

# Lars Kaderali

## List of Publications by Year in descending order

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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	Recruitment and Activation of a Lipid Kinase by Hepatitis C Virus NS5A Is Essential for Integrity of the Membranous Replication Compartment. <i>Cell Host and Microbe</i> , 2011, 9, 32-45.	5.1	435
2	Dynamic Oscillation of Translation and Stress Granule Formation Mark the Cellular Response to Virus Infection. <i>Cell Host and Microbe</i> , 2012, 12, 71-85.	5.1	166
3	Identification of type I and type II interferon-induced effectors controlling hepatitis C virus replication. <i>Hepatology</i> , 2012, 56, 2082-2093.	3.6	138
4	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
5	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
6	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
7	Hypertension delays viral clearance and exacerbates airway hyperinflammation in patients with COVID-19. <i>Nature Biotechnology</i> , 2021, 39, 705-716.	9.4	129
8	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. <i>American Journal of Gastroenterology</i> , 2010, 105, 2060-2071.	0.2	126
9	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
10	Molecular Mechanism of Signal Perception and Integration by the Innate Immune Sensor Retinoic Acid-inducible Gene-I (RIG-I). <i>Journal of Biological Chemistry</i> , 2011, 286, 27278-27287.	1.6	112
11	MAP-Kinase Regulated Cytosolic Phospholipase A2 Activity Is Essential for Production of Infectious Hepatitis C Virus Particles. <i>PLoS Pathogens</i> , 2012, 8, e1002829.	2.1	110
12	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
13	Hepatitis C Virus p7 is Critical for Capsid Assembly and Envelopment. <i>PLoS Pathogens</i> , 2013, 9, e1003355.	2.1	102
14	Impaired detection of omicron by SARS-CoV-2 rapid antigen tests. <i>Medical Microbiology and Immunology</i> , 2022, 211, 105-117.	2.6	94
15	Accurate prediction of neuroblastoma outcome based on miRNA expression profiles. <i>International Journal of Cancer</i> , 2010, 127, 2374-2385.	2.3	88
16	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
17	Replication Vesicles are Load- and Choke-Points in the Hepatitis C Virus Lifecycle. <i>PLoS Pathogens</i> , 2013, 9, e1003561.	2.1	77
18	Hepatitis C Virus Replication Depends on Endosomal Cholesterol Homeostasis. <i>Journal of Virology</i> , 2018, 92, .	1.5	75

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19	Primer-design for multiplexed genotyping. <i>Nucleic Acids Research</i> , 2003, 31, 1796-1802.	6.5	73
20	Tec-Kinase-Mediated Phosphorylation of Fibroblast Growth Factor 2 is Essential for Unconventional Secretion. <i>Traffic</i> , 2010, 11, 813-826.	1.3	72
21	Aging is associated with highly defined epigenetic changes in the human epidermis. <i>Epigenetics and Chromatin</i> , 2013, 6, 36.	1.8	72
22	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
23	Reduced <scp>DNA</scp> methylation patterning and transcriptional connectivity define human skin aging. <i>Aging Cell</i> , 2016, 15, 563-571.	3.0	65
24	Flunarizine prevents hepatitis C virus membrane fusion in a genotypeâ€dependent manner by targeting the potential fusion peptide within E1. <i>Hepatology</i> , 2016, 63, 49-62.	3.6	64
25	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
26	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
27	Identification of HNRNPK as Regulator of Hepatitis C Virus Particle Production. <i>PLoS Pathogens</i> , 2015, 11, e1004573.	2.1	56
28	Decline in Pathogenic Antibodies over Time in VITT. <i>New England Journal of Medicine</i> , 2021, 385, 1815-1816.	13.9	56
29	Isolate-dependent use of claudins for cell entry by hepatitis C virus. <i>Hepatology</i> , 2014, 59, 24-34.	3.6	54
30	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
31	Whither systems medicine?. <i>Experimental and Molecular Medicine</i> , 2018, 50, e453-e453.	3.2	49
32	RNAither, an automated pipeline for the statistical analysis of high-throughput RNAi screens. <i>Bioinformatics</i> , 2009, 25, 678-679.	1.8	48
33	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
34	Proteome analysis of the HIV-1 Gag interactome. <i>Virology</i> , 2014, 460-461, 194-206.	1.1	46
35	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
36	Transcriptome analysis reveals a classical interferon signature induced by IFNÎ»4 in human primary cells. <i>Genes and Immunity</i> , 2015, 16, 414-421.	2.2	44

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37	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
38	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
39	Hepatitis C virus complete life cycle screen for identification of small molecules with pro- or antiviral activity. <i>Antiviral Research</i> , 2011, 89, 136-148.	1.9	41
40	Comparative proteomics reveals a diagnostic signature for pulmonary head&neck cancer&metastasis. <i>EMBO Molecular Medicine</i> , 2018, 10, .	3.3	41
41	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
42	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
43	Reconstructing nonlinear dynamic models of gene regulation using stochastic sampling. <i>BMC Bioinformatics</i> , 2009, 10, 448.	1.2	39
44	From experimental setup to bioinformatics: An RNAi screening platform to identify host factors involved in HIV&replication. <i>Biotechnology Journal</i> , 2010, 5, 39-49.	1.8	39
45	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
46	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
47	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
48	Reconstructing signaling pathways from RNAi data using probabilistic Boolean threshold networks. <i>Bioinformatics</i> , 2009, 25, 2229-2235.	1.8	35
49	miR-17-5p Regulates Endocytic Trafficking through Targeting TBC1D2/Arms. <i>PLoS ONE</i> , 2012, 7, e52555.	1.1	34
50	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
51	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
52	Rif2 Promotes a Telomere Fold-Back Structure through Rpd3L Recruitment in Budding Yeast. <i>PLoS Genetics</i> , 2012, 8, e1002960.	1.5	30
53	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
54	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

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55	Most anti-PF4 antibodies in vaccine-induced immune thrombotic thrombocytopenia are transient. <i>Blood</i> , 2022, 139, 1903-1907.	0.6	30
56	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
57	Translating Expression Profiling into a Clinically Feasible Test to Predict Neuroblastoma Outcome. <i>Clinical Cancer Research</i> , 2007, 13, 1459-1465.	3.2	28
58	Hub-Centered Gene Network Reconstruction Using Automatic Relevance Determination. <i>PLoS ONE</i> , 2012, 7, e35077.	1.1	28
59	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
60	Modeling transcriptomic age using knowledge-primed artificial neural networks. <i>Npj Aging and Mechanisms of Disease</i> , 2021, 7, 15.	4.5	27
61	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
62	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
63	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
64	The SUMOylation Pathway Restricts Gene Transduction by Adeno-Associated Viruses. <i>PLoS Pathogens</i> , 2015, 11, e1005281.	2.1	25
65	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
66	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
67	Normalizing for individual cell population context in the analysis of high-content cellular screens. <i>BMC Bioinformatics</i> , 2011, 12, 485.	1.2	22
68	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
69	A fractional programming approach to efficient DNA melting temperature calculation. <i>Bioinformatics</i> , 2005, 21, 2375-2382.	1.8	18
70	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
71	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
72	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

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73	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
74	Novel CIC Point Mutations and an Exon-Spanning, Homozygous Deletion Identified in Oligodendroglial Tumors by a Comprehensive Genomic Approach Including Transcriptome Sequencing. <i>PLoS ONE</i> , 2013, 8, e76623.	1.1	16
75	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
76	Detecting host factors involved in virus infection by observing the clustering of infected cells in siRNA screening images. <i>Bioinformatics</i> , 2010, 26, i653-i658.	1.8	15
77	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
78	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
79	A New Stochastic Model for Subgenomic Hepatitis C Virus Replication Considers Drug Resistant Mutants. <i>PLoS ONE</i> , 2014, 9, e91502.	1.1	12
80	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
81	High-throughput RNA interference screens integrative analysis: Towards a comprehensive understanding of the virus-host interplay. <i>World Journal of Virology</i> , 2013, 2, 18.	1.3	11
82	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
83	Reconstruction of Cellular Signal Transduction Networks Using Perturbation Assays and Linear Programming. <i>PLoS ONE</i> , 2013, 8, e69220.	1.1	10
84	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
85	Dynamic probabilistic threshold networks to infer signaling pathways from time-course perturbation data. <i>BMC Bioinformatics</i> , 2014, 15, 250.	1.2	10
86	Autocrine TGF- $\beta$ 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
87	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
88	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
89	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
90	Postoperative course and prognostic value of circulating angiogenic cytokines after pancreatic cancer resection. <i>Oncotarget</i> , 2017, 8, 72315-72323.	0.8	10

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91	Concomitant DNA methylation and transcriptome signatures define epidermal responses to acute solar UV radiation. <i>Scientific Reports</i> , 2020, 10, 12918.	1.6	9
92	Incorporation of primary patient-derived glycoproteins into authentic infectious hepatitis C virus particles. <i>Hepatology</i> , 2014, 60, 508-520.	3.6	7
93	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
94	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
95	Mathematical modeling of hepatitis C RNA replication, exosome secretion and virus release. <i>PLoS Computational Biology</i> , 2020, 16, e1008421.	1.5	7
96	Inference of an oscillating model for the yeast cell cycle. <i>Discrete Applied Mathematics</i> , 2009, 157, 2285-2295.	0.5	6
97	Can Supervised Learning Be Used to Classify Cardiac Rhythms?. , 0, , .		6
98	Well-being and return rate of first-time whole blood donors. <i>Vox Sanguinis</i> , 2019, 114, 154-161.	0.7	6
99	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
100	ITN-VIROINF: Understanding (Harmful) Virus-Host Interactions by Linking Virology and Bioinformatics. <i>Viruses</i> , 2021, 13, 766.	1.5	5
101	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
102	Constitutional de novo and postzygotic mutations in isolated cases of cerebral cavernous malformations. <i>Molecular Genetics &amp; Genomic Medicine</i> , 2017, 5, 21-27.	0.6	4
103	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
104	Primer Design for Multiplexed Genotyping. <i>Methods in Molecular Biology</i> , 2007, 402, 269-285.	0.4	4
105	lpNet: a linear programming approach to reconstruct signal transduction networks. <i>Bioinformatics</i> , 2015, 31, 3231-3233.	1.8	3
106	Comparison of Cell Arrays and Multi-Well Plates in Microscopy-Based Screening. <i>High-Throughput</i> , 2018, 7, 13.	4.4	3
107	Detecting Non-Uniform Clusters in Large-Scale Interaction Graphs. <i>Journal of Computational Biology</i> , 2014, 21, 173-183.	0.8	2
108	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

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109	Genome-Wide DNA Alterations in X-Irradiated Human Gingiva Fibroblasts. International Journal of Molecular Sciences, 2020, 21, 5778.	1.8	2
110	The Importance and Challenges of Bayesian Parameter Learning in Systems Biology. Contributions in Mathematical and Computational Sciences, 2013, , 145-156.	0.3	2
111	Editorial: Integrative Computational Systems Biology Approaches in Immunology and Medicine. Frontiers in Microbiology, 2019, 9, 3338.	1.5	1
112	Efficient inactivation of pseudotyped HIV-based lentiviral vectors and infectious HIV. Journal of Virological Methods, 2020, 276, 113768.	1.0	1
113	Ionizing Radiation Alters the Transition/Transversion Ratio in the Exome of Human Gingiva Fibroblasts. Health Physics, 2020, 119, 109-117.	0.3	1
114	Deep sequencing of a recurrent oligodendroglioma and the derived xenografts reveals new insights into the evolution of human oligodendroglioma and candidate driver genes. Oncotarget, 2019, 10, 3641-3653.	0.8	1
115	6. Prevention of inadequate sarcoma operations. , 2016, , 373-410.		0
116	Systems biology of viral infection. Virus Research, 2016, 218, 1.	1.1	0
117	Abstract 3387: Upregulation of gene expression in oligodendrogliomas is linked to an increase in GA binding protein alpha transcription. , 2014, , .		0
118	Deciphering the Origin and Evolution of Hepatitis B Viruses. SSRN Electronic Journal, 0, , .	0.4	0
119	Title is missing!. , 2020, 16, e1007587.		0
120	Title is missing!. , 2020, 16, e1007587.		0
121	Title is missing!. , 2020, 16, e1007587.		0
122	Title is missing!. , 2020, 16, e1007587.		0