Nikos Darzentas

List of Publications by Year
in descending order

90 papers	4,226 citations	186265 28 h-index	114465 63 g-index
92 all docs	92 docs citations	92 times ranked	5584 citing authors

#	Article	IF	Citations
1	Expansion of the BioCyc collection of pathway/genome databases to 160 genomes. Nucleic Acids Research, 2005, 33, 6083-6089.	14.5	570
2	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
3	Circoletto: visualizing sequence similarity with Circos. Bioinformatics, 2010, 26, 2620-2621.	4.1	293
4	Stereotyped patterns of somatic hypermutation in subsets of patients with chronic lymphocytic leukemia: implications for the role of antigen selection in leukemogenesis. Blood, 2008, 111, 1524-1533.	1.4	285
5	Molecular Subsets of Mantle Cell Lymphoma Defined by the <i>IGHV</i> Mutational Status and SOX11 Expression Have Distinct Biologic and Clinical Features. Cancer Research, 2012, 72, 5307-5316.	0.9	231
6	The net of life: Reconstructing the microbial phylogenetic network. Genome Research, 2005, 15, 954-959.	5.5	211
7	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. Leukemia, 2019, 33, 2241-2253.	7.2	177
8	Is there a role for antigen selection in mantle cell lymphoma? Immunogenetic support from a series of 807 cases. Blood, 2011, 118, 3088-3095.	1.4	149
9	A minimal estimate for the gene content of the last universal common ancestor—exobiology from a terrestrial perspective. Research in Microbiology, 2006, 157, 57-68.	2.1	130
10	A different ontogenesis for chronic lymphocytic leukemia cases carrying stereotyped antigen receptors: molecular and computational evidence. Leukemia, 2010, 24, 125-132.	7.2	109
11	Clinical effect of stereotyped B-cell receptor immunoglobulins in chronic lymphocytic leukaemia: a retrospective multicentre study. Lancet Haematology,the, 2014, 1, e74-e84.	4.6	93
12	Multiple evidence for the role of an Ovate-like gene in determining fruit shape in pepper. BMC Plant Biology, 2011, 11, 46.	3.6	92
13	Next-generation sequencing of immunoglobulin gene rearrangements for clonality assessment: a technical feasibility study by EuroClonality-NGS. Leukemia, 2019, 33, 2227-2240.	7.2	92
14	The normal IGHV1-69–derived B-cell repertoire contains stereotypic patterns characteristic of unmutated CLL. Blood, 2010, 115, 71-77.	1.4	83
15	Barcode High Resolution Melting (Bar-HRM) analysis for detection and quantification of PDO "Fava Santorinis"(Lathyrus clymenum) adulterants. Food Chemistry, 2012, 133, 505-512.	8.2	76
16	Molecular evidence for EBV and CMV persistence in a subset of patients with chronic lymphocytic leukemia expressing stereotyped IGHV4-34 B-cell receptors. Leukemia, 2009, 23, 919-924.	7.2	72
17	Evidence for the significant role of immunoglobulin light chains in antigen recognition and selection in chronic lymphocytic leukemia. Blood, 2009, 113, 403-411.	1.4	71
18	Not all IGHV3-21 chronic lymphocytic leukemias are equal: prognostic considerations. Blood, 2015, 125, 856-859.	1.4	70

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19	Quality control and quantification in IG/TR next-generation sequencing marker identification: protocols and bioinformatic functionalities by EuroClonality-NGS. Leukemia, 2019, 33, 2254-2265.	7.2	70
20	Extensive intraclonal diversification in a subgroup of chronic lymphocytic leukemia patients with stereotyped IGHV4-34 receptors: implications for ongoing interactions with antigen. Blood, 2009, 114, 4460-4468.	1.4	64
21	High-Throughput Immunogenetics for Clinical and Research Applications in Immunohematology: Potential and Challenges. Journal of Immunology, 2017, 198, 3765-3774.	0.8	61
22	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
23	Intraclonal diversification of immunoglobulin light chains in a subset of chronic lymphocytic leukemia alludes to antigen-driven clonal evolution. Leukemia, 2010, 24, 1317-1324.	7.2	50
24	Analysis of xyloglucan endotransglycosylase/hydrolase (XTH) genes from allotetraploid (Gossypium) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 5 Physiology, 2009, 166, 403-416.	3.5	44
25	ARResT/AssignSubsets: a novel application for robust subclassification of chronic lymphocytic leukemia based on B cell receptor IG stereotypy. Bioinformatics, 2015, 31, 3844-3846.	4.1	43
26	Antigen selection in B-cell lymphomas—Tracing the evidence. Seminars in Cancer Biology, 2013, 23, 399-409.	9.6	38
27	The study of the E-class SEPALLATA3-like MADS-box genes in wild-type and mutant flowers of cultivated saffron crocus (Crocus sativus L.) and its putative progenitors. Journal of Plant Physiology, 2011, 168, 1675-1684.	3.5	36
28	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
29	Genome coverage, literally speaking. EMBO Reports, 2005, 6, 397-399.	4.5	34
30	The study of a SPATULA-like bHLH transcription factor expressed during peach (Prunus persica) fruit development. Plant Physiology and Biochemistry, 2011, 49, 654-663.	5.8	31
31	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
32	Chronic Lymphocytic Leukemia with Mutated IGHV4-34 Receptors: Shared and Distinct Immunogenetic Features and Clinical Outcomes. Clinical Cancer Research, 2017, 23, 5292-5301.	7.0	27
33	Highly conserved motifs in non-coding regions of Sirevirus retrotransposons: the key for their pattern of distribution within and across plants?. BMC Genomics, 2010, 11, 89.	2.8	25
34	Next-Generation Sequencing—Based Clonality Assessment of Ig Gene Rearrangements. Journal of Molecular Diagnostics, 2021, 23, 1105-1115.	2.8	25
35	MASiVEdb: the Sirevirus Plant Retrotransposon Database. BMC Genomics, 2012, 13, 158.	2.8	24
36	Beyond 100 genomes. Genome Biology, 2003, 4, 402.	9.6	23

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37	CoGenT++: an extensive and extensible data environment for computational genomics. Bioinformatics, 2005, 21, 3806-3810.	4.1	22
38	Stereotyped B Cell Receptors in B Cell Leukemias and Lymphomas. Methods in Molecular Biology, 2013, 971, 135-148.	0.9	22
39	A role for palindromic structures in the <i>cis</i>-region of maize Sirevirus LTRs in transposable element evolution and host epigenetic response. Genome Research, 2016, 26, 226-237.	5.5	22
40	Immunoglobulin heavy variable (IGHV) genes and alleles: new entities, new names and implications for research and prognostication in chronic lymphocytic leukaemia. Immunogenetics, 2015, 67, 61-66.	2.4	20
41	Lack of common TCRA and TCRB clonotypes in CD8+/TCRαβ+ 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
42	An Immunogenetic Signature of Ongoing Antigen Interactions in Splenic Marginal Zone Lymphoma Expressing IGHV1-2*04 Receptors. Clinical Cancer Research, 2016, 22, 2032-2040.	7.0	17
43	The presence of CLL-associated stereotypic B cell receptors in the normal BCR repertoire from healthy individuals increases with age. Immunity and Ageing, 2019, 16, 22.	4.2	17
44	Gene capture by transposable elements leads to epigenetic conflict in maize. Molecular Plant, 2021, 14, 237-252.	8.3	17
45	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
46	Sirevirus LTR retrotransposons: phylogenetic misconceptions in the plant world. Mobile DNA, 2013, 4, 9.	3.6	16
47	No improvement in long-term survival over time for chronic lymphocytic leukemia patients in stereotyped subsets #1 and #2 treated with chemo(immuno)therapy. Haematologica, 2018, 103, e158-e161.	3.5	16
48	High resolution IgH repertoire analysis reveals fetal liver as the likely origin of life-long, innate B lymphopoiesis in humans. Clinical Immunology, 2017, 183, 8-16.	3.2	15
49	Automation of Amplicon-Based Library Preparation for Next-Generation Sequencing by Centrifugal Microfluidics. Analytical Chemistry, 2020, 92, 12833-12841.	6.5	15
50	The Significance of Stereotyped B-Cell Receptors in Chronic Lymphocytic Leukemia. Hematology/Oncology Clinics of North America, 2013, 27, 237-250.	2.2	13
51	A restricted clonal T-cell receptor αβ repertoire in Sézary syndrome is indicative of superantigenic stimulation. British Journal of Dermatology, 2011, 165, 78-84.	1.5	11
52	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
53	Considerations and complications of mapping small RNA high-throughput data to transposable elements. Mobile DNA, 2017, 8, 3.	3.6	11
54	Composite lymphoma of concurrent T zone lymphoma and large cell B cell lymphoma in a dog. BMC Veterinary Research, 2019, 15, 413.	1.9	10

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55	Characterization of the canine immunoglobulin heavy chain repertoire by next generation sequencing. Veterinary Immunology and Immunopathology, 2018, 202, 181-190.	1.2	9
56	Multiple Immunoglobulin Îº Gene Rearrangements within a Single Clone Unraveled by Next-Generation Sequencingâ€"Based Clonality Assessment. Journal of Molecular Diagnostics, 2021, 23, 1097-1104.	2.8	8
57	Sensitive detection of sequence similarity using combinatorial pattern discovery: A challenging study of two distantly related protein families. Proteins: Structure, Function and Bioinformatics, 2005, 61, 926-937.	2.6	7
58	T Cell Receptor Gene Repertoire Restriction in Chronic Lymphocytic Leukemia with Stereotyped IGHV4â€"34/IGKV2â€"30 Antigen Receptors. Blood, 2012, 120, 3908-3908.	1.4	6
59	Consistent B Cell Receptor Immunoglobulin Features Between Siblings in Familial Chronic Lymphocytic Leukemia. Frontiers in Oncology, 2021, 11, 740083.	2.8	5
60	A review of canine B cell clonality assays and primer set optimization using large-scale repertoire data. Veterinary Immunology and Immunopathology, 2019, 209, 45-52.	1.2	4
61	Euroclonality-NGS DNA Capture Panel for Integrated Analysis of IG/TR Rearrangements, Translocations, Copy Number and Sequence Variation in Lymphoproliferative Disorders. Blood, 2019, 134, 888-888.	1.4	4
62	Science communication media for scientists and the public. EMBO Reports, 2007, 8, 886-887.	4.5	3
63	Potential and pitfalls of whole transcriptome-based immunogenetic marker identification in acute lymphoblastic leukemia; a EuroMRD and EuroClonality-NGS Working Group study. Leukemia, 2021, 35, 924-928.	7.2	3
64	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. Preparative Biochemistry and Biotechnology, 2010, 40, 177-187.	1.9	2
65	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?. Blood, 2010, 116, 43-43.	1.4	2
66	Over 30% of Patients with Splenic Marginal Zone Lymphoma Express Distinctive Antigen Receptors Utilizing a Single Immunoglogulin Variable Gene: Implications for the Origin and Selection of the Neoplastic Cells. Blood, 2010, 116, 634-634.	1.4	2
67	The IG/TR Next Generation Marker Screening Developed within Euroclonality-NGS Consortium Is Successful in 94% of Acute Lymphoblastic Leukemia Samples. Blood, 2018, 132, 2830-2830.	1.4	2
68	Validation of the EuroClonality-NGS DNA capture panel as an integrated genomic tool for lymphoproliferative disorders. Blood Advances, 2021, 5, 3188-3198.	5.2	2
69	NGS-Based MRD Quantitation: An Alternative to qPCR Validated on a Large Consecutive Cohort of Children with ALL. Blood, 2021, 138, 1314-1314.	1.4	2
70	Evidence for Antigen-Driven Development of Molecularly Classified Burkitt Lymphomas.. Blood, 2009, 114, 317-317.	1.4	1
71	Library Preparation Is the Major Factor Affecting Differences in Results of Immunoglobulin Gene Rearrangements Detection on Two Major Next-Generation Sequencing Platforms. Blood, 2015, 126, 1411-1411.	1.4	1
72	Reappraising Immunoglobulin Repertoire Restrictions in Chronic Lymphocytic Leukemia: Focus on Major Stereotyped Subsets and Closely Related Satellites. Blood, 2016, 128, 4376-4376.	1.4	1

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73	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. Blood, 2012, 120, 1777-1777.	1.4	1
74	Coexistence of different types of biallelic immunoglobulin heavy variable gene replacement events in a case of pediatric B precursor acute lymphoblastic leukemia. Leukemia and Lymphoma, 2010, 51, 1748-1750.	1.3	0
75	Stereotyped Patterns of Somatic Hypermutation (SHM) in Subsets of Patients with Chronic Lymphocytic Leukemia (CLL): Implications for the Role of Antigen Selection in Leukemogenesis.. Blood, 2007, 110, 744-744.	1.4	0
76	A Different Ontogenesis for CLL Cases Carrying Stereotyped Antigen Receptors: Molecular and Computational Evidence. Blood, 2008, 112, 777-777.	1.4	0
77	The Normal IGHV1-69-derived B Cell Repertoire Contains â€œStereotypicâ€•Patterns Characteristic of Unmutated CLL.. Blood, 2009, 114, 4370-4370.	1.4	0
78	Distinctive Patterns of Intraclonal Diversification In IGHV1-2*04 Immunoglobulin Receptors of Patients with Splenic Marginal Zone Lymphoma: A of Ongoing Interactions with Antigen?. Blood, 2011, 118, 2638-2638.	1.4	0
79	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. Blood, 2012, 120, 831-831.	1.4	0
80	Clonal Selection in the Ontogeny and Evolution of Splenic Marginal Zone Lymphoma Confirming the Existence of Distinct Molecular Subtypes. Blood, 2012, 120, 1556-1556.	1.4	0
81	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
82	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
83	Clinical Impact of Stereotyped Antigen Receptors in Chronic Lymphocytic Leukemia. Blood, 2014, 124, 3280-3280.	1.4	0
84	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. Blood, 2015, 126, 3159-3159.	1.4	0
85	CLL with Mutated IGHV4-34 Antigen Receptors Is Clinically Heterogeneous: Antigen Receptor Stereotypy Makes the Difference. Blood, 2015, 126, 5263-5263.	1.4	0
86	A Versatile DNA/RNA NGS Targeted Capture Strategy for Detection of Fusion Genes in Pediatric ALL. Blood, 2016, 128, 2913-2913.	1.4	0
87	Monitoring of the Clonal Architecture of B-Cell Precursor ALL during Induction Chemoimmunotherapy. Blood, 2018, 132, 1555-1555.	1.4	0
88	Deep Immunoprofiling By Flow Cytometry and NGS Reveals Distinct T Cell Profile in Pediatric Hepatitis-Associated Aplastic Anemia. Blood, 2019, 134, 2508-2508.	1.4	0
89	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. Blood, 2021, 138, 3498-3498.	1.4	0
90	Karyosequencing: Integrating Genome-Wide and Targeted Sequencing for Comprehensive Diagnosis of Lymphoproliferative Disorders. Blood, 2021, 138, 272-272.	1.4	0