

Lars Kaderali

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3525071/publications.pdf>

Version: 2024-02-01

122
papers

4,829
citations

87843

38
h-index

114418

63
g-index

129
all docs

129
docs citations

129
times ranked

7833
citing authors

#	ARTICLE	IF	CITATIONS
1	Stimulation of soluble guanylyl cyclase (sGC) by riociguat attenuates heart failure and pathological cardiac remodelling. <i>British Journal of Pharmacology</i> , 2022, 179, 2430-2442.	2.7	15
2	Most anti-PF4 antibodies in vaccine-induced immune thrombotic thrombocytopenia are transient. <i>Blood</i> , 2022, 139, 1903-1907.	0.6	30
3	Impaired detection of omicron by SARS-CoV-2 rapid antigen tests. <i>Medical Microbiology and Immunology</i> , 2022, 211, 105-117.	2.6	94
4	Computational strategies to combat COVID-19: useful tools to accelerate SARS-CoV-2 and coronavirus research. <i>Briefings in Bioinformatics</i> , 2021, 22, 642-663.	3.2	110
5	Hypertension delays viral clearance and exacerbates airway hyperinflammation in patients with COVID-19. <i>Nature Biotechnology</i> , 2021, 39, 705-716.	9.4	129
6	From heterogeneous healthcare data to disease-specific biomarker networks: A hierarchical Bayesian network approach. <i>PLoS Computational Biology</i> , 2021, 17, e1008735.	1.5	10
7	ITNâ€™VIROINF: Understanding (Harmful) Virus-Host Interactions by Linking Virology and Bioinformatics. <i>Viruses</i> , 2021, 13, 766.	1.5	5
8	Modeling transcriptomic age using knowledge-primed artificial neural networks. <i>Npj Aging and Mechanisms of Disease</i> , 2021, 7, 15.	4.5	27
9	Comparison of four commercial, automated antigen tests to detect SARS-CoV-2 variants of concern. <i>Medical Microbiology and Immunology</i> , 2021, 210, 263-275.	2.6	47
10	Decline in Pathogenic Antibodies over Time in VITT. <i>New England Journal of Medicine</i> , 2021, 385, 1815-1816.	13.9	56
11	Evaluation of two rapid antigen tests to detect SARS-CoV-2 in a hospital setting. <i>Medical Microbiology and Immunology</i> , 2021, 210, 65-72.	2.6	66
12	Convergent use of phosphatidic acid for hepatitis C virus and SARS-CoV-2 replication organelle formation. <i>Nature Communications</i> , 2021, 12, 7276.	5.8	37
13	Evidence for increased SARS-CoV-2 susceptibility and COVID-19 severity related to pre-existing immunity to seasonal coronaviruses. <i>Cell Reports</i> , 2021, 37, 110169.	2.9	34
14	Efficient inactivation of pseudotyped HIV-based lentiviral vectors and infectious HIV. <i>Journal of Virological Methods</i> , 2020, 276, 113768.	1.0	1
15	Identifying Differentially Expressed MicroRNAs, Target Genes, and Key Pathways Deregulated in Patients with Liver Diseases. <i>International Journal of Molecular Sciences</i> , 2020, 21, 7368.	1.8	7
16	Concomitant DNA methylation and transcriptome signatures define epidermal responses to acute solar UV radiation. <i>Scientific Reports</i> , 2020, 10, 12918.	1.6	9
17	Genome-Wide DNA Alterations in X-Irradiated Human Gingiva Fibroblasts. <i>International Journal of Molecular Sciences</i> , 2020, 21, 5778.	1.8	2
18	A Coupled Mathematical Model of the Intracellular Replication of Dengue Virus and the Host Cell Immune Response to Infection. <i>Frontiers in Microbiology</i> , 2020, 11, 725.	1.5	28

#	ARTICLE	IF	CITATIONS
19	Ionizing Radiation Alters the Transition/Transversion Ratio in the Exome of Human Gingiva Fibroblasts. <i>Health Physics</i> , 2020, 119, 109-117.	0.3	1
20	Interaction of <i>Staphylococcus aureus</i> and Host Cells upon Infection of Bronchial Epithelium during Different Stages of Regeneration. <i>ACS Infectious Diseases</i> , 2020, 6, 2279-2290.	1.8	4
21	Host factor prioritization for pan-viral genetic perturbation screens using random intercept models and network propagation. <i>PLoS Computational Biology</i> , 2020, 16, e1007587.	1.5	11
22	Mechanistic modeling explains the dsRNA length-dependent activation of the RIG-I mediated immune response. <i>Journal of Theoretical Biology</i> , 2020, 500, 110336.	0.8	5
23	Multi-omics network analysis reveals distinct stages in the human aging progression in epidermal tissue. <i>Aging</i> , 2020, 12, 12393-12409.	1.4	21
24	Mathematical modeling of hepatitis C RNA replication, exosome secretion and virus release. <i>PLoS Computational Biology</i> , 2020, 16, e1008421.	1.5	7
25	Title is missing!. , 2020, 16, e1007587.		0
26	Title is missing!. , 2020, 16, e1007587.		0
27	Title is missing!. , 2020, 16, e1007587.		0
28	Title is missing!. , 2020, 16, e1007587.		0
29	Selective inactivation of hypomethylating agents by SAMHD1 provides a rationale for therapeutic stratification in AML. <i>Nature Communications</i> , 2019, 10, 3475.	5.8	43
30	Benign uterine massâ€™ discrimination from leiomyosarcoma by a preoperative risk score: a multicenter cohort study. <i>Archives of Gynecology and Obstetrics</i> , 2019, 300, 1719-1727.	0.8	18
31	Wellâ€™being and return rate of firstâ€™time whole blood donors. <i>Vox Sanguinis</i> , 2019, 114, 154-161.	0.7	6
32	Reciprocal Effects of Fibroblast Growth Factor Receptor Signaling on Dengue Virus Replication and Virion Production. <i>Cell Reports</i> , 2019, 27, 2579-2592.e6.	2.9	17
33	Metabolic Cross-talk Between Human Bronchial Epithelial Cells and Internalized <i>Staphylococcus aureus</i> as a Driver for Infection*. <i>Molecular and Cellular Proteomics</i> , 2019, 18, 892a-908.	2.5	32
34	Editorial: Integrative Computational Systems Biology Approaches in Immunology and Medicine. <i>Frontiers in Microbiology</i> , 2019, 9, 3338.	1.5	1
35	Deep sequencing of a recurrent oligodendroglioma and the derived xenografts reveals new insights into the evolution of human oligodendroglioma and candidate driver genes. <i>Oncotarget</i> , 2019, 10, 3641-3653.	0.8	1
36	Whither systems medicine?. <i>Experimental and Molecular Medicine</i> , 2018, 50, e453-e453.	3.2	49

#	ARTICLE	IF	CITATIONS
37	The biological age linked to oxidative stress modifies breast cancer aggressiveness. <i>Free Radical Biology and Medicine</i> , 2018, 120, 133-146.	1.3	17
38	Hepatitis C Virus Replication Depends on Endosomal Cholesterol Homeostasis. <i>Journal of Virology</i> , 2018, 92, .	1.5	75
39	A convolutional neural network for ECG annotation as the basis for classification of cardiac rhythms. <i>Physiological Measurement</i> , 2018, 39, 104005.	1.2	60
40	The structural basis for cancer drug interactions with the catalytic and allosteric sites of SAMHD1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10022-E10031.	3.3	30
41	Mathematical Analysis of Viral Replication Dynamics and Antiviral Treatment Strategies: From Basic Models to Age-Based Multi-Scale Modeling. <i>Frontiers in Microbiology</i> , 2018, 9, 1546.	1.5	61
42	Comparison of Cell Arrays and Multi-Well Plates in Microscopy-Based Screening. <i>High-Throughput</i> , 2018, 7, 13.	4.4	3
43	Hepatitis C virus enters liver cells using the CD81 receptor complex proteins calpain-5 and CBLB. <i>PLoS Pathogens</i> , 2018, 14, e1007111.	2.1	46
44	Comparative proteomics reveals a diagnostic signature for pulmonary head&neck cancer&metastasis. <i>EMBO Molecular Medicine</i> , 2018, 10, .	3.3	41
45	Exome Sequencing Discloses Ionizing-radiation-induced DNA Variants in the Genome of Human Gingiva Fibroblasts. <i>Health Physics</i> , 2018, 115, 151-160.	0.3	5
46	Supplementary data for the biological age linked to oxidative stress modifies breast cancer aggressiveness. <i>Data in Brief</i> , 2018, 18, 1172-1184.	0.5	2
47	Synthetic lethality in <i>CCNE1</i> -amplified high grade serous ovarian cancer through combined inhibition of Polo-like kinase 1 and microtubule dynamics. <i>Oncotarget</i> , 2018, 9, 25842-25859.	0.8	24
48	Phosphorylation-Dependent Feedback Inhibition of RIG-I by DAPK1 Identified by Kinome-wide siRNA Screening. <i>Molecular Cell</i> , 2017, 65, 403-415.e8.	4.5	40
49	Constitutional de novo and postzygotic mutations in isolated cases of cerebral cavernous malformations. <i>Molecular Genetics & Genomic Medicine</i> , 2017, 5, 21-27.	0.6	4
50	SAMHD1 is a biomarker for cytarabine response and a therapeutic target in acute myeloid leukemia. <i>Nature Medicine</i> , 2017, 23, 250-255.	15.2	121
51	Deciphering the Origin and Evolution of Hepatitis B Viruses by Means of a Family of Non-enveloped Fish Viruses. <i>Cell Host and Microbe</i> , 2017, 22, 387-399.e6.	5.1	134
52	High-throughput sequencing of the entire genomic regions of CCM1/KRIT1, CCM2 and CCM3/PDCD10 to search for pathogenic deep-intronic splice mutations in cerebral cavernous malformations. <i>European Journal of Medical Genetics</i> , 2017, 60, 479-484.	0.7	10
53	Postoperative course and prognostic value of circulating angiogenic cytokines after pancreatic cancer resection. <i>Oncotarget</i> , 2017, 8, 72315-72323.	0.8	10
54	6. Prevention of inadequate sarcoma operations. , 2016, , 373-410.		0

#	ARTICLE	IF	CITATIONS
55	Flunarizine prevents hepatitis C virus membrane fusion in a genotype-dependent manner by targeting the potential fusion peptide within E1. <i>Hepatology</i> , 2016, 63, 49-62.	3.6	64
56	Reduced DNA methylation patterning and transcriptional connectivity define human skin aging. <i>Aging Cell</i> , 2016, 15, 563-571.	3.0	65
57	Systems biology of viral infection. <i>Virus Research</i> , 2016, 218, 1.	1.1	0
58	Autocrine TGF- β 2/ZEB/microRNA-200 signal transduction drives epithelial-mesenchymal transition: Kinetic models predict minimal drug dose to inhibit metastasis. <i>Cellular Signalling</i> , 2016, 28, 861-870.	1.7	10
59	Multi-scale model for hepatitis C viral load kinetics under treatment with direct acting antivirals. <i>Virus Research</i> , 2016, 218, 96-101.	1.1	18
60	ABHD5/CGI-58, the Chanarin-Dorfman Syndrome Protein, Mobilises Lipid Stores for Hepatitis C Virus Production. <i>PLoS Pathogens</i> , 2016, 12, e1005568.	2.1	26
61	Oral Health and Quality of Life in Old Age: A Cross-Sectional Pilot Project in Germany and Poland. <i>Advances in Clinical and Experimental Medicine</i> , 2016, 25, 951-959.	0.6	10
62	Comparison of Microbiomes from Different Niches of Upper and Lower Airways in Children and Adolescents with Cystic Fibrosis. <i>PLoS ONE</i> , 2015, 10, e0116029.	1.1	133
63	lpNet: a linear programming approach to reconstruct signal transduction networks. <i>Bioinformatics</i> , 2015, 31, 3231-3233.	1.8	3
64	Retrospective survival analysis of 237 consecutive patients with multiple pulmonary metastases from advanced renal cell carcinoma exclusively resected by a 1318-nm laser. <i>Interactive Cardiovascular and Thoracic Surgery</i> , 2015, 21, 211-217.	0.5	16
65	Quantitative Proteomics Identifies Serum Response Factor Binding Protein 1 as a Host Factor for Hepatitis C Virus Entry. <i>Cell Reports</i> , 2015, 12, 864-878.	2.9	50
66	Transcriptome analysis reveals a classical interferon signature induced by IFN γ 4 in human primary cells. <i>Genes and Immunity</i> , 2015, 16, 414-421.	2.2	44
67	Identification of HNRNPK as Regulator of Hepatitis C Virus Particle Production. <i>PLoS Pathogens</i> , 2015, 11, e1004573.	2.1	56
68	An integrative approach for a network based meta-analysis of viral RNAi screens. <i>Algorithms for Molecular Biology</i> , 2015, 10, 6.	0.3	7
69	Clearance of persistent hepatitis C virus infection in humanized mice using a claudin-1-targeting monoclonal antibody. <i>Nature Biotechnology</i> , 2015, 33, 549-554.	9.4	129
70	Several Human Liver Cell Expressed Apolipoproteins Complement HCV Virus Production with Varying Efficacy Conferring Differential Specific Infectivity to Released Viruses. <i>PLoS ONE</i> , 2015, 10, e0134529.	1.1	30
71	The SUMOylation Pathway Restricts Gene Transduction by Adeno-Associated Viruses. <i>PLoS Pathogens</i> , 2015, 11, e1005281.	2.1	25
72	A New Stochastic Model for Subgenomic Hepatitis C Virus Replication Considers Drug Resistant Mutants. <i>PLoS ONE</i> , 2014, 9, e91502.	1.1	12

#	ARTICLE	IF	CITATIONS
73	Detecting Non-Uniform Clusters in Large-Scale Interaction Graphs. <i>Journal of Computational Biology</i> , 2014, 21, 173-183.	0.8	2
74	RNAi screen identifies KIF15 as a novel regulator of integrin endocytic trafficking. <i>Journal of Cell Science</i> , 2014, 127, 2433-47.	1.2	25
75	Apolipoprotein E Codetermines Tissue Tropism of Hepatitis C Virus and Is Crucial for Viral Cell-to-Cell Transmission by Contributing to a Postenvelopment Step of Assembly. <i>Journal of Virology</i> , 2014, 88, 1433-1446.	1.5	88
76	Cell entry, efficient RNA replication, and production of infectious hepatitis C virus progeny in mouse liver-derived cells. <i>Hepatology</i> , 2014, 59, 78-88.	3.6	40
77	Role of Hypervariable Region 1 for the Interplay of Hepatitis C Virus with Entry Factors and Lipoproteins. <i>Journal of Virology</i> , 2014, 88, 12644-12655.	1.5	42
78	Impact of raltegravir on HIV-1 RNA and DNA forms following initiation of antiretroviral therapy in treatment-naive patients. <i>Journal of Antimicrobial Chemotherapy</i> , 2014, 69, 2809-2818.	1.3	10
79	AAV8-Mediated In Vivo Overexpression of miR-155 Enhances the Protective Capacity of Genetically Attenuated Malarial Parasites. <i>Molecular Therapy</i> , 2014, 22, 2130-2141.	3.7	25
80	Dynamic probabilistic threshold networks to infer signaling pathways from time-course perturbation data. <i>BMC Bioinformatics</i> , 2014, 15, 250.	1.2	10
81	Incorporation of primary patient-derived glycoproteins into authentic infectious hepatitis C virus particles. <i>Hepatology</i> , 2014, 60, 508-520.	3.6	7
82	Proteome analysis of the HIV-1 Gag interactome. <i>Virology</i> , 2014, 460-461, 194-206.	1.1	46
83	Isolate-dependent use of claudins for cell entry by hepatitis C virus. <i>Hepatology</i> , 2014, 59, 24-34.	3.6	54
84	Abstract 3387: Upregulation of gene expression in oligodendrogliomas is linked to an increase in GA binding protein alpha transcription. , 2014, , .		0
85	Aging is associated with highly defined epigenetic changes in the human epidermis. <i>Epigenetics and Chromatin</i> , 2013, 6, 36.	1.8	72
86	Mining Quasi-Bicliques from HIV-1-Human Protein Interaction Network: A Multiobjective Biclustering Approach. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013, 10, 423-435.	1.9	29
87	Hepatitis C Virus p7 is Critical for Capsid Assembly and Envelopment. <i>PLoS Pathogens</i> , 2013, 9, e1003355.	2.1	102
88	Replication Vesicles are Load- and Choke-Points in the Hepatitis C Virus Lifecycle. <i>PLoS Pathogens</i> , 2013, 9, e1003561.	2.1	77
89	A Novel, Diffusely Infiltrative Xenograft Model of Human Anaplastic Oligodendroglioma with Mutations in FUBP1, CIC, and IDH1. <i>PLoS ONE</i> , 2013, 8, e59773.	1.1	39
90	Reconstruction of Cellular Signal Transduction Networks Using Perturbation Assays and Linear Programming. <i>PLoS ONE</i> , 2013, 8, e69220.	1.1	10

#	ARTICLE	IF	CITATIONS
91	Novel CIC Point Mutations and an Exon-Spanning, Homozygous Deletion Identified in Oligodendroglial Tumors by a Comprehensive Genomic Approach Including Transcriptome Sequencing. PLoS ONE, 2013, 8, e76623.	1.1	16
92	The Importance and Challenges of Bayesian Parameter Learning in Systems Biology. Contributions in Mathematical and Computational Sciences, 2013, , 145-156.	0.3	2
93	High-throughput RNA interference screens integrative analysis: Towards a comprehensive understanding of the virus-host interplay. World Journal of Virology, 2013, 2, 18.	1.3	11
94	Rif2 Promotes a Telomere Fold-Back Structure through Rpd3L Recruitment in Budding Yeast. PLoS Genetics, 2012, 8, e1002960.	1.5	30
95	MAP-Kinase Regulated Cytosolic Phospholipase A2 Activity Is Essential for Production of Infectious Hepatitis C Virus Particles. PLoS Pathogens, 2012, 8, e1002829.	2.1	110
96	Dynamic Oscillation of Translation and Stress Granule Formation Mark the Cellular Response to Virus Infection. Cell Host and Microbe, 2012, 12, 71-85.	5.1	166
97	Identification of type I and type II interferon-induced effectors controlling hepatitis C virus replication. Hepatology, 2012, 56, 2082-2093.	3.6	138
98	Hub-Centered Gene Network Reconstruction Using Automatic Relevance Determination. PLoS ONE, 2012, 7, e35077.	1.1	28
99	miR-17-5p Regulates Endocytic Trafficking through Targeting TBC1D2/Arms. PLoS ONE, 2012, 7, e52555.	1.1	34
100	Recruitment and Activation of a Lipid Kinase by Hepatitis C Virus NS5A Is Essential for Integrity of the Membranous Replication Compartment. Cell Host and Microbe, 2011, 9, 32-45.	5.1	435
101	Hepatitis C virus complete life cycle screen for identification of small molecules with pro- or antiviral activity. Antiviral Research, 2011, 89, 136-148.	1.9	41
102	Normalizing for individual cell population context in the analysis of high-content cellular screens. BMC Bioinformatics, 2011, 12, 485.	1.2	22
103	Molecular Mechanism of Signal Perception and Integration by the Innate Immune Sensor Retinoic Acid-inducible Gene-I (RIG-I). Journal of Biological Chemistry, 2011, 286, 27278-27287.	1.6	112
104	From experimental setup to bioinformatics: An RNAi screening platform to identify host factors involved in HIV-1 replication. Biotechnology Journal, 2010, 5, 39-49.	1.8	39
105	Accurate prediction of neuroblastoma outcome based on miRNA expression profiles. International Journal of Cancer, 2010, 127, 2374-2385.	2.3	88
106	Tec-Kinase-Mediated Phosphorylation of Fibroblast Growth Factor 2 is Essential for Unconventional Secretion. Traffic, 2010, 11, 813-826.	1.3	72
107	Autoantibodies Against the Exocrine Pancreas in Autoimmune Pancreatitis: Gene and Protein Expression Profiling and Immunoassays Identify Pancreatic Enzymes as a Major Target of the Inflammatory Process. American Journal of Gastroenterology, 2010, 105, 2060-2071.	0.2	126
108	Detecting host factors involved in virus infection by observing the clustering of infected cells in siRNA screening images. Bioinformatics, 2010, 26, i653-i658.	1.8	15

#	ARTICLE	IF	CITATIONS
109	Biological Signature Characteristics of Primary Isolates from Human Immunodeficiency Virus Type 1 Group O in Ex Vivo Human Tonsil Histocultures. <i>Journal of Virology</i> , 2009, 83, 10494-10503.	1.5	12
110	RNAither, an automated pipeline for the statistical analysis of high-throughput RNAi screens. <i>Bioinformatics</i> , 2009, 25, 678-679.	1.8	48
111	Reconstructing signaling pathways from RNAi data using probabilistic Boolean threshold networks. <i>Bioinformatics</i> , 2009, 25, 2229-2235.	1.8	35
112	Reconstructing nonlinear dynamic models of gene regulation using stochastic sampling. <i>BMC Bioinformatics</i> , 2009, 10, 448.	1.2	39
113	Inference of an oscillating model for the yeast cell cycle. <i>Discrete Applied Mathematics</i> , 2009, 157, 2285-2295.	0.5	6
114	Reanalysis of neuroblastoma expression profiling data using improved methodology and extended follow-up increases validity of outcome prediction. <i>Cancer Letters</i> , 2009, 282, 55-62.	3.2	10
115	Subclassification and Individual Survival Time Prediction from Gene Expression Data of Neuroblastoma Patients by Using CASPAR. <i>Clinical Cancer Research</i> , 2008, 14, 6590-6601.	3.2	23
116	Translating Expression Profiling into a Clinically Feasible Test to Predict Neuroblastoma Outcome. <i>Clinical Cancer Research</i> , 2007, 13, 1459-1465.	3.2	28
117	Primer Design for Multiplexed Genotyping. <i>Methods in Molecular Biology</i> , 2007, 402, 269-285.	0.4	4
118	CASPAR: a hierarchical bayesian approach to predict survival times in cancer from gene expression data. <i>Bioinformatics</i> , 2006, 22, 1495-1502.	1.8	37
119	A fractional programming approach to efficient DNA melting temperature calculation. <i>Bioinformatics</i> , 2005, 21, 2375-2382.	1.8	18
120	Primer-design for multiplexed genotyping. <i>Nucleic Acids Research</i> , 2003, 31, 1796-1802.	6.5	73
121	Can Supervised Learning Be Used to Classify Cardiac Rhythms?. , 0, , .		6
122	Deciphering the Origin and Evolution of Hepatitis B Viruses. <i>SSRN Electronic Journal</i> , 0, , .	0.4	0