

# Sonja Lehtinen

## List of Publications by Citations

**Source:** <https://exaly.com/author-pdf/4424462/sonja-lehtinen-publications-by-citations.pdf>

**Version:** 2024-04-28

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

23  
papers

745  
citations

11  
h-index

27  
g-index

29  
ext. papers

1,025  
ext. citations

7.8  
avg, IF

4.5  
L-index

#	Paper	IF	Citations
23	CATH: comprehensive structural and functional annotations for genome sequences. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D376-81	20.1	335
22	Evolution of antibiotic resistance is linked to any genetic mechanism affecting bacterial duration of carriage. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , <b>2017</b> , 114, 1075-1080	11.5	81
21	COVID-19 infectivity profile correction. <i>Swiss Medical Weekly</i> , <b>2020</b> , 150, w20336	3.1	50
20	Gene3D: expanding the utility of domain assignments. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D404-9	20.1	47
19	Quantifying the impact of quarantine duration on COVID-19 transmission. <i>ELife</i> , <b>2021</b> , 10,	8.9	32
18	On the evolutionary ecology of multidrug resistance in bacteria. <i>PLoS Pathogens</i> , <b>2019</b> , 15, e1007763	7.6	30
17	The evolution of antibiotic resistance in a structured host population. <i>Journal of the Royal Society Interface</i> , <b>2018</b> , 15,	4.1	25
16	On the relationship between serial interval, infectiousness profile and generation time. <i>Journal of the Royal Society Interface</i> , <b>2021</b> , 18, 20200756	4.1	24
15	Estimating the effects of non-pharmaceutical interventions on the number of new infections with COVID-19 during the first epidemic wave. <i>PLoS ONE</i> , <b>2021</b> , 16, e0252827	3.7	23
14	Mathematical modelling for antibiotic resistance control policy: do we know enough?. <i>BMC Infectious Diseases</i> , <b>2019</b> , 19, 1011	4	21
13	Stress induces remodelling of yeast interaction and co-expression networks. <i>Molecular BioSystems</i> , <b>2013</b> , 9, 1697-707		18
12	Gene Function Prediction from Functional Association Networks Using Kernel Partial Least Squares Regression. <i>PLoS ONE</i> , <b>2015</b> , 10, e0134668	3.7	11
11	Horizontal gene transfer rate is not the primary determinant of observed antibiotic resistance frequencies in. <i>Science Advances</i> , <b>2020</b> , 6, eaaz6137	14.3	10
10	Factors favouring the evolution of multidrug resistance in bacteria. <i>Journal of the Royal Society Interface</i> , <b>2020</b> , 17, 20200105	4.1	10
9	Quantifying the impact of quarantine duration on COVID-19 transmission		8
8	Evolutionary mechanisms that determine which bacterial genes are carried on plasmids. <i>Evolution Letters</i> , <b>2021</b> , 5, 290-301	5.3	6
7	Estimating the effects of non-pharmaceutical interventions on the number of new infections with COVID-19 during the first epidemic wave		4

6	On the relationship between serial interval, infectiousness profile and generation time		3
5	Plasmid co-infection: linking biological mechanisms to ecological and evolutionary dynamics. <i>Philosophical Transactions of the Royal Society B: Biological Sciences</i> , <b>2022</b> , 377, 20200478	5.8	2
4	Quantifying the impact of test-trace-isolate-quarantine (TTIQ) strategies on COVID-19 transmission		2
3	Evolutionary mechanisms that determine which bacterial genes are carried on plasmids		2
2	Test-trace-isolate-quarantine (TTIQ) intervention strategies after symptomatic COVID-19 case identification.. <i>PLoS ONE</i> , <b>2022</b> , 17, e0263597	3.7	1
1	Co-colonisation and coexistence. <i>Nature Ecology and Evolution</i> , <b>2019</b> , 3, 334-335	12.3	