

# Thomas K F Wong

## 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.

30  
papers

5,873  
citations

9  
h-index

37  
g-index

37  
ext. papers

9,418  
ext. citations

5.2  
avg, IF

6.05  
L-index

#	Paper	IF	Citations
30	An assembly-free method of phylogeny reconstruction using short-read sequences from pooled samples without barcodes. <i>PLoS Computational Biology</i> , <b>2021</b> , 17, e1008949	5	
29	Genetic Variants of and Are Associated With Risk of Non-Small Cell Lung Cancer. <i>Frontiers in Oncology</i> , <b>2021</b> , 11, 709829	5.3	1
28	A minimum reporting standard for multiple sequence alignments. <i>NAR Genomics and Bioinformatics</i> , <b>2020</b> , 2, lqaa024	3.7	24
27	Effective machine-learning assembly for next-generation amplicon sequencing with very low coverage. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 654	3.6	1
26	Complete mitochondrial genome of the green-lipped mussel, (Mollusca: Mytiloidea), from long nanopore sequencing reads. <i>Mitochondrial DNA Part B: Resources</i> , <b>2018</b> , 3, 175-176	0.5	9
25	HaploJuice : accurate haplotype assembly from a pool of sequences with known relative concentrations. <i>BMC Bioinformatics</i> , <b>2018</b> , 19, 389	3.6	1
24	Reassembling haplotypes in a mixture of pooled amplicons when the relative concentrations are known: A proof-of-concept study on the efficient design of next-generation sequencing strategies. <i>PLoS ONE</i> , <b>2018</b> , 13, e0195090	3.7	3
23	Mitochondrial DNA and trade data support multiple origins of <i>Helicoverpa armigera</i> (Lepidoptera, Noctuidae) in Brazil. <i>Scientific Reports</i> , <b>2017</b> , 7, 45302	4.9	45
22	ModelFinder: fast model selection for accurate phylogenetic estimates. <i>Nature Methods</i> , <b>2017</b> , 14, 587-596	39.6	3957
21	Phylogenomics resolves the timing and pattern of insect evolution. <i>Science</i> , <b>2014</b> , 346, 763-7	33.3	1489
20	Mixture models of nucleotide sequence evolution that account for heterogeneity in the substitution process across sites and across lineages. <i>Systematic Biology</i> , <b>2014</b> , 63, 726-42	8.4	47
19	Computational identification of protein binding sites on RNAs using high-throughput RNA structure-probing data. <i>Bioinformatics</i> , <b>2014</b> , 30, 1049-1055	7.2	5
18	SOAP3-dp: fast, accurate and sensitive GPU-based short read aligner. <i>PLoS ONE</i> , <b>2013</b> , 8, e65632	3.7	76
17	A Local Structural Prediction Algorithm for RNA Triple Helix Structure. <i>Lecture Notes in Computer Science</i> , <b>2013</b> , 102-113	0.9	
16	Memory efficient algorithms for structural alignment of RNAs with pseudoknots. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2012</b> , 9, 161-8	3	4
15	SOAP3: ultra-fast GPU-based parallel alignment tool for short reads. <i>Bioinformatics</i> , <b>2012</b> , 28, 878-9	7.2	158
14	An efficient alignment algorithm for searching simple pseudoknots over long genomic sequence. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2012</b> , 9, 1629-38	3	

13	Structural alignment of RNA with triple helix structure. <i>Journal of Computational Biology</i> , <b>2012</b> , 19, 365-78	7.8	5
12	Structural alignment of RNA with complex pseudoknot structure. <i>Journal of Computational Biology</i> , <b>2011</b> , 18, 97-108	1.7	11
11	RNASAlign: RNA structural alignment system. <i>Bioinformatics</i> , <b>2011</b> , 27, 2151-2	7.2	5
10	Structural Alignment of RNAs with Pseudoknots <b>2011</b> , 550-571		
9	Improving the accuracy of signal transduction pathway construction using Level-2 neighbours. <i>International Journal of Bioinformatics Research and Applications</i> , <b>2010</b> , 6, 542-55	0.9	
8	Refining orthologue groups at the transcript level. <i>BMC Genomics</i> , <b>2010</b> , 11 Suppl 4, S11	4.5	4
7	Adjacent nucleotide dependence in ncRNA and order-1 SCFG for ncRNA identification. <i>PLoS ONE</i> , <b>2010</b> , 5, e12848	3.7	1
6	Correcting short reads with high error rates for improved sequencing result. <i>International Journal of Bioinformatics Research and Applications</i> , <b>2009</b> , 5, 224-37	0.9	2
5	Structural Alignment of RNA with Complex Pseudoknot Structure. <i>Lecture Notes in Computer Science</i> , <b>2009</b> , 403-414	0.9	1
4	Promoter-sharing by different genes in human genome--CPNE1 and RBM12 gene pair as an example. <i>BMC Genomics</i> , <b>2008</b> , 9, 456	4.5	18
3	Finding alternative splicing patterns with strong support from expressed sequences on individual exons/introns. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2008</b> , 6, 1021-33	1	3
2	A MEMORY EFFICIENT ALGORITHM FOR STRUCTURAL ALIGNMENT OF RNAs WITH EMBEDDED SIMPLE PSEUDOKNOTS <b>2007</b> ,		2
1	HaploJuice: Accurate haplotype assembly from a pool of sequences with known relative concentrations		1