Claudia Sala

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/4736242/publications.pdf

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89 papers 4,548 citations

32 h-index 63 g-index

94 all docs 94 docs citations 94 times ranked 6789 citing authors

#	Article	IF	CITATIONS
1	Pilot Study on Poultry Meat from Antibiotic Free and Conventional Farms: Can Metagenomics Detect Any Difference?. Foods, 2022, 11, 249.	4.3	13
2	Early downregulation of hsa-miR-144-3p in serum from drug-naÃ⁻ve Parkinson's disease patients. Scientific Reports, 2022, 12, 1330.	3.3	14
3	Metabolite and lipoprotein profiles reveal sex-related oxidative stress imbalance in de novo drug-naive Parkinson's disease patients. Npj Parkinson's Disease, 2022, 8, 14.	5. 3	11
4	Canine smooth muscle tumors: A clinicopathological study. Veterinary Pathology, 2022, 59, 244-255.	1.7	1
5	Prediction of Overall Survival in Cervical Cancer Patients Using PET/CT Radiomic Features. Applied Sciences (Switzerland), 2022, 12, 5946.	2.5	4
6	Evaluation of different computational methods for DNA methylation-based biological age. Briefings in Bioinformatics, 2022, 23, .	6.5	4
7	Commensal-driven immune zonation of the liver promotes host defence. Nature, 2021, 589, 131-136.	27.8	141
8	Antibodies, epicenter of SARS-CoV-2 immunology. Cell Death and Differentiation, 2021, 28, 821-824.	11.2	9
9	Comparison between 16S rRNA and shotgun sequencing data for the taxonomic characterization of the gut microbiota. Scientific Reports, $2021, 11, 3030$.	3.3	208
10	Impact of concurrency on the performance of a whole exome sequencing pipeline. BMC Bioinformatics, 2021, 22, 60.	2.6	3
11	A geroscience approach for Parkinson's disease: Conceptual framework and design of PROPAG-AGEING project. Mechanisms of Ageing and Development, 2021, 194, 111426.	4.6	14
12	A Meta-Analysis of Brain DNA Methylation Across Sex, Age, and Alzheimer's Disease Points for Accelerated Epigenetic Aging in Neurodegeneration. Frontiers in Aging Neuroscience, 2021, 13, 639428.	3.4	45
13	Classification and Personalized Prognostic Assessment on the Basis of Clinical and Genomic Features in Myelodysplastic Syndromes. Journal of Clinical Oncology, 2021, 39, 1223-1233.	1.6	127
14	Whole-genome sequencing analysis of semi-supercentenarians. ELife, 2021, 10, .	6.0	37
15	Estimage: a webserver hub for the computation of methylation age. Nucleic Acids Research, 2021, 49, W199-W206.	14.5	9
16	Clinical relevance of clonal hematopoiesis in persons aged ≥80 years. Blood, 2021, 138, 2093-2105.	1.4	37
17	Elevated metallothionein expression in long-lived species mediates the influence of cadmium accumulation on aging. GeroScience, 2021, 43, 1975-1993.	4.6	6
18	Heterogeneity of prodromal Parkinson symptoms in siblings of Parkinson disease patients. Npj Parkinson's Disease, 2021, 7, 78.	5. 3	2

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19	DNA methylation correlation structure of chromosome 21 in Down syndrome Theoretical Biology Forum, 2021, 114, 89-113.	0.2	0
20	Insights From Liverâ€Humanized Mice on Cholesterol Lipoprotein Metabolism and LXRâ€Agonist Pharmacodynamics in Humans. Hepatology, 2020, 72, 656-670.	7.3	23
21	Multicenter analysis of sputum microbiota in tuberculosis patients. PLoS ONE, 2020, 15, e0240250.	2.5	10
22	FasR Regulates Fatty Acid Biosynthesis and Is Essential for Virulence of Mycobacterium tuberculosis. Frontiers in Microbiology, 2020, 11, 586285.	3.5	1
23	Metagenomics-Based Proficiency Test of Smoked Salmon Spiked with a Mock Community. Microorganisms, 2020, 8, 1861.	3.6	4
24	Vaccines as remedy for antimicrobial resistance and emerging infections. Current Opinion in Immunology, 2020, 65, 102-106.	5.5	11
25	Proficiency Testing of Metagenomics-Based Detection of Food-Borne Pathogens Using a Complex Artificial Sequencing Dataset. Frontiers in Microbiology, 2020, 11, 575377.	3.5	7
26	Analysis of Epigenetic Age Predictors in Pain-Related Conditions. Frontiers in Public Health, 2020, 8, 172.	2.7	8
27	Evaluation of pre-processing on the meta-analysis of DNA methylation data from the Illumina HumanMethylation450 BeadChip platform. PLoS ONE, 2020, 15, e0229763.	2.5	12
28	Depression and Microbiomeâ€"Study on the Relation and Contiguity between Dogs and Humans. Applied Sciences (Switzerland), 2020, 10, 573.	2.5	2
29	Methylation data imputation performances under different representations and missingness patterns. BMC Bioinformatics, 2020, 21, 268.	2.6	15
30	Effect of Lactobacillus acidophilus D2/CSL (CECT 4529) supplementation in drinking water on chicken crop and caeca microbiome. PLoS ONE, 2020, 15, e0228338.	2.5	25
31	Small extracellular vesicles deliver miRâ€21 and miRâ€217 as proâ€senescence effectors to endothelial cells. Journal of Extracellular Vesicles, 2020, 9, 1725285.	12.2	104
32	Polarly Localized EccE ₁ Is Required for ESX-1 Function and Stabilization of ESX-1 Membrane Proteins in Mycobacterium tuberculosis. Journal of Bacteriology, 2020, 202, .	2.2	7
33	Host-Directed Therapies and Anti-Virulence Compounds to Address Anti-Microbial Resistant Tuberculosis Infection. Applied Sciences (Switzerland), 2020, 10, 2688.	2.5	6
34	Gut microbiota ecology: Biodiversity estimated from hybrid neutral-niche model increases with health status and aging. PLoS ONE, 2020, 15, e0237207.	2.5	4
35	Editorial on Special Issue "Tuberculosis Drug Discovery and Development 2019― Applied Sciences (Switzerland), 2020, 10, 6069.	2.5	0
36	Impact of a probiotic-based cleaning product on the microbiological profile of broiler litters and chicken caeca microbiota. Poultry Science, 2019, 98, 3602-3610.	3.4	27

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37	Missing value estimation methods for DNA methylation data. Bioinformatics, 2019, 35, 3786-3793.	4.1	39
38	Effect of a low protein diet on chicken ceca microbiome and productive performances. Poultry Science, 2019, 98, 3963-3976.	3.4	31
39	Promoter mutagenesis for fineâ€tuning expression of essential genes in <i>Mycobacterium tuberculosis</i> . Microbial Biotechnology, 2018, 11, 238-247.	4.2	13
40	EspL is essential for virulence and stabilizes EspE, EspF and EspH levels in Mycobacterium tuberculosis. PLoS Pathogens, 2018, 14, e1007491.	4.7	33
41	Essential Nucleoid Associated Protein mIHF (Rv1388) Controls Virulence and Housekeeping Genes in Mycobacterium tuberculosis. Scientific Reports, 2018, 8, 14214.	3.3	19
42	Genomic profiles of primary and metastatic esophageal adenocarcinoma identified via digital sorting of pure cell populations: results from a case report. BMC Cancer, 2018, 18, 889.	2.6	3
43	Rv3852 (H-NS) of Mycobacterium tuberculosis Is Not Involved in Nucleoid Compaction and Virulence Regulation. Journal of Bacteriology, 2017, 199, .	2.2	9
44	Identification of a T cell gene expression clock obtained by exploiting a MZ twin design. Scientific Reports, 2017, 7, 6005.	3.3	5
45	<pre><scp>E</scp>sp<scp>C</scp> forms a filamentous structure in the cell envelope of <scp><i>M</i></scp><i>ycobacterium tuberculosis</i> and impacts <scp>ESX</scp>â€1 secretion. Molecular Microbiology, 2017, 103, 26-38.</pre>	2.5	77
46	The Inosine Monophosphate Dehydrogenase, GuaB2, Is a Vulnerable New Bactericidal Drug Target for Tuberculosis. ACS Infectious Diseases, 2017, 3, 5-17.	3.8	83
47	Transcription facilitated genome-wide recruitment of topoisomerase I and DNA gyrase. PLoS Genetics, 2017, 13, e1006754.	3.5	56
48	Acceleration of leukocytes' epigenetic age as an early tumor and sex-specific marker of breast and colorectal cancer. Oncotarget, 2017, 8, 23237-23245.	1.8	90
49	Mycobacterium ulcerans Mouse Model Refinement for Pre-Clinical Profiling of Vaccine Candidates. PLoS ONE, 2016, 11, e0167059.	2.5	12
50	Characterization of DprE1-Mediated Benzothiazinone Resistance in Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2016, 60, 6451-6459.	3.2	36
51	Genomic and transcriptomic analysis of the streptomycin-dependent Mycobacterium tuberculosis strain 18b. BMC Genomics, 2016, 17, 190.	2.8	18
52	Methods for the integration of multi-omics data: mathematical aspects. BMC Bioinformatics, 2016, 17, 15.	2.6	316
53	Stochastic neutral modelling of the Gut Microbiota's relative species abundance from next generation sequencing data. BMC Bioinformatics, 2016, 17, 16.	2.6	19
54	Systems medicine of inflammaging. Briefings in Bioinformatics, 2016, 17, 527-540.	6.5	35

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55	Master equation and relative species abundance distribution for Lotka-Volterra models of interacting ecological communities. Theoretical Biology Forum, 2016, 109, 37-47.	0.2	3
56	Mycobacterium tuberculosis Differentially Activates cGAS- and Inflammasome-Dependent Intracellular Immune Responses through ESX-1. Cell Host and Microbe, 2015, 17, 799-810.	11.0	341
57	Statistical strategies and stochastic predictive models for the MARK-AGE data. Mechanisms of Ageing and Development, 2015, 151, 45-53.	4.6	3
58	Lansoprazole is an antituberculous prodrug targeting cytochrome bc1. Nature Communications, 2015, 6, 7659.	12.8	141
59	Bioluminescence for Assessing Drug Potency against Nonreplicating Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2015, 59, 4012-4019.	3.2	30
60	Whole-Transcriptome Sequencing for High-Resolution Transcriptomic Analysis in Mycobacterium tuberculosis. Methods in Molecular Biology, 2015, 1285, 17-30.	0.9	10
61	GtrA Protein Rv3789 Is Required for Arabinosylation of Arabinogalactan in Mycobacterium tuberculosis. Journal of Bacteriology, 2015, 197, 3686-3697.	2.2	26
62	Whole-Genome Sequencing for Comparative Genomics and De Novo Genome Assembly. Methods in Molecular Biology, 2015, 1285, 1-16.	0.9	15
63	Erratum for Boldrin et al., The Phosphatidyl- <i>myo</i> -Inositol Mannosyltransferase PimA Is Essential for Mycobacterium tuberculosis Growth <i>In Vitro</i> and <i>In Vivo</i> Journal of Bacteriology, 2014, 196, 4197-4197.	2.2	1
64	The PhoP-Dependent ncRNA Mcr7 Modulates the TAT Secretion System in Mycobacterium tuberculosis. PLoS Pathogens, 2014, 10, e1004183.	4.7	127
65	In VitroandIn VivoActivities of Three Oxazolidinones against Nonreplicating Mycobacterium tuberculosis. Antimicrobial Agents and Chemotherapy, 2014, 58, 3217-3223.	3.2	53
66	The role of low-grade inflammation and metabolic flexibility in aging and nutritional modulation thereof: A systems biology approach. Mechanisms of Ageing and Development, 2014, 136-137, 138-147.	4.6	80
67	<scp>EspI</scp> regulates the <scp>ESX</scp> â€1 secretion system in response to <scp>ATP</scp> levels in <scp><i>M</i></scp> <i>ycobacterium tuberculosis</i> . Molecular Microbiology, 2014, 93, 1057-1065.	2.5	27
68	Assessing the essentiality of the decaprenylâ€phosphoâ€ <scp>d</scp> â€arabinofuranose pathway in <scp><i>M</i></scp> <ii>ycobacterium tuberculosisi> using conditional mutants. Molecular Microbiology, 2014, 92, 194-211.</ii>	2.5	76
69	Assessing essentiality of transketolase in <i>Mycobacterium tuberculosis</i> using an inducible protein degradation system. FEMS Microbiology Letters, 2014, 358, 30-35.	1.8	8
70	The Phosphatidyl- <i>myo</i> -lnositol Mannosyltransferase PimA Is Essential for Mycobacterium tuberculosis Growth <i>In Vitro</i> and <i>In Vivo</i> Journal of Bacteriology, 2014, 196, 3441-3451.	2.2	37
71	Anticytolytic Screen Identifies Inhibitors of Mycobacterial Virulence Protein Secretion. Cell Host and Microbe, 2014, 16, 538-548.	11.0	83
72	High-resolution detection of DNA binding sites of the global transcriptional regulator GlxR in Corynebacterium glutamicum. Microbiology (United Kingdom), 2013, 159, 12-22.	1.8	44

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73	High-resolution transcriptome and genome-wide dynamics of RNA polymerase and NusA in Mycobacterium tuberculosis. Nucleic Acids Research, 2013, 41, 961-977.	14.5	41
74	Streptomycin-Starved Mycobacterium tuberculosis 18b, a Drug Discovery Tool for Latent Tuberculosis. Antimicrobial Agents and Chemotherapy, 2012, 56, 5782-5789.	3.2	88
75	Genome-Wide Definition of the SigF Regulon in Mycobacterium tuberculosis. Journal of Bacteriology, 2012, 194, 2001-2009.	2.2	46
76	Towards a new tuberculosis drug: pyridomycin – nature's isoniazid. EMBO Molecular Medicine, 2012, 4, 1032-1042.	6.9	175
77	Virulence Regulator EspR of Mycobacterium tuberculosis Is a Nucleoid-Associated Protein. PLoS Pathogens, 2012, 8, e1002621.	4.7	115
78	Tuberculosis drugs: new candidates and how to find more. Future Microbiology, 2011, 6, 617-633.	2.0	36
79	Sigma Factor F Does Not Prevent Rifampin Inhibition of RNA Polymerase or Cause Rifampin Tolerance in <i>Mycobacterium tuberculosis</i>). Journal of Bacteriology, 2010, 192, 5472-5479.	2.2	14
80	Simple Model for Testing Drugs against Nonreplicating <i>Mycobacterium tuberculosis</i> Antimicrobial Agents and Chemotherapy, 2010, 54, 4150-4158.	3.2	117
81	Development of a repressible mycobacterial promoter system based on two transcriptional repressors. Nucleic Acids Research, 2010, 38, e134-e134.	14.5	74
82	Genomeâ€wide regulon and crystal structure of Blal (Rv1846c) from <i>Mycobacterium tuberculosis</i> . Molecular Microbiology, 2009, 71, 1102-1116.	2.5	61
83	Dissecting Regulatory Networks in Host-Pathogen Interaction Using ChIP-on-chip Technology. Cell Host and Microbe, 2009, 5, 430-437.	11.0	14
84	Benzothiazinones Kill <i>Mycobacterium tuberculosis</i> by Blocking Arabinan Synthesis. Science, 2009, 324, 801-804.	12.6	660
85	The katG mRNA of Mycobacterium tuberculosis and Mycobacterium smegmatis is processed at its 5' end and is stabilized by both a polypurine sequence and translation initiation. BMC Molecular Biology, 2008, 9, 33.	3.0	22
86	Bacteriophage P4 sut1: a mutation suppressing transcription termination. Journal of General Virology, 2007, 88, 1041-1047.	2.9	0
87	DNA replication in phage P4: Characterization of replicon II. Plasmid, 2006, 56, 216-222.	1.4	2
88	Mycobacterium tuberculosis FurA Autoregulates Its Own Expression. Journal of Bacteriology, 2003, 185, 5357-5362.	2.2	61
89	Transcriptional Regulation of furA and katG upon Oxidative Stress in Mycobacterium smegmatis. Journal of Bacteriology, 2001, 183, 6801-6806.	2.2	67