# Hon Wai Leong

List of Publications by Year
in descending order

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|---|---|---|---|
| **53** papers | **993** citations | 567281 **15** h-index | 454955 **30** g-index |
| **54** all docs | **54** docs citations | **54** times ranked | **999** citing authors |

| # | Article | IF | Citations |
|---|---------|----|-----------|
| 1 | A 2-Approximation Scheme for Sorting Signed Permutations by Reversals, Transpositions, Transreversals, and Block-Interchanges. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2019, 16, 1702-1711. | 3.0 | 0 |
| 2 | GI-Cluster: Detecting genomic islands via consensus clustering on multiple features. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840010. | 0.8 | 7 |
| 3 | Genome-scale metabolic network of Cordyceps militaris useful for comparative analysis of entomopathogenic fungi. Gene, 2017, 626, 132-139. | 2.2 | 35 |
| 4 | A program to compute the soft Robinson–Foulds distance between phylogenetic networks. BMC Genomics, 2017, 18, 111. | 2.8 | 11 |
| 5 | An O(n3) algorithm for sorting signed genomes by reversals, transpositions, transreversals and block-interchanges. Journal of Bioinformatics and Computational Biology, 2016, 14, 1640002. | 0.8 | 3 |
| 6 | Computational methods for predicting genomic islands in microbial genomes. Computational and Structural Biotechnology Journal, 2016, 14, 200-206. | 4.1 | 54 |
| 7 | GI-SVM: A sensitive method for predicting genomic islands based on unannotated sequence of a single genome. Journal of Bioinformatics and Computational Biology, 2016, 14, 1640003. | 0.8 | 21 |
| 8 | Reading Digital Video Clocks. International Journal of Pattern Recognition and Artificial Intelligence, 2015, 29, 1555006. | 1.2 | 10 |
| 9 | EnzDP: Improved enzyme annotation for metabolic network reconstruction based on domain composition profiles. Journal of Bioinformatics and Computational Biology, 2015, 13, 1543003. | 0.8 | 11 |
| 10 | Evolution and Controllability of Cancer Networks: A Boolean Perspective. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 83-94. | 3.0 | 34 |
| 11 | Identifying conserved protein complexes between species by constructing interolog networks. BMC Bioinformatics, 2013, 14, S8. | 2.6 | 34 |
| 12 | A SURVEY OF COMPUTATIONAL METHODS FOR PROTEIN COMPLEX PREDICTION FROM PROTEIN INTERACTION NETWORKS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1230002. | 0.8 | 106 |
| 13 | HOMOLOGOUS SYNTENY BLOCK DETECTION BASED ON SUFFIX TREE ALGORITHMS. Journal of Bioinformatics and Computational Biology, 2013, 11, 1343004. | 0.8 | 1 |
| 14 | ON TWO VARIATIONS OF THE REVERSAL MEDIAN PROBLEM. International Journal of Modern Physics Conference Series, 2012, 09, 285-292. | 0.7 | 0 |
| 15 | Employing functional interactions for characterisation and detection of sparse complexes from yeast PPI networks. International Journal of Bioinformatics Research and Applications, 2012, 8, 286. | 0.2 | 29 |
| 16 | 3-D–2-D spatiotemporal registration for sports motion analysis. Machine Vision and Applications, 2012, 23, 1177-1194. | 2.7 | 4 |
| 17 | TUTORIAL ON DE NOVO PEPTIDE SEQUENCING USING MS/MS MASS SPECTROMETRY. Journal of Bioinformatics and Computational Biology, 2012, 10, 1231002. | 0.8 | 8 |
| 18 | Temporal dynamics of protein complexes in PPI Networks: a case study using yeast cell cycle dynamics. BMC Bioinformatics, 2012, 13, S16. | 2.6 | 47 |

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|---|---------|-----|-----------|
| 19 | BBH-LS: an algorithm for computing positional homologs using sequence and gene context similarity. BMC Systems Biology, 2012, 6, S22. | 3.0 | 8 |
| 20 | A Parent Mass Filter Algorithm for Peptide Sequencing from Tandem Mass Spectra. , 2011, , . | | 0 |
| 21 | Identifying positional homologs as bidirectional best hits of sequence and gene context similarity. , 2011, , . | | 0 |
| 22 | Analysis of the relationships among Longest Common Subsequences, Shortest Common Supersequences and patterns and its application on pattern discovery in biological sequences. International Journal of Data Mining and Bioinformatics, 2011, 5, 611. | 0.1 | 3 |
| 23 | The multiple sequence sets: problem and heuristic algorithms. Journal of Combinatorial Optimization, 2011, 22, 778-796. | 1.3 | 4 |
| 24 | Algorithms for Computing Bidirectional Best Hit r-Window Gene Clusters. Lecture Notes in Computer Science, 2011, , 275-286. | 1.3 | 0 |
| 25 | MCL-CAw: a refinement of MCL for detecting yeast complexes from weighted PPI networks by incorporating core-attachment structure. BMC Bioinformatics, 2010, 11, 504. | 2.6 | 63 |
| 26 | Examination of the relationship between essential genes in PPI network and hub proteins in reverse nearest neighbor topology. BMC Bioinformatics, 2010, 11, 505. | 2.6 | 78 |
| 27 | Bidirectional best hit r-window gene clusters. BMC Bioinformatics, 2010, 11, S63. | 2.6 | 16 |
| 28 | Two-phase Filtering Strategy for Efficient Peptide Identification from Mass Spectrometry. Journal of Proteomics and Bioinformatics, 2010, 03, 121-129. | 0.4 | 0 |
| 29 | Gene Team Tree: A Hierarchical Representation of Gene Teams for All Gap Lengths. Journal of Computational Biology, 2009, 16, 1383-1398. | 1.6 | 11 |
| 30 | Interactive broadcast services for live soccer video based on instant semantics acquisition. Journal of Visual Communication and Image Representation, 2009, 20, 117-130. | 2.8 | 10 |
| 31 | Automatic camera calibration of broadcast tennis video with applications to 3D virtual content insertion and ball detection and tracking. Computer Vision and Image Understanding, 2009, 113, 643-652. | 4.7 | 37 |
| 32 | REFINING MARKOV CLUSTERING FOR PROTEIN COMPLEX PREDICTION BY INCORPORATING CORE-ATTACHMENT STRUCTURE. , 2009, , . | | 16 |
| 33 | Refining Markov Clustering for protein complex prediction by incorporating core-attachment structure. Genome Informatics, 2009, 23, 159-68. | 0.4 | 8 |
| 34 | ON PREPROCESSING AND ANTISYMMETRY IN DE NOVO PEPTIDE SEQUENCING: IMPROVING EFFICIENCY AND ACCURACY. Journal of Bioinformatics and Computational Biology, 2008, 06, 467-492. | 0.8 | 9 |
| 35 | USING INDIRECT PROTEINâ€"PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION. Journal of Bioinformatics and Computational Biology, 2008, 06, 435-466. | 0.8 | 123 |
| 36 | 3D-2D spatiotemporal registration for sports motion analysis. , 2008, , . | | 4 |

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|---|---------|-----|-----------|
| 37 | A Merge-Decoupling Dead End Elimination algorithm for protein side-chain conformation. International Journal of Data Mining and Bioinformatics, 2007, 1, 372. | 0.1 | 2 |
| 38 | USING INDIRECT PROTEIN-PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION. , 2007, , . | | 33 |
| 39 | AN ACCURATE AND EFFICIENT ALGORITHM FOR PEPTIDE AND PTM IDENTIFICATION BY TANDEM MASS SPECTROMETRY. , 2007, , . | | 0 |
| 40 | ALGORITHM FOR PEPTIDE SEQUENCING BY TANDEM MASS SPECTROMETRY BASED ON BETTER PREPROCESSING AND ANTI-SYMMETRIC COMPUTATIONAL MODEL. , 2007, , . | | 5 |
| 41 | Using indirect protein-protein interactions for protein complex predication. Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference, 2007, 6, 97-109. | 0.4 | 9 |
| 42 | An accurate and efficient algorithm for Peptide and ptm identification by tandem mass spectrometry. Genome Informatics, 2007, 19, 119-30. | 0.4 | 2 |
| 43 | Finding Patterns in Biological Sequences by Longest Common Subsequencesand Shortest Common Supersequences. , 2006, , . | | 6 |
| 44 | Trajectory-Based Ball Detection and Tracking in Broadcast Soccer Video. IEEE Transactions on Multimedia, 2006, 8, 1164-1178. | 7.2 | 85 |
| 45 | Towards a better solution to the shortest common supersequence problem: the deposition and reduction algorithm. BMC Bioinformatics, 2006, 7, S12. | 2.6 | 19 |
| 46 | Towards a Better Solution to the Shortest Common Supersequence Problem: A Post. , 2006, , . | | 2 |
| 47 | MODELING AND CHARACTERIZATION OF MULTI-CHARGE MASS SPECTRA FOR PEPTIDE SEQUENCING. Journal of Bioinformatics and Computational Biology, 2006, 04, 1329-1352. | 0.8 | 7 |
| 48 | The distribution and deposition algorithm for multiple oligo nucleotide arrays. Genome Informatics, 2006, 17, 89-99. | 0.4 | 1 |
| 49 | PepSOM: an algorithm for peptide identification by tandem mass spectrometry based on SOM. Genome Informatics, 2006, 17, 194-205. | 0.4 | 2 |
| 50 | IMPROVED ALGORITHMS FOR LOW POWER MULTIPLEXOR DECOMPOSITION. Journal of Circuits, Systems and Computers, 2005, 14, 1085-1099. | 1.5 | 0 |
| 51 | A post-processing method for optimizing synthesis strategy for oligonucleotide microarrays. Nucleic Acids Research, 2005, 33, e144-e144. | 14.5 | 10 |
| 52 | Efficient algorithm for path-based range query in spatial databases. , 0, , . | | 0 |
| 53 | Least-cost path in public transportation systems with fare rebates that are path- and time-dependent. , 0, , . | | 1 |