCyc collection of pathway/genome databases to 160 genomes. <i>Nucleic Acids Research</i> , 2005, 33, 6083-6089.	14.5	570
88	CoGenT++: an extensive and extensible data environment for computational genomics. <i>Bioinformatics</i> , 2005, 21, 3806-3810.	4.1	22
89	The net of life: Reconstructing the microbial phylogenetic network. <i>Genome Research</i> , 2005, 15, 954-959.	5.5	211
90	Beyond 100 genomes. <i>Genome Biology</i> , 2003, 4, 402.	9.6	23