Thomas K F Wong

List of Publications by Citations

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	ModelFinder: fast model selection for accurate phylogenetic estimates. *Nature Methods*, **2017**, 14, 587-589	36.6	3957
29	Phylogenomics resolves the timing and pattern of insect evolution. *Science*, **2014**, 346, 763-7	33.3	1489
28	SOAP3: ultra-fast GPU-based parallel alignment tool for short reads. *Bioinformatics*, **2012**, 28, 878-9	7.2	158
27	SOAP3-dp: fast, accurate and sensitive GPU-based short read aligner. *PLoS ONE*, **2013**, 8, e65632	3.7	76
26	Mixture models of nucleotide sequence evolution that account for heterogeneity in the substitution process across sites and across lineages. *Systematic Biology*, **2014**, 63, 726-42	8.4	47
25	Mitochondrial DNA and trade data support multiple origins of Helicoverpa armigera (Lepidoptera, Noctuidae) in Brazil. *Scientific Reports*, **2017**, 7, 45302	4.9	45
24	A minimum reporting standard for multiple sequence alignments. *NAR Genomics and Bioinformatics*, **2020**, 2, lqaa024	3.7	24
23	Promoter-sharing by different genes in human genome--CPNE1 and RBM12 gene pair as an example. *BMC Genomics*, **2008**, 9, 456	4.5	18
22	Structural alignment of RNA with complex pseudoknot structure. *Journal of Computational Biology*, **2011**, 18, 97-108	1.7	11
21	Complete mitochondrial genome of the green-lipped mussel, (Mollusca: Mytiloidea), from long nanopore sequencing reads. *Mitochondrial DNA Part B: Resources*, **2018**, 3, 175-176	0.5	9
20	Computational identification of protein binding sites on RNAs using high-throughput RNA structure-probing data. *Bioinformatics*, **2014**, 30, 1049-1055	7.2	5
19	RNASAlign: RNA structural alignment system. *Bioinformatics*, **2011**, 27, 2151-2	7.2	5
18	Structural alignment of RNA with triple helix structure. *Journal of Computational Biology*, **2012**, 19, 365-78	1.7	5
17	Memory efficient algorithms for structural alignment of RNAs with pseudoknots. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2012**, 9, 161-8	3	4
16	Refining orthologue groups at the transcript level. *BMC Genomics*, **2010**, 11 Suppl 4, S11	4.5	4
15	Finding alternative splicing patterns with strong support from expressed sequences on individual exons/introns. *Journal of Bioinformatics and Computational Biology*, **2008**, 6, 1021-33	1	3
14	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. *PLoS ONE*, **2018**, 13, e0195090	3.7	3

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13	Correcting short reads with high error rates for improved sequencing result. *International Journal of Bioinformatics Research and Applications*, **2009**, 5, 224-37	0.9	2
12	A MEMORY EFFICIENT ALGORITHM FOR STRUCTURAL ALIGNMENT OF RNAs WITH EMBEDDED SIMPLE PSEUDOKNOTS **2007**,		2
11	HaploJuice: Accurate haplotype assembly from a pool of sequences with known relative concentrations		1
10	Structural Alignment of RNA with Complex Pseudoknot Structure. *Lecture Notes in Computer Science*, **2009**, 403-414	0.9	1
9	Adjacent nucleotide dependence in ncRNA and order-1 SCFG for ncRNA identification. *PLoS ONE*, **2010**, 5, e12848	3.7	1
8	Effective machine-learning assembly for next-generation amplicon sequencing with very low coverage. *BMC Bioinformatics*, **2019**, 20, 654	3.6	1
7	HaploJuice : accurate haplotype assembly from a pool of sequences with known relative concentrations. *BMC Bioinformatics*, **2018**, 19, 389	3.6	1
6	Genetic Variants of and Are Associated With Risk of Non-Small Cell Lung Cancer. *Frontiers in Oncology*, **2021**, 11, 709829	5.3	1
5	An efficient alignment algorithm for searching simple pseudoknots over long genomic sequence. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2012**, 9, 1629-38	3	
4	Improving the accuracy of signal transduction pathway construction using Level-2 neighbours. *International Journal of Bioinformatics Research and Applications*, **2010**, 6, 542-55	0.9	
3	Structural Alignment of RNAs with Pseudoknots **2011**, 550-571		
2	A Local Structural Prediction Algorithm for RNA Triple Helix Structure. *Lecture Notes in Computer Science*, **2013**, 102-113	0.9	
1	An assembly-free method of phylogeny reconstruction using short-read sequences from pooled samples without barcodes. *PLoS Computational Biology*, **2021**, 17, e1008949	5	