## Sabri Saeed Sanabani

List of Publications by Year in descending order

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84 1,494 22 papers citations h-index

93 93 93 2135
all docs docs citations times ranked citing authors

395702

33

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#	Article	IF	CITATIONS
1	lgG from Adult Atopic Dermatitis (AD) Patients Induces Nonatopic Neonatal Thymic Gamma–Delta T Cells (ĴĴT) to Acquire IL-22/IL-17 Secretion Profile with Skin-Homing Properties and Epigenetic Implications Mediated by miRNA. International Journal of Molecular Sciences, 2022, 23, 6872.	4.1	7
2	lgG from Adult Atopic Dermatitis (AD) Patients Induces Thymic IL-22 Production and CLA Expression on CD4+ T Cells: Possible Epigenetic Implications Mediated by miRNA. International Journal of Molecular Sciences, 2022, 23, 6867.	4.1	5
3	Altered RNome expression in Murine Gastrocnemius Muscle following Exposure to Jararhagin, a Metalloproteinase from Bothrops jararaca Venom. Toxins, 2022, 14, 472.	3.4	1
4	Global expression of noncoding RNome reveals dysregulation of small RNAs in patients with HTLV-1–associated adult T-cell leukemia: a pilot study. Infectious Agents and Cancer, 2021, 16, 4.	2.6	9
5	Zika virus in Brazil. , 2021, , 341-349.		O
6	Preconceptional Immunization Can Modulate Offspring Intrathymic IL-17-Producing γÎT Cells with Epigenetic Implications Mediated by microRNAs. International Journal of Molecular Sciences, 2021, 22, 6633.	4.1	1
7	A new class of antimicrobial molecules derived from kefir, effective against Pseudomonas aeruginosa and methicillin resistant Staphylococcus aureus (MRSA) strains. Scientific Reports, 2020, 10, 17434.	3.3	8
8	Bacterial community composition and potential pathogens along the Pinheiros River in the southeast of Brazil. Scientific Reports, 2020, 10, 9331.	3.3	20
9	Bacterial diversity associated with the abdomens of naturally Plasmodium-infected and non-infected Nyssorhynchus darlingi. BMC Microbiology, 2020, 20, 180.	3.3	7
10	The Vaginal Microbiome as a Tool to Predict rASRM Stage of Disease in Endometriosis: a Pilot Study. Reproductive Sciences, 2020, 27, 1064-1073.	2.5	35
11	Zika Virus Amplification Using Strand Displacement Isothermal Method and Sequencing Using Nanopore Technology. Methods in Molecular Biology, 2020, 2142, 123-136.	0.9	2
12	Rabies virus diversification in aerial and terrestrial mammals. Genetics and Molecular Biology, 2020, 43, e20190370.	1.3	10
13	Asaia (Rhodospirillales: Acetobacteraceae) and Serratia (Enterobacterales: Yersiniaceae) associated with Nyssorhynchus braziliensis and Nyssorhynchus darlingi (Diptera: Culicidae). Revista Brasileira De Entomologia, 2020, 64, .	0.4	7
14	Small RNA profiles of HTLVâ $\in$ 1 asymptomatic carriers with monoclonal and polyclonal rearrangement of the Tâ $\in$ cell antigen receptor γâ $\in$ chain using massively parallel sequencing: A pilot study. Oncology Letters, 2020, 20, 2311-2321.	1.8	11
15	Dataset of the microbiome composition in skin lesions caused by lumpy skin disease virus via 16s rRNA massive parallel sequencing. Data in Brief, 2019, 27, 104764.	1.0	5
16	Carbapenem-resistant Pseudomonas aeruginosa carrying blaVIM-36 assigned to ST308: Indicated non-virulence in a Galleria mellonella model. Journal of Global Antimicrobial Resistance, 2019, 16, 92-97.	2.2	4
17	Diagnosing Zika virus infection against a background of other flaviviruses: Studies in high resolution serological analysis. Scientific Reports, 2019, 9, 3648.	3.3	11
18	IgG From HIV-1–Exposed Seronegative and HIV-1–Infected Subjects Differently Modulates IFN-γ Production by Thymic T and B Cells. Journal of Acquired Immune Deficiency Syndromes (1999), 2019, 82, e56-e60.	2.1	12

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19	Shifts in intestinal microbiota after duodenal exclusion favor glycemic control and weight loss: a randomized controlled trial. Surgery for Obesity and Related Diseases, 2018, 14, 1748-1754.	1.2	27
20	Combination random isothermal amplification and nanopore sequencing for rapid identification of the causative agent of an outbreak. Journal of Clinical Virology, 2018, 106, 23-27.	3.1	15
21	High prevalence of HIV-1 transmitted drug-resistance mutations from proviral DNA massively parallel sequencing data of therapy-naÃve chronically infected Brazilian blood donors. PLoS ONE, 2017, 12, e0185559.	2.5	10
22	Rapid Molecular Detection of Zika Virus in Acute-Phase Urine Samples Using the Recombinase Polymerase Amplification Assay. PLOS Currents, 2017, 9, .	1.4	20
23	HIV-1 Diversity in Brazil. , 2017, , 55-70.		0
24	The microbiological signature of human cutaneous leishmaniasis lesions exhibits restricted bacterial diversity compared to healthy skin. Memorias Do Instituto Oswaldo Cruz, 2016, 111, 241-251.	1.6	28
25	Diversity of Bacterial Communities on Four Frequently Used Surfaces in a Large Brazilian Teaching Hospital. International Journal of Environmental Research and Public Health, 2016, 13, 152.	2.6	21
26	Ultra-Deep Sequencing of HIV-1 near Full-Length and Partial Proviral Genomes Reveals High Genetic Diversity among Brazilian Blood Donors. PLoS ONE, 2016, 11, e0152499.	2.5	28
27	Data on global expression of non-coding RNome in mice gastrocnemius muscle exposed to jararhagin, snake venom metalloproteinase. Data in Brief, 2016, 9, 685-688.	1.0	6
28	Frequent detection of CXCR4-using viruses among Brazilian blood donors with HIV-1 long-standing infection and unknown clinical stage: Analysis of massive parallel sequencing data. Data in Brief, 2016, 6, 267-274.	1.0	0
29	Investigation Into an Outbreak of Dengue-like Illness in Pernambuco, Brazil, Revealed a Cocirculation of Zika, Chikungunya, and Dengue Virus Type 1. Medicine (United States), 2016, 95, e3201.	1.0	91
30	Mitochondrial Genomes of <i> Anopheles </i> ( <i> Kerteszia </i> ) (Diptera: Culicidae) From the Atlantic Forest, Brazil. Journal of Medical Entomology, 2016, 53, 790-797.	1.8	17
31	Molecular investigation of bacterial communities: Data from two frequently used surfaces in the São Paulo Institute of Tropical Medicine. Data in Brief, 2016, 8, 399-403.	1.0	4
32	Comparative study of different methodologies to detect the JAK2 V617F mutation in chronic BCR-ABL1 negative myeloproliferative neoplasms. Practical Laboratory Medicine, 2016, 4, 30-37.	1.3	16
33	Detection of Zika virus in Brazilian patients during the first five days of infection – urine versus plasma. Eurosurveillance, 2016, 21, .	7.0	16
34	Mitochondrial genomes and comparative analyses of Culex camposi, Culex coronator, Culex usquatus and Culex usquatissimus (Diptera:Culicidae), members of the coronator group. BMC Genomics, 2015, 16, 831.	2.8	35
35	Frequency of coreceptor tropism in PBMC samples from HIV-1 recently infected blood donors by massively parallel sequencing: the REDS II study. Virology Journal, 2015, 12, 74.	3.4	4
36	Molecular Analysis of Bacterial Microbiota on Brazilian Currency Note Surfaces. International Journal of Environmental Research and Public Health, 2015, 12, 13276-13288.	2.6	24

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37	Enhanced detection of viral diversity using partial and near fullâ€length genomes of human immunodeficiency virus <scp>T</scp> ype 1 provirus deep sequencing data from recently infected donors at four blood centers in <scp>B</scp> razil. Transfusion, 2015, 55, 980-990.	1.6	12
38	Molecular Characterization of Human T-Cell Lymphotropic Virus Type 1 Full and Partial Genomes by Illumina Massively Parallel Sequencing Technology. PLoS ONE, 2014, 9, e93374.	2.5	45
39	Identification of a Novel HIV-1 Circulating Recombinant Form (CRF72_BF1) in Deep Sequencing Data from Blood Donors in Southeastern Brazil. Genome Announcements, 2014, 2, .	0.8	13
40	Genetic Characterization of HIV-1 Subtype D Near-Full-Length Proviral Genomes by Illumina Massively Parallel Sequencing Technology. Genome Announcements, 2014, 2, .	0.8	3
41	Short Communication: HIV Type 1 Subtype BF Leads to Faster CD4+ T Cell Loss Compared to Subtype B. AIDS Research and Human Retroviruses, 2014, 30, 190-194.	1.1	13
42	Deep Sequencing of HIV-1 near Full-Length Proviral Genomes Identifies High Rates of BF1 Recombinants Including Two Novel Circulating Recombinant Forms (CRF) 70_BF1 and a Disseminating 71_BF1 among Blood Donors in Pernambuco, Brazil. PLoS ONE, 2014, 9, e112674.	2.5	27
43	Investigation of human parvovirus B19 occurrence and genetic variability in different leukaemia entities. Clinical Microbiology and Infection, 2013, 19, E31-E43.	6.0	21
44	Expansion in CD39+ CD4+ Immunoregulatory T Cells and Rarity of Th17 Cells in HTLV-1 Infected Patients Is Associated with Neurological Complications. PLoS Neglected Tropical Diseases, 2013, 7, e2028.	3.0	27
45	Variability of HIV-1 Genomes among Children and Adolescents from São Paulo, Brazil. PLoS ONE, 2013, 8, e62552.	2.5	18
46	Evaluation of HIV-1 resistance to antiretroviral drugs among 150 patients after six months of therapeutic interruption. International Journal of STD and AIDS, 2012, 23, 120-125.	1.1	7
47	HIV-1 Proviral DNA Loads (as Determined by Quantitative PCR) in Patients Subjected to Structured Treatment Interruption after Antiretroviral Therapy Failure. Journal of Clinical Microbiology, 2012, 50, 2132-2133.	3.9	17
48	Dasatinib Overrides Imatinib Resistance Mediated by the F359I Residue Mutation in Two Patients with Chronic Myeloid Leukemia. Acta Haematologica, 2012, 127, 56-59.	1.4	1
49	Simultaneous Occurrence of Biphenotypic T Cell/Myeloid Lesions Involving t(12;13)(p13;q14) in a Pediatric Patient. Acta Haematologica, 2012, 127, 165-169.	1.4	4
50	Evaluation of Long-Term Outcomes, Cytogenetic and Molecular Responses with Imatinib Mesylate in Early and Late Chronic-Phase Chronic Myeloid Leukemia: A Report from a Single Institute. Acta Haematologica, 2012, 128, 223-232.	1.4	8
51	Low-Cost Ultra-Wide Genotyping Using Roche/454 Pyrosequencing for Surveillance of HIV Drug Resistance. PLoS ONE, 2012, 7, e36494.	2.5	75
52	Analysis of Transmitted Resistance to Raltegravir and Selective Pressure among HIV-1-Infected Patients on a Failing HAART in São Paulo, Brazil. Journal of Clinical Microbiology, 2012, 50, 2122-2125.	3.9	4
53	Lack of evidence to support the association of a single IL28B genotype SNP rs12979860 with the HTLV-1 clinical outcomes and proviral load. BMC Infectious Diseases, 2012, 12, 374.	2.9	12
54	Frequency of subtype B and F1 dual infection in HIV-1 positive, Brazilian men who have sex with men. Virology Journal, 2012, 9, 223.	3.4	11

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55	Pretherapeutic Expression of the <i>hOCT1</i> Gene Predicts a Complete Molecular Response to Imatinib Mesylate in Chronic-Phase Chronic Myeloid Leukemia. Acta Haematologica, 2012, 127, 228-234.	1.4	23
56	Frequency of subtype B and F1 dual infection in HIV-1 positive, Brazilian men who have sex with men. Retrovirology, 2012, 9, .	2.0	0
57	Genetic variability and high proportion of HIV-1 BF1 recombinant strains among vertically infected children in SÃ $\pm$ o Paulo, Brazil. Retrovirology, 2012, 9, .	2.0	1
58	Faster HIV-1 Disease Progression among Brazilian Individuals Recently Infected with CXCR4-Utilizing Strains. PLoS ONE, 2012, 7, e30292.	2.5	29
59	Correlation between LTR point mutations and proviral load levels among Human T cell Lymphotropic Virus type 1 (HTLV-1) asymptomatic carriers. Virology Journal, 2011, 8, 535.	3.4	13
60	Prognostic impact of <i>MYCN, DDX1, TrkA</i> , and <i>TrkC</i> gene transcripts expression in neuroblastoma. Pediatric Blood and Cancer, 2011, 56, 749-756.	1.5	8
61	Parvovirus among Patients with Cytopenia of Unknown Origin in Brazil: a Case-Control Study. Journal of Clinical Microbiology, 2011, 49, 1578-1580.	3.9	8
62	HTLV-1 Tax Specific CD8+ T Cells Express Low Levels of Tim-3 in HTLV-1 Infection: Implications for Progression to Neurological Complications. PLoS Neglected Tropical Diseases, 2011, 5, e1030.	3.0	29
63	Characterization of Partial and Near Full-Length Genomes of HIV-1 Strains Sampled from Recently Infected Individuals in São Paulo, Brazil. PLoS ONE, 2011, 6, e25869.	2.5	31
64	Molecular measurement of BCR-ABL transcript variations in chronic myeloid leukemia patients in cytogenetic remission. BMC Hematology, 2010, $10, 7$ .	2.6	6
65	Unexpected Diversity of Cellular Immune Responses against Nef and Vif in HIV-1-Infected Patients Who Spontaneously Control Viral Replication. PLoS ONE, 2010, 5, e11436.	2.5	10
66	Efficacy and Tolerability after Unusually Low Doses of Dasatinib in Chronic Myeloid Leukemia Patients Intolerant to Standard-Dose Dasatinib Therapy. Clinical Medicine Insights: Oncology, 2010, 4, CMO.S6413.	1.3	7
67	Early Detection of t(8;21) Chromosomal Translocations during Treatment of <i>PML-RARA</i> Positive Acute Promyelocytic Leukemia: A Case Study. Clinical Medicine Insights: Oncology, 2010, 4, CMO.S6446.	1.3	3
68	Successful Pregnancy and Delivery in a Patient with Chronic Myeloid Leukemia while on Dasatinib Therapy. Advances in Hematology, 2010, 2010, 1-4.	1.0	42
69	Whole-Genome Characterization of Human and Simian Immunodeficiency Virus Intrahost Diversity by Ultradeep Pyrosequencing. Journal of Virology, 2010, 84, 12087-12092.	3.4	63
70	Achievement of complete donor-type chimerism and remission with dasatinib in Philadelphia chromosome-positive ALL relapsing after allogeneic transplantation. Bone Marrow Transplantation, 2010, 45, 1125-1126.	2.4	3
71	Characterization and frequency of a newly identified HIV-1 BF1 intersubtype circulating recombinant form in São Paulo, Brazil. Virology Journal, 2010, 7, 74.	3.4	26
72	Doenças hematológicas associadas ao eritrovÃrus. Revista Brasileira De Hematologia E Hemoterapia, 2009, 31, 285-290.	0.7	0

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73	The performance of semi-quantitative differential PCR is similar to that of real-time PCR for the detection of the MYCN gene in neuroblastomas. Brazilian Journal of Medical and Biological Research, 2009, 42, 791-795.	1.5	8
74	The Use of Imatinib Mesylate as a Lifesaving Treatment of Chronic Myeloid Leukemia Relapse after Bone Marrow Transplantation. Journal of Transplantation, 2009, 2009, 1-4.	0.5	2
75	HIVSetSubtype., 2009,,.		0
76	Near full-length genome analysis of low prevalent human immunodeficiency virus type 1 subclade F1 in São Paulo, Brazil. Virology Journal, 2009, 6, 78.	3.4	10
77	Two successful pregnancies in a woman with chronic myeloid leukemia exposed to nilotinib during the first trimester of her second pregnancy: case study. Journal of Hematology and Oncology, 2009, 2, 42.	17.0	69
78	Selective regimes and evolutionary rates of HIV-1 subtype B V3 variants in the Brazilian epidemic. Virology, 2008, 381, 184-193.	2.4	19
79	Characterization of the Full-Length Human Immunodeficiency Virus-1 Genome from Recently Infected Subjects in Brazil. AIDS Research and Human Retroviruses, 2007, 23, 1087-1094.	1.1	7
80	Analysis of the near full length genomes of HIV-1 subtypes B, F and BF recombinant from a cohort of 14 patients in $S\tilde{A}$ Paulo, Brazil. Infection, Genetics and Evolution, 2006, 6, 368-377.	2.3	48
81	Sequence Variability of Human Erythroviruses Present in Bone Marrow of Brazilian Patients with Various Parvovirus B19-Related Hematological Symptoms. Journal of Clinical Microbiology, 2006, 44, 604-606.	3.9	86
82	Full-Length Genome Analysis of Human Immunodeficiency Virus Type 1 Subtype C in Brazil. AIDS Research and Human Retroviruses, 2006, 22, 171-176.	1.1	39
83	Analysis of Full-Length Human Immunodeficiency Virus Type 1 Genome Reveals a Variable Spectrum of Subtypes B and F Recombinants in São Paulo, Brazil. AIDS Research and Human Retroviruses, 2005, 21, 145-151.	1.1	43
84	Human herpesvirus type 8 among Brazilian blood donors. Transfusion, 2003, 43, 1764-1765.	1.6	18