

Chee Keong Kwoh

List of Publications by Year in descending order

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134
papers

5,058
citations

117625

34
h-index

106344

65
g-index

141
all docs

141
docs citations

141
times ranked

5611
citing authors

#	ARTICLE	IF	CITATIONS
1	A core-attachment based method to detect protein complexes in PPI networks. BMC Bioinformatics, 2009, 10, 169.	2.6	319
2	The effect of genotype and in utero environment on interindividual variation in neonate DNA methylomes. Genome Research, 2014, 24, 1064-1074.	5.5	317
3	Computational approaches for detecting protein complexes from protein interaction networks: a survey. BMC Genomics, 2010, 11, S3.	2.8	284
4	Ultra-Scalable Spectral Clustering and Ensemble Clustering. IEEE Transactions on Knowledge and Data Engineering, 2020, 32, 1212-1226.	5.7	248
5	An Attention-Based Deep Learning Approach for Sleep Stage Classification With Single-Channel EEG. IEEE Transactions on Neural Systems and Rehabilitation Engineering, 2021, 29, 809-818.	4.9	225
6	Fast, accurate, and reliable molecular docking with QuickVina 2. Bioinformatics, 2015, 31, 2214-2216.	4.1	189
7	Protein-Ligand Blind Docking Using QuickVina-W With Inter-Process Spatio-Temporal Integration. Scientific Reports, 2017, 7, 15451.	3.3	182
8	Computational prediction of drug-target interactions using chemogenomic approaches: an empirical survey. Briefings in Bioinformatics, 2019, 20, 1337-1357.	6.5	182
9	Enhanced Ensemble Clustering via Fast Propagation of Cluster-Wise Similarities. IEEE Transactions on Systems, Man, and Cybernetics: Systems, 2021, 51, 508-520.	9.3	120
10	CovalentDock: Automated covalent docking with parameterized covalent linkage energy estimation and molecular geometry constraints. Journal of Computational Chemistry, 2013, 34, 326-336.	3.3	117
11	MULTiPly: a novel multi-layer predictor for discovering general and specific types of promoters. Bioinformatics, 2019, 35, 2957-2965.	4.1	109
12	Time-Series Representation Learning via Temporal and Contextual Contrasting. , 2021, , .		102
13	Drug-target interaction prediction via class imbalance-aware ensemble learning. BMC Bioinformatics, 2016, 17, 509.	2.6	88
14	Drug-target interaction prediction using ensemble learning and dimensionality reduction. Methods, 2017, 129, 81-88.	3.8	88
15	Review of tandem repeat search tools: a systematic approach to evaluating algorithmic performance. Briefings in Bioinformatics, 2013, 14, 67-81.	6.5	85
16	Inferring Gene-Phenotype Associations via Global Protein Complex Network Propagation. PLoS ONE, 2011, 6, e21502.	2.5	83
17	Predicting human microbe-drug associations via graph convolutional network with conditional random field. Bioinformatics, 2020, 36, 4918-4927.	4.1	82
18	Feasibility Structure Modeling: An Effective Chaperone for Constrained Memetic Algorithms. IEEE Transactions on Evolutionary Computation, 2010, 14, 740-758.	10.0	79

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19	Quantitative model of R-loop forming structures reveals a novel level of RNA-DNA interactome complexity. <i>Nucleic Acids Research</i> , 2012, 40, e16-e16.	14.5	78
20	Ensemble Positive Unlabeled Learning for Disease Gene Identification. <i>PLoS ONE</i> , 2014, 9, e97079.	2.5	78
21	The safety issues of medical robotics. <i>Reliability Engineering and System Safety</i> , 2001, 73, 183-192.	8.9	67
22	Contrastive Adversarial Domain Adaptation for Machine Remaining Useful Life Prediction. <i>IEEE Transactions on Industrial Informatics</i> , 2021, 17, 5239-5249.	11.3	65
23	Graph representation learning in bioinformatics: trends, methods and applications. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	64
24	Binding Affinity Prediction for Protein-Ligand Complexes Based on \hat{I}^2 Contacts and B Factor. <i>Journal of Chemical Information and Modeling</i> , 2013, 53, 3076-3085.	5.4	53
25	Gene, Environment and Methylation (GEM): a tool suite to efficiently navigate large scale epigenome wide association studies and integrate genotype and interaction between genotype and environment. <i>BMC Bioinformatics</i> , 2016, 17, 299.	2.6	53
26	QuickVina: Accelerating AutoDock Vina Using Gradient-Based Heuristics for Global Optimization. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2012, 9, 1266-1272.	3.0	49
27	A random forest based computational model for predicting novel lncRNA-disease associations. <i>BMC Bioinformatics</i> , 2020, 21, 126.	2.6	49
28	Comparison of Methyl-capture Sequencing vs. Infinium 450K methylation array for methylome analysis in clinical samples. <i>Epigenetics</i> , 2016, 11, 36-48.	2.7	47
29	Simulations of mutant p53 DNA binding domains reveal a novel druggable pocket. <i>Nucleic Acids Research</i> , 2019, 47, 1637-1652.	14.5	43
30	Tempel: time-series mutation prediction of influenza A viruses via attention-based recurrent neural networks. <i>Bioinformatics</i> , 2020, 36, 2697-2704.	4.1	43
31	Prediction of supertype-specific HLA class I binding peptides using support vector machines. <i>Journal of Immunological Methods</i> , 2007, 320, 143-154.	1.4	41
32	Predicting antigenic variants of H1N1 influenza virus based on epidemics and pandemics using a stacking model. <i>PLoS ONE</i> , 2018, 13, e0207777.	2.5	40
33	Cross-Examination for Angle-Closure Glaucoma Feature Detection. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2016, 20, 343-354.	6.3	39
34	Ensemble Prediction of Synergistic Drug Combinations Incorporating Biological, Chemical, Pharmacological, and Network Knowledge. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2019, 23, 1336-1345.	6.3	39
35	Learning ECOC Code Matrix for Multiclass Classification with Application to Glaucoma Diagnosis. <i>Journal of Medical Systems</i> , 2016, 40, 78.	3.6	37
36	Discovery of Protein Complexes with Core-Attachment Structures from Tandem Affinity Purification (TAP) Data. <i>Journal of Computational Biology</i> , 2012, 19, 1027-1042.	1.6	36

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37	DeepCPP: a deep neural network based on nucleotide bias information and minimum distribution similarity feature selection for RNA coding potential prediction. <i>Briefings in Bioinformatics</i> , 2021, 22, 2073-2084.	6.5	36
38	Automated anterior segment OCT image analysis for Angle Closure Glaucoma mechanisms classification. <i>Computer Methods and Programs in Biomedicine</i> , 2016, 130, 65-75.	4.7	35
39	Adversarial Multiple-Target Domain Adaptation for Fault Classification. <i>IEEE Transactions on Instrumentation and Measurement</i> , 2021, 70, 1-11.	4.7	35
40	Attention-based sequence to sequence model for machine remaining useful life prediction. <i>Neurocomputing</i> , 2021, 466, 58-68.	5.9	35
41	Conditional Contrastive Domain Generalization for Fault Diagnosis. <i>IEEE Transactions on Instrumentation and Measurement</i> , 2022, 71, 1-12.	4.7	35
42	Outlining the prostate boundary using the harmonics method. <i>Medical and Biological Engineering and Computing</i> , 1998, 36, 768-771.	2.8	34
43	Construction of co-complex score matrix for protein complex prediction from AP-MS data. <i>Bioinformatics</i> , 2011, 27, i159-i166.	4.1	34
44	Modeling the full length HIV-1 Gag polyprotein reveals the role of its p6 subunit in viral maturation and the effect of non-cleavage site mutations in protease drug resistance. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018, 36, 4366-4377.	3.5	34
45	Ensembling graph attention networks for human microbe-drug association prediction. <i>Bioinformatics</i> , 2020, 36, i779-i786.	4.1	34
46	Genetic studies of diseases. <i>Cellular and Molecular Life Sciences</i> , 2007, 64, 1739-1751.	5.4	32
47	An improved random forest-based computational model for predicting novel miRNA-disease associations. <i>BMC Bioinformatics</i> , 2019, 20, 624.	2.6	30
48	A Feature Subset Selection Method Based On High-Dimensional Mutual Information. <i>Entropy</i> , 2011, 13, 860-901.	2.2	29
49	Automatic glaucoma diagnosis through medical imaging informatics. <i>Journal of the American Medical Informatics Association: JAMIA</i> , 2013, 20, 1021-1027.	4.4	29
50	Classifying Vulnerability to Sleep Deprivation Using Baseline Measures of Psychomotor Vigilance. <i>Sleep</i> , 2015, 38, 723-734.	1.1	29
51	Integrating node embeddings and biological annotations for genes to predict disease-gene associations. <i>BMC Systems Biology</i> , 2018, 12, 138.	3.0	29
52	CovalentDock Cloud: a web server for automated covalent docking. <i>Nucleic Acids Research</i> , 2013, 41, W329-W332.	14.5	27
53	SparseHC: A Memory-efficient Online Hierarchical Clustering Algorithm. <i>Procedia Computer Science</i> , 2014, 29, 8-19.	2.0	26
54	Chromatin interaction neural network (ChINN): a machine learning-based method for predicting chromatin interactions from DNA sequences. <i>Genome Biology</i> , 2021, 22, 226.	8.8	26

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55	Pre-training graph neural networks for link prediction in biomedical networks. <i>Bioinformatics</i> , 2022, 38, 2254-2262.	4.1	26
56	Graph contextualized attention network for predicting synthetic lethality in human cancers. <i>Bioinformatics</i> , 2021, 37, 2432-2440.	4.1	25
57	In Silico Prediction of Synthetic Lethality by Meta-Analysis of Genetic Interactions, Functions, and Pathways in Yeast and Human Cancer. <i>Cancer Informatics</i> , 2014, 13s3, CIN.S14026.	1.9	24
58	Predicting vulnerability to sleep deprivation using diffusion model parameters. <i>Journal of Sleep Research</i> , 2014, 23, 576-584.	3.2	24
59	Computational Prediction of Drug-Target Interactions via Ensemble Learning. <i>Methods in Molecular Biology</i> , 2019, 1903, 239-254.	0.9	23
60	Automatic Diagnosis of Pathological Myopia from Heterogeneous Biomedical Data. <i>PLoS ONE</i> , 2013, 8, e65736.	2.5	23
61	Deep learning based DNA:RNA triplex forming potential prediction. <i>BMC Bioinformatics</i> , 2020, 21, 522.	2.6	22
62	Using causality modeling and Fuzzy Lattice Reasoning algorithm for predicting blood glucose. <i>Expert Systems With Applications</i> , 2013, 40, 7354-7366.	7.6	21
63	Experimental study of transurethral robotic laser resection of the prostate using the LaserTrode lightguide. <i>Journal of Biomedical Optics</i> , 2001, 6, 244.	2.6	18
64	Identifying protein complexes from heterogeneous biological data. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 2023-2033.	2.6	18
65	Evaluating Temporal Factors in Combined Interventions of Workforce Shift and School Closure for Mitigating the Spread of Influenza. <i>PLoS ONE</i> , 2012, 7, e32203.	2.5	18
66	Reliable Feature Selection for Automated Angle Closure Glaucoma Mechanism Detection. <i>Journal of Medical Systems</i> , 2015, 39, 21.	3.6	17
67	Heterogeneous information network and its application to human health and disease. <i>Briefings in Bioinformatics</i> , 2020, 21, 1327-1346.	6.5	17
68	Predicting the interaction biomolecule types for lncRNA: an ensemble deep learning approach. <i>Briefings in Bioinformatics</i> , 2020, 22, .	6.5	16
69	Clustering based active learning for biomedical Named Entity Recognition. , 2016, , .		15
70	Time series computational prediction of vaccines for influenza A H3N2 with recurrent neural networks. <i>Journal of Bioinformatics and Computational Biology</i> , 2020, 18, 2040002.	0.8	14
71	Benchmarking Human Protein Complexes to Investigate Drug-Related Systems and Evaluate Predicted Protein Complexes. <i>PLoS ONE</i> , 2013, 8, e53197.	2.5	14
72	Microarray profiling shows distinct differences between primary tumors and commonly used preclinical models in hepatocellular carcinoma. <i>BMC Cancer</i> , 2015, 15, 828.	2.6	13

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73	DL-CRISPR: A Deep Learning Method for Off-Target Activity Prediction in CRISPR/Cas9 With Data Augmentation. <i>IEEE Access</i> , 2020, 8, 76610-76617.	4.2	13
74	Computer-assisted transurethral laser resection of the prostate (CALRP): theoretical and experimental motion plan. <i>IEEE Transactions on Biomedical Engineering</i> , 2001, 48, 1125-1133.	4.2	12
75	Integrating diverse biological and computational sources for reliable protein-protein interactions. <i>BMC Bioinformatics</i> , 2010, 11, S8.	2.6	12
76	Temporal factors in school closure policy for mitigating the spread of influenza. <i>Journal of Public Health Policy</i> , 2011, 32, 180-197.	2.0	12
77	Computational identification of physicochemical signatures for host tropism of influenza A virus. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840023.	0.8	12
78	Spectral Clustering by Subspace Randomization and Graph Fusion for High-Dimensional Data. <i>Lecture Notes in Computer Science</i> , 2020, , 330-342.	1.3	12
79	HopPER: an adaptive model for probability estimation of influenza reassortment through host prediction. <i>BMC Medical Genomics</i> , 2020, 13, 9.	1.5	12
80	Rules of co-occurring mutations characterize the antigenic evolution of human influenza A/H3N2, A/H1N1 and B viruses. <i>BMC Medical Genomics</i> , 2016, 9, 69.	1.5	11
81	Complex wavelet based quality assessment for AS-OCT images with application to Angle Closure Glaucoma diagnosis. <i>Computer Methods and Programs in Biomedicine</i> , 2016, 130, 13-21.	4.7	11
82	Water-Bridge Mediates Recognition of mRNA Cap in eIF4E. <i>Structure</i> , 2017, 25, 188-194.	3.3	10
83	A context-free encoding scheme of protein sequences for predicting antigenicity of diverse influenza A viruses. <i>BMC Genomics</i> , 2018, 19, 936.	2.8	9
84	VirPreNet: a weighted ensemble convolutional neural network for the virulence prediction of influenza A virus using all eight segments. <i>Bioinformatics</i> , 2021, 37, 737-743.	4.1	9
85	Self-Supervised Autoregressive Domain Adaptation for Time Series Data. <i>IEEE Transactions on Neural Networks and Learning Systems</i> , 2024, 35, 1341-1351.	11.3	9
86	Dynamic algorithm for inferring qualitative models of Gene Regulatory Networks. <i>International Journal of Data Mining and Bioinformatics</i> , 2006, 1, 111.	0.1	8
87	Extracting Protein-Protein Interactions from MEDLINE using the Hidden Vector State model. <i>International Journal of Bioinformatics Research and Applications</i> , 2008, 4, 64.	0.2	8
88	Computational analysis of the receptor binding specificity of novel influenza A/H7N9 viruses. <i>BMC Genomics</i> , 2018, 19, 88.	2.8	8
89	Heterogeneous graph attention networks for drug virus association prediction. <i>Methods</i> , 2021, 198, 11-11.	3.8	8
90	Brief Overview of Bioinformatics Activities in Singapore. <i>PLoS Computational Biology</i> , 2009, 5, e1000508.	3.2	7

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91	Feature Selection for Computer-Aided Angle Closure Glaucoma Mechanism Detection. Journal of Medical Imaging and Health Informatics, 2012, 2, 438-444.	0.3	7
92	Active learning for ontological event extraction incorporating named entity recognition and unknown word handling. Journal of Biomedical Semantics, 2016, 7, 22.	1.6	7
93	Packpred: Predicting the Functional Effect of Missense Mutations. Frontiers in Molecular Biosciences, 2021, 8, 646288.	3.5	7
94	Beta Atomic Contacts: Identifying Critical Specific Contacts in Protein Binding Interfaces. PLoS ONE, 2013, 8, e59737.	2.5	6
95	Identification of Potential Critical Virulent Sites Based on Hemagglutinin of Influenza A Virus in Past Pandemic Strains. , 2017, , .		6
96	Rule-based meta-analysis reveals the major role of PB2 in influencing influenza A virus virulence in mice. BMC Genomics, 2019, 20, 973.	2.8	6
97	The pattern classification based on the nearest feature midpoints. , 2004, , .		5
98	High Performance Protein Sequence Database Scanning on the Cell Broadband Engine. Scientific Programming, 2009, 17, 97-111.	0.7	5
99	Meta-analysis of Genomic and Proteomic Features to Predict Synthetic Lethality of Yeast and Human Cancer. , 2013, , .		5
100	Molecular insights into evolution, mutations and receptor-binding specificity of influenza A and B viruses from outpatients and hospitalized patients in Singapore. International Journal of Infectious Diseases, 2020, 90, 84-96.	3.3	5
101	Chromatin loop anchors predict transcript and exon usage. Briefings in Bioinformatics, 2021, 22, .	6.5	5
102	Semi-supervised learning of the hidden vector state model for extracting proteinâ€“protein interactions. Artificial Intelligence in Medicine, 2007, 41, 209-222.	6.5	4
103	Proposing drug fragments for dengue virus NS5 protein. Journal of Bioinformatics and Computational Biology, 2018, 16, 1840017.	0.8	4
104	Characterization of Hydration Properties in Structural Ensembles of Biomolecules. Journal of Chemical Information and Modeling, 2019, 59, 3316-3329.	5.4	4
105	u-Genome: a database on genome design in unicellular genomes. In Silico Biology, 2005, 5, 611-5.	0.9	4
106	Using survival models to analyze the effects of social attributes on length of stay of stroke patients. , 2009, , .		3
107	Comparison of Structure-based Tools for the Prediction of Ligand Binding Site Residues in Apo-structures. Procedia Computer Science, 2012, 11, 115-126.	2.0	3
108	Identify Predictive SNP groups in Genome Wide Association Study: A Sparse Learning Approach. Procedia Computer Science, 2012, 11, 107-114.	2.0	3

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109	Improved Time Complexities for Learning Boolean Networks. <i>Entropy</i> , 2013, 15, 3762-3795.	2.2	3
110	Comprehensive detection of cancer gene expression profiles and gene networks are impacted by the choice of pre-processing algorithm and gene-selection method. <i>International Journal of Data Mining and Bioinformatics</i> , 2013, 7, 416.	0.1	3
111	Facial Scanning With a Digital Camera. <i>Journal of Glaucoma</i> , 2015, 24, 522-526.	1.6	3
112	Efficient agglomerative hierarchical clustering for biological sequence analysis. , 2015, , .		3
113	Informative MicroRNA Expression Patterns for Cancer Classification. <i>Lecture Notes in Computer Science</i> , 2006, , 143-154.	1.3	3
114	Measuring Similarity by Prediction Class between Biomedical Datasets via Fuzzy Unordered Rule Induction. <i>International Journal of Bio-Science and Bio-Technology</i> , 2014, 6, 159-168.	0.2	2
115	LDSplitDB: a database for studies of meiotic recombination hotspots in MHC using human genomic data. <i>BMC Medical Genomics</i> , 2018, 11, 27.	1.5	2
116	An Efficient Multiresolution Clustering for Motif Discovery in Complex Networks. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 284-294.	3.0	2
117	Predicting Drugs for COVID-19/SARS-CoV-2 via Heterogeneous Graph Attention Networks. , 2020, , .		2
118	Class similarity network for coding and long non-coding RNA classification. <i>BMC Bioinformatics</i> , 2021, 22, 609.	2.6	2
119	Outcomes of gene association analysis of cancer microarray data are impacted by pre-processing algorithms. , 2010, , .		1
120	A possible mutation that enables H1N1 influenza a virus to escape antibody recognition. , 2010, , .		1
121	An Encoding Scheme Capturing Generic Priors and Properties of Amino Acids Improves Protein Classification. <i>IEEE Access</i> , 2019, 7, 7348-7356.	4.2	1
122	ncRNA2MetS: a manually curated database for non-coding RNAs associated with metabolic syndrome. <i>PeerJ</i> , 2019, 7, e7909.	2.0	1
123	Exploring the Lethality of Human-Adapted Coronavirus Through Alignment-Free Machine Learning Approaches Using Genomic Sequences. <i>Current Genomics</i> , 2021, 22, 583-595.	1.6	1
124	Functional Prediction of Snake Neurotoxins. , 2006, , .		0
125	Semi-supervised Learning of the Hidden Vector State Model for Protein-Protein Interactions Extraction. , 2007, , .		0
126	Semantic Labeling to Identify Reliable Interactions in the Protein Interaction Network. , 2008, , .		0

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127	Structural analysis of (TCR—)HLA/peptide complexes: An initial study. , 2010, , .		0
128	Bioinformatics approaches in tuberculosis vaccination strategies by whole genome sequence. , 2010, , .		0
129	A ranking-based method to predict protein function in terms of gene ontology. , 2011, , .		0
130	Analyzing Trends of Hospital Length of Stay Using Phase-Type Distributions. , 2011, , .		0
131	Preface: Computational Systems-Biology and Bioinformatics. Procedia Computer Science, 2012, 11, 1-3.	2.0	0
132	Power-Law Modeling of Cancer Cell Fates Driven by Signaling Data to Reveal Drug Effects. PLoS ONE, 2016, 11, e0165049.	2.5	0
133	AI and Big Data Analytics for Health and Bioinformatics. , 2017, , .		0
134	Inference of Sequence Homology by BLAST visualization of Influenza Genome set. , 2018, , .		0