

Hon Wai Leong

List of Publications by Year in descending order

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53
papers

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567281

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citing authors

#	ARTICLE	IF	CITATIONS
1	USING INDIRECT PROTEIN-PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 435-466.	0.8	123
2	A SURVEY OF COMPUTATIONAL METHODS FOR PROTEIN COMPLEX PREDICTION FROM PROTEIN INTERACTION NETWORKS. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1230002.	0.8	106
3	Trajectory-Based Ball Detection and Tracking in Broadcast Soccer Video. <i>IEEE Transactions on Multimedia</i> , 2006, 8, 1164-1178.	7.2	85
4	Examination of the relationship between essential genes in PPI network and hub proteins in reverse nearest neighbor topology. <i>BMC Bioinformatics</i> , 2010, 11, 505.	2.6	78
5	MCL-CAw: a refinement of MCL for detecting yeast complexes from weighted PPI networks by incorporating core-attachment structure. <i>BMC Bioinformatics</i> , 2010, 11, 504.	2.6	63
6	Computational methods for predicting genomic islands in microbial genomes. <i>Computational and Structural Biotechnology Journal</i> , 2016, 14, 200-206.	4.1	54
7	Temporal dynamics of protein complexes in PPI Networks: a case study using yeast cell cycle dynamics. <i>BMC Bioinformatics</i> , 2012, 13, S16.	2.6	47
8	Automatic camera calibration of broadcast tennis video with applications to 3D virtual content insertion and ball detection and tracking. <i>Computer Vision and Image Understanding</i> , 2009, 113, 643-652.	4.7	37
9	Genome-scale metabolic network of <i>Cordyceps militaris</i> useful for comparative analysis of entomopathogenic fungi. <i>Gene</i> , 2017, 626, 132-139.	2.2	35
10	Identifying conserved protein complexes between species by constructing interolog networks. <i>BMC Bioinformatics</i> , 2013, 14, S8.	2.6	34
11	Evolution and Controllability of Cancer Networks: A Boolean Perspective. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014, 11, 83-94.	3.0	34
12	USING INDIRECT PROTEIN-PROTEIN INTERACTIONS FOR PROTEIN COMPLEX PREDICTION. , 2007, , .		33
13	Employing functional interactions for characterisation and detection of sparse complexes from yeast PPI networks. <i>International Journal of Bioinformatics Research and Applications</i> , 2012, 8, 286.	0.2	29
14	GI-SVM: A sensitive method for predicting genomic islands based on unannotated sequence of a single genome. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1640003.	0.8	21
15	Towards a better solution to the shortest common supersequence problem: the deposition and reduction algorithm. <i>BMC Bioinformatics</i> , 2006, 7, S12.	2.6	19
16	Bidirectional best hit r-window gene clusters. <i>BMC Bioinformatics</i> , 2010, 11, S63.	2.6	16
17	REFINING MARKOV CLUSTERING FOR PROTEIN COMPLEX PREDICTION BY INCORPORATING CORE-ATTACHMENT STRUCTURE. , 2009, , .		16
18	Gene Team Tree: A Hierarchical Representation of Gene Teams for All Gap Lengths. <i>Journal of Computational Biology</i> , 2009, 16, 1383-1398.	1.6	11

#	ARTICLE	IF	CITATIONS
19	EnzDP: Improved enzyme annotation for metabolic network reconstruction based on domain composition profiles. <i>Journal of Bioinformatics and Computational Biology</i> , 2015, 13, 1543003.	0.8	11
20	A program to compute the soft Robinson-Foulds distance between phylogenetic networks. <i>BMC Genomics</i> , 2017, 18, 111.	2.8	11
21	A post-processing method for optimizing synthesis strategy for oligonucleotide microarrays. <i>Nucleic Acids Research</i> , 2005, 33, e144-e144.	14.5	10
22	Interactive broadcast services for live soccer video based on instant semantics acquisition. <i>Journal of Visual Communication and Image Representation</i> , 2009, 20, 117-130.	2.8	10
23	Reading Digital Video Clocks. <i>International Journal of Pattern Recognition and Artificial Intelligence</i> , 2015, 29, 1555006.	1.2	10
24	ON PREPROCESSING AND ANTISYMMETRY IN DE NOVO PEPTIDE SEQUENCING: IMPROVING EFFICIENCY AND ACCURACY. <i>Journal of Bioinformatics and Computational Biology</i> , 2008, 06, 467-492.	0.8	9
25	Using indirect protein-protein interactions for protein complex predication. <i>Computational Systems Bioinformatics / Life Sciences Society Computational Systems Bioinformatics Conference</i> , 2007, 6, 97-109.	0.4	9
26	TUTORIAL ON DE NOVO PEPTIDE SEQUENCING USING MS/MS MASS SPECTROMETRY. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1231002.	0.8	8
27	BBH-LS: an algorithm for computing positional homologs using sequence and gene context similarity. <i>BMC Systems Biology</i> , 2012, 6, S22.	3.0	8
28	Refining Markov Clustering for protein complex prediction by incorporating core-attachment structure. <i>Genome Informatics</i> , 2009, 23, 159-68.	0.4	8
29	MODELING AND CHARACTERIZATION OF MULTI-CHARGE MASS SPECTRA FOR PEPTIDE SEQUENCING. <i>Journal of Bioinformatics and Computational Biology</i> , 2006, 04, 1329-1352.	0.8	7
30	GI-Cluster: Detecting genomic islands via consensus clustering on multiple features. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840010.	0.8	7
31	Finding Patterns in Biological Sequences by Longest Common Subsequences and Shortest Common Supersequences. , 2006, , .		6
32	ALGORITHM FOR PEPTIDE SEQUENCING BY TANDEM MASS SPECTROMETRY BASED ON BETTER PREPROCESSING AND ANTI-SYMMETRIC COMPUTATIONAL MODEL. , 2007, , .		5
33	3D-2D spatiotemporal registration for sports motion analysis. , 2008, , .		4
34	The multiple sequence sets: problem and heuristic algorithms. <i>Journal of Combinatorial Optimization</i> , 2011, 22, 778-796.	1.3	4
35	3-D ⁺ 2-D spatiotemporal registration for sports motion analysis. <i>Machine Vision and Applications</i> , 2012, 23, 1177-1194.	2.7	4
36	Analysis of the relationships among Longest Common Subsequences, Shortest Common Supersequences and patterns and its application on pattern discovery in biological sequences. <i>International Journal of Data Mining and Bioinformatics</i> , 2011, 5, 611.	0.1	3

#	ARTICLE	IF	CITATIONS
37	An $O(n^3)$ algorithm for sorting signed genomes by reversals, transpositions, transreversals and block-interchanges. <i>Journal of Bioinformatics and Computational Biology</i> , 2016, 14, 1640002.	0.8	3
38	Towards a Better Solution to the Shortest Common Supersequence Problem: A Post. , 2006, , .		2
39	A Merge-Decoupling Dead End Elimination algorithm for protein side-chain conformation. <i>International Journal of Data Mining and Bioinformatics</i> , 2007, 1, 372.	0.1	2
40	PepSOM: an algorithm for peptide identification by tandem mass spectrometry based on SOM. <i>Genome Informatics</i> , 2006, 17, 194-205.	0.4	2
41	An accurate and efficient algorithm for Peptide and ptm identification by tandem mass spectrometry. <i>Genome Informatics</i> , 2007, 19, 119-30.	0.4	2
42	Least-cost path in public transportation systems with fare rebates that are path- and time-dependent. , 0, , .		1
43	HOMOLOGOUS SYNTENY BLOCK DETECTION BASED ON SUFFIX TREE ALGORITHMS. <i>Journal of Bioinformatics and Computational Biology</i> , 2013, 11, 1343004.	0.8	1
44	The distribution and deposition algorithm for multiple oligo nucleotide arrays. <i>Genome Informatics</i> , 2006, 17, 89-99.	0.4	1
45	Efficient algorithm for path-based range query in spatial databases. , 0, , .		0
46	IMPROVED ALGORITHMS FOR LOW POWER MULTIPLEXOR DECOMPOSITION. <i>Journal of Circuits, Systems and Computers</i> , 2005, 14, 1085-1099.	1.5	0
47	AN ACCURATE AND EFFICIENT ALGORITHM FOR PEPTIDE AND PTM IDENTIFICATION BY TANDEM MASS SPECTROMETRY. , 2007, , .		0
48	A Parent Mass Filter Algorithm for Peptide Sequencing from Tandem Mass Spectra. , 2011, , .		0
49	Identifying positional homologs as bidirectional best hits of sequence and gene context similarity. , 2011, , .		0
50	ON TWO VARIATIONS OF THE REVERSAL MEDIAN PROBLEM. <i>International Journal of Modern Physics Conference Series</i> , 2012, 09, 285-292.	0.7	0
51	A 2-Approximation Scheme for Sorting Signed Permutations by Reversals, Transpositions, Transreversals, and Block-Interchanges. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2019, 16, 1702-1711.	3.0	0
52	Two-phase Filtering Strategy for Efficient Peptide Identification from Mass Spectrometry. <i>Journal of Proteomics and Bioinformatics</i> , 2010, 03, 121-129.	0.4	0
53	Algorithms for Computing Bidirectional Best Hit r-Window Gene Clusters. <i>Lecture Notes in Computer Science</i> , 2011, , 275-286.	1.3	0