Steven Kelk

List of Publications by Year
in descending order

46 papers	707 citations	687363 13 h-index	580821 25 g-index
47 all docs	47 docs citations	47 times ranked	482 citing authors

#	Article	IF	Citations
1	Networks: expanding evolutionary thinking. Trends in Genetics, 2013, 29, 439-441.	6.7	176
2	Constructing Level-2 Phylogenetic Networks from Triplets. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2009, 6, 667-681.	3.0	51
3	Phylogenetic networks do not need to be complex: using fewer reticulations to represent conflicting clusters. Bioinformatics, 2010, 26, i124-i131.	4.1	47
4	The Complexity of the Single Individual SNP Haplotyping Problem. Algorithmica, 2007, 49, 13-36.	1.3	45
5	Constructing the Simplest Possible Phylogenetic Network from Triplets. Algorithmica, 2011, 60, 207-235.	1.3	35
6	UNIQUENESS, INTRACTABILITY AND EXACT ALGORITHMS: REFLECTIONS ON LEVEL-K PHYLOGENETIC NETWORKS. Journal of Bioinformatics and Computational Biology, 2009, 07, 597-623.	0.8	27
7	Worst-case optimal approximation algorithms for maximizing triplet consistency within phylogenetic networks. Journal of Discrete Algorithms, 2010, 8, 65-75.	0.7	22
8	On the Maximum Parsimony Distance Between Phylogenetic Trees. Annals of Combinatorics, 2016, 20, 87-113.	0.6	21
9	When two trees go to war. Journal of Theoretical Biology, 2011, 269, 245-255.	1.7	18
10	Cycle Killer...Qu'est-ce que c'est? On the Comparative Approximability of Hybridization Number and Directed Feedback Vertex Set. SIAM Journal on Discrete Mathematics, 2012, 26, 1635-1656.	0.8	18
11	On Computing the Maximum Parsimony Score of a Phylogenetic Network. SIAM Journal on Discrete Mathematics, 2015, 29, 559-585.	0.8	17
12	Constructing Minimal Phylogenetic Networks from Softwired Clusters is Fixed Parameter Tractable. Algorithmica, 2014, 68, 886-915.	1.3	16
13	Prefix Reversals on Binary and Ternary Strings. SIAM Journal on Discrete Mathematics, 2007, 21, 592-611.	0.8	15
14	On Unrooted and Root-Uncertain Variants of Several Well-Known Phylogenetic Network Problems. Algorithmica, 2018, 80, 2993-3022.	1.3	14
15	The Complexity of Choosing an H-Coloring (Nearly) Uniformly at Random. SIAM Journal on Computing, 2004, 33, 416-432.	1.0	13
16	Approximation Algorithms for Nonbinary Agreement Forests. SIAM Journal on Discrete Mathematics, 2014, 28, 49-66.	0.8	12
17	Hybridization Number on Three Rooted Binary Trees is EPT. SIAM Journal on Discrete Mathematics, 2016, 30, 1607-1631.	0.8	11
18	Kernelizations for the hybridization number problem on multiple nonbinary trees. Journal of Computer and System Sciences, 2016, 82, 1075-1089.	1.2	11

#	Article	IF	Citations
19	On the Complexity of Computing MP Distance Between Binary Phylogenetic Trees. Annals of Combinatorics, 2017, 21, 573-604.	0.6	11
20	On the Elusiveness of Clusters. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 517-534.	3.0	10
21	Phylogenetic incongruence through the lens of Monadic Second Order logic. Journal of Graph Algorithms and Applications, 2016, 20, 189-215.	0.4	10
22	Shorelines of Islands of Tractability: Algorithms for Parsimony and Minimum Perfect Phylogeny Haplotyping Problems. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2008, 5, 301-312.	3.0	9
23	A practical approximation algorithm for solving massive instances of hybridization number for binary and nonbinary trees. BMC Bioinformatics, 2014, 15, 127.	2.6	9
24	Reduction rules for the maximum parsimony distance on phylogenetic trees. Theoretical Computer Science, 2016, 646, 1-15.	0.9	8
25	Do Branch Lengths Help to Locate a Tree in a Phylogenetic Network?. Bulletin of Mathematical Biology, 2016, 78, 1773-1795.	1.9	8
26	On the challenge of reconstructing level-1 phylogenetic networks from triplets and clusters. Journal of Mathematical Biology, 2017, 74, 1729-1751.	1.9	8
27	A Tight Kernel for Computing the Tree Bisection and Reconnection Distance between Two Phylogenetic Trees. SIAM Journal on Discrete Mathematics, 2019, 33, 1556-1574.	0.8	7
28	The agreement problem for unrooted phylogenetic trees is FPT. Journal of Graph Algorithms and Applications, 2014, 18, 385-392.	0.4	7
29	A note on convex characters, Fibonacci numbers and exponential-time algorithms. Advances in Applied Mathematics, 2017, 84, 34-46.	0.7	6
30	Deciding the existence of a cherry-picking sequence is hard on two trees. Discrete Applied Mathematics, 2019, 260, 131-143.	0.9	5
31	Reflections on kernelizing and computing unrooted agreement forests. Annals of Operations Research, 2022, 309, 425-451.	4.1	5
32	Phylogenetic Networks: Concepts, Algorithms and Applications. Systematic Biology, 2012, 61, 174-175.	5.6	4
33	New Reduction Rules for the Tree Bisection and Reconnection Distance. Annals of Combinatorics, 2020, 24, 475-502.	0.6	4
34	Maximum parsimony distance on phylogenetic trees: A linear kernel and constant factor approximation algorithm. Journal of Computer and System Sciences, 2021, 117, 165-181.	1.2	4
35	On Low Treewidth Graphs and Supertrees. Journal of Graph Algorithms and Applications, 2015, 19, 325-343.	0.4	4
36	Treewidth of display graphs: bounds, brambles and applications. Journal of Graph Algorithms and Applications, 2019, 23, 715-743.	0.4	4

#	Article	IF	Citations
37	Treewidth distance on phylogenetic trees. Theoretical Computer Science, 2018, 731, 99-117.	0.9	3
38	ToTo: An open database for computation, storage and retrieval of tree decompositions. Discrete Applied Mathematics, 2017, 217, 389-393.	0.9	2
39	A Third Strike Against Perfect Phylogeny. Systematic Biology, 2019, 68, 814-827.	5.6	2
40	Applicability of several rooted phylogenetic network algorithms for representing the evolutionary history of SARS-CoV-2. Bmc Ecology and Evolution, 2021, 21, 220.	1.6	2
41	A Resolution of the Static Formulation Question for the Problem of Computing the History Bound. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 404-417.	3.0	1
42	Integrality gaps for colorful matchings. Discrete Optimization, 2019, 32, 73-92.	0.9	1
43	Finding a most parsimonious or likely tree in a network with respect to an alignment. Journal of Mathematical Biology, 2019, 78, 527-547.	1.9	1
44	A Practical Approximation Algorithm for Solving Massive Instances of Hybridization Number. Lecture Notes in Computer Science, 2012, , 430-440.	1.3	1
45	New FPT Algorithms for Finding the Temporal Hybridization Number for Sets of Phylogenetic Trees. Algorithmica, 0, , .	1.3	1
46	A Machine Learning Approach to Algorithm Selection for Exact Computation of Treewidth. Algorithms, 2019, 12, 200.	2.1	0