

# Szymon Wasik

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3713855/publications.pdf>

Version: 2024-02-01

17  
papers

363  
citations

1039406

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h-index

1058022

14  
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17  
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17  
docs citations

17  
times ranked

397  
citing authors

#	ARTICLE	IF	CITATIONS
1	Chessboard and Chess Piece Recognition With the Support of Neural Networks. Foundations of Computing and Decision Sciences, 2020, 45, 257-280.	0.5	11
2	Searching for the Origins of Life – Detecting RNA Life Signatures Using Learning Vector Quantization. Advances in Intelligent Systems and Computing, 2020, , 324-333.	0.5	0
3	A Survey on Online Judge Systems and Their Applications. ACM Computing Surveys, 2019, 51, 1-34.	16.1	99
4	Detecting life signatures with RNA sequence similarity measures. Journal of Theoretical Biology, 2019, 463, 110-120.	0.8	5
5	VirDB: Crowdsourced Database for Evaluation of Dynamical Viral Infection Models. Current Bioinformatics, 2019, 14, 740-748.	0.7	0
6	Submit a Topic Page to PLOS Computational Biology and Wikipedia. PLoS Computational Biology, 2018, 14, e1006137.	1.5	7
7	Modeling Biological Systems Using Crowdsourcing. Foundations of Computing and Decision Sciences, 2018, 43, 219-243.	0.5	2
8	Understanding Life: A Bioinformatics Perspective. European Review, 2017, 25, 231-245.	0.4	7
9	Simulating the origins of life: The dual role of RNA replicases as an obstacle to evolution. PLoS ONE, 2017, 12, e0180827.	1.1	9
10	Computer Representations of Bioinformatics Models. Current Bioinformatics, 2016, 11, 551-560.	0.7	11
11	Hypercycle. PLoS Computational Biology, 2016, 12, e1004853.	1.5	29
12	Optil.io: Cloud Based Platform For Solving Optimization Problems Using Crowdsourcing Approach. , 2016, , .		7
13	Inferring Mathematical Equations Using Crowdsourcing. PLoS ONE, 2015, 10, e0145557.	1.1	9
14	Multi-agent model of hepatitis C virus infection. Artificial Intelligence in Medicine, 2014, 60, 123-131.	3.8	17
15	ModeLang: A New Approach for Experts-Friendly Viral Infections Modeling. Computational and Mathematical Methods in Medicine, 2013, 2013, 1-8.	0.7	11
16	RNA FRABASE 2.0: an advanced web-accessible database with the capacity to search the three-dimensional fragments within RNA structures. BMC Bioinformatics, 2010, 11, 231.	1.2	130
17	Towards Prediction of HCV Therapy Efficiency. Computational and Mathematical Methods in Medicine, 2010, 11, 185-199.	0.7	9