## Sonja Lehtinen

## List of Publications by Year in Descending Order

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

23	745	11	<b>27</b>
papers	citations	h-index	g-index
29	1,025	7.8	4.5
ext. papers	ext. citations	avg, IF	L-index

#	Paper	IF	Citations
23	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
22	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
21	Evolutionary mechanisms that determine which bacterial genes are carried on plasmids. <i>Evolution Letters</i> , <b>2021</b> , 5, 290-301	5.3	6
20	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
19	Quantifying the impact of quarantine duration on COVID-19 transmission. <i>ELife</i> , <b>2021</b> , 10,	8.9	32
18	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
17	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
16	COVID-19 infectivity profile correction. Swiss Medical Weekly, <b>2020</b> , 150, w20336	3.1	50
15	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
14	On the evolutionary ecology of multidrug resistance in bacteria. <i>PLoS Pathogens</i> , <b>2019</b> , 15, e1007763	7.6	30
13	Co-colonisation and coexistence. <i>Nature Ecology and Evolution</i> , <b>2019</b> , 3, 334-335	12.3	
12	Mathematical modelling for antibiotic resistance control policy: do we know enough?. <i>BMC Infectious Diseases</i> , <b>2019</b> , 19, 1011	4	21
11	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
10	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, 10	75-168	081
9	Gene3D: expanding the utility of domain assignments. <i>Nucleic Acids Research</i> , <b>2016</b> , 44, D404-9	20.1	47
8	CATH: comprehensive structural and functional annotations for genome sequences. <i>Nucleic Acids Research</i> , <b>2015</b> , 43, D376-81	20.1	335
7	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

## LIST OF PUBLICATIONS

6	Stress induces remodelling of yeast interaction and co-expression networks. <i>Molecular BioSystems</i> , <b>2013</b> , 9, 1697-707	18
5	Quantifying the impact of test-trace-isolate-quarantine (TTIQ) strategies on COVID-19 transmission	2
4	Evolutionary mechanisms that determine which bacterial genes are carried on plasmids	2
3	On the relationship between serial interval, infectiousness profile and generation time	3
2	Quantifying the impact of quarantine duration on COVID-19 transmission	8
1	Estimating the effects of non-pharmaceutical interventions on the number of new infections with COVID-19 during the first epidemic wave	4