

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	Self-Supervised Autoregressive Domain Adaptation for Time Series Data. IEEE Transactions on Neural Networks and Learning Systems, 2024, 35, 1341-1351.	11.3	9
2	An Efficient Multiresolution Clustering for Motif Discovery in Complex Networks. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 284-294.	3.0	2
3	Graph representation learning in bioinformatics: trends, methods and applications. Briefings in Bioinformatics, 2022, 23, .	6.5	64
4	Conditional Contrastive Domain Generalization for Fault Diagnosis. IEEE Transactions on Instrumentation and Measurement, 2022, 71, 1-12.	4.7	35
5	Pre-training graph neural networks for link prediction in biomedical networks. Bioinformatics, 2022, 38, 2254-2262.	4.1	26
6	DeepCPP: a deep neural network based on nucleotide bias information and minimum distribution similarity feature selection for RNA coding potential prediction. Briefings in Bioinformatics, 2021, 22, 2073-2084.	6.5	36
7	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
8	Contrastive Adversarial Domain Adaptation for Machine Remaining Useful Life Prediction. IEEE Transactions on Industrial Informatics, 2021, 17, 5239-5249.	11.3	65
9	Adversarial Multiple-Target Domain Adaptation for Fault Classification. IEEE Transactions on Instrumentation and Measurement, 2021, 70, 1-11.	4.7	35
10	VirPreNet: a weighted ensemble convolutional neural network for the virulence prediction of influenza A virus using all eight segments. Bioinformatics, 2021, 37, 737-743.	4.1	9
11	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
12	Graph contextualized attention network for predicting synthetic lethality in human cancers. Bioinformatics, 2021, 37, 2432-2440.	4.1	25
13	Chromatin loop anchors predict transcript and exon usage. Briefings in Bioinformatics, 2021, 22, .	6.5	5
14	Heterogeneous graph attention networks for drug virus association prediction. Methods, 2021, 198, 11-11.	3.8	8
15	Chromatin interaction neural network (ChINN): a machine learning-based method for predicting chromatin interactions from DNA sequences. Genome Biology, 2021, 22, 226.	8.8	26
16	Time-Series Representation Learning via Temporal and Contextual Contrasting. , 2021, , .		102
17	Packpred: Predicting the Functional Effect of Missense Mutations. Frontiers in Molecular Biosciences, 2021, 8, 646288.	3.5	7
18	Attention-based sequence to sequence model for machine remaining useful life prediction. Neurocomputing, 2021, 466, 58-68.	5.9	35

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19	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
20	Class similarity network for coding and long non-coding RNA classification. <i>BMC Bioinformatics</i> , 2021, 22, 609.	2.6	2
21	Ultra-Scalable Spectral Clustering and Ensemble Clustering. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2020, 32, 1212-1226.	5.7	248
22	Heterogeneous information network and its application to human health and disease. <i>Briefings in Bioinformatics</i> , 2020, 21, 1327-1346.	6.5	17
23	Molecular insights into evolution, mutations and receptor-binding specificity of influenza A and B viruses from outpatients and hospitalized patients in Singapore. <i>International Journal of Infectious Diseases</i> , 2020, 90, 84-96.	3.3	5
24	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
25	Deep learning based DNA:RNA triplex forming potential prediction. <i>BMC Bioinformatics</i> , 2020, 21, 522.	2.6	22
26	Predicting the interaction biomolecule types for lncRNA: an ensemble deep learning approach. <i>Briefings in Bioinformatics</i> , 2020, 22, .	6.5	16
27	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
28	Predicting human microbe-drug associations via graph convolutional network with conditional random field. <i>Bioinformatics</i> , 2020, 36, 4918-4927.	4.1	82
29	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
30	A random forest based computational model for predicting novel lncRNA-disease associations. <i>BMC Bioinformatics</i> , 2020, 21, 126.	2.6	49
31	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
32	Ensembling graph attention networks for human microbe-drug association prediction. <i>Bioinformatics</i> , 2020, 36, i779-i786.	4.1	34
33	HopPER: an adaptive model for probability estimation of influenza reassortment through host prediction. <i>BMC Medical Genomics</i> , 2020, 13, 9.	1.5	12
34	Predicting Drugs for COVID-19/SARS-CoV-2 via Heterogeneous Graph Attention Networks. , 2020, , .		2
35	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
36	MULTiPLY: a novel multi-layer predictor for discovering general and specific types of promoters. <i>Bioinformatics</i> , 2019, 35, 2957-2965.	4.1	109

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37	Simulations of mutant p53 DNA binding domains reveal a novel druggable pocket. <i>Nucleic Acids Research</i> , 2019, 47, 1637-1652.	14.5	43
38	Characterization of Hydration Properties in Structural Ensembles of Biomolecules. <i>Journal of Chemical Information and Modeling</i> , 2019, 59, 3316-3329.	5.4	4
39	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
40	Rule-based meta-analysis reveals the major role of PB2 in influencing influenza A virus virulence in mice. <i>BMC Genomics</i> , 2019, 20, 973.	2.8	6
41	An improved random forest-based computational model for predicting novel miRNA-disease associations. <i>BMC Bioinformatics</i> , 2019, 20, 624.	2.6	30
42	Computational Prediction of Drug-Target Interactions via Ensemble Learning. <i>Methods in Molecular Biology</i> , 2019, 1903, 239-254.	0.9	23
43	Computational prediction of drug-target interactions using chemogenomic approaches: an empirical survey. <i>Briefings in Bioinformatics</i> , 2019, 20, 1337-1357.	6.5	182
44	ncRNA2MetS: a manually curated database for non-coding RNAs associated with metabolic syndrome. <i>PeerJ</i> , 2019, 7, e7909.	2.0	1
45	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
46	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
47	Inference of Sequence Homology by BLAST visualization of Influenza Genome set. , 2018, , .		0
48	Integrating node embeddings and biological annotations for genes to predict disease-gene associations. <i>BMC Systems Biology</i> , 2018, 12, 138.	3.0	29
49	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
50	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
51	Proposing drug fragments for dengue virus NS5 protein. <i>Journal of Bioinformatics and Computational Biology</i> , 2018, 16, 1840017.	0.8	4
52	Computational analysis of the receptor binding specificity of novel influenza A/H7N9 viruses. <i>BMC Genomics</i> , 2018, 19, 88.	2.8	8
53	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
54	Water-Bridge Mediates Recognition of mRNA Cap in eIF4E. <i>Structure</i> , 2017, 25, 188-194.	3.3	10

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55	Drug-target interaction prediction using ensemble learning and dimensionality reduction. <i>Methods</i> , 2017, 129, 81-88.	3.8	88
56	Protein-Ligand Blind Docking Using QuickVina-W With Inter-Process Spatio-Temporal Integration. <i>Scientific Reports</i> , 2017, 7, 15451.	3.3	182
57	AI and Big Data Analytics for Health and Bioinformatics. , 2017, , .		0
58	Identification of Potential Critical Virulent Sites Based on Hemagglutinin of Influenza a Virus in Past Pandemic Strains. , 2017, , .		6
59	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
60	Power-Law Modeling of Cancer Cell Fates Driven by Signaling Data to Reveal Drug Effects. <i>PLoS ONE</i> , 2016, 11, e0165049.	2.5	0
61	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
62	Clustering based active learning for biomedical Named Entity Recognition. , 2016, , .		15
63	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
64	Drug-target interaction prediction via class imbalance-aware ensemble learning. <i>BMC Bioinformatics</i> , 2016, 17, 509.	2.6	88
65	Active learning for ontological event extraction incorporating named entity recognition and unknown word handling. <i>Journal of Biomedical Semantics</i> , 2016, 7, 22.	1.6	7
66	Cross-Examination for Angle-Closure Glaucoma Feature Detection. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2016, 20, 343-354.	6.3	39
67	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
68	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
69	Learning ECOC Code Matrix for Multiclass Classification with Application to Glaucoma Diagnosis. <i>Journal of Medical Systems</i> , 2016, 40, 78.	3.6	37
70	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
71	Classifying Vulnerability to Sleep Deprivation Using Baseline Measures of Psychomotor Vigilance. <i>Sleep</i> , 2015, 38, 723-734.	1.1	29
72	Facial Scanning With a Digital Camera. <i>Journal of Glaucoma</i> , 2015, 24, 522-526.	1.6	3

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73	Reliable Feature Selection for Automated Angle Closure Glaucoma Mechanism Detection. Journal of Medical Systems, 2015, 39, 21.	3.6	17
74	Efficient agglomerative hierarchical clustering for biological sequence analysis. , 2015, , .		3
75	Fast, accurate, and reliable molecular docking with QuickVina 2. Bioinformatics, 2015, 31, 2214-2216.	4.1	189
76	In Silico Prediction of Synthetic Lethality by Meta-Analysis of Genetic Interactions, Functions, and Pathways in Yeast and Human Cancer. Cancer Informatics, 2014, 13s3, CIN.S14026.	1.9	24
77	Measuring Similarity by Prediction Class between Biomedical Datasets via Fuzzy Unordered Rule Induction. International Journal of Bio-Science and Bio-Technology, 2014, 6, 159-168.	0.2	2
78	The effect of genotype and in utero environment on interindividual variation in neonate DNA methylomes. Genome Research, 2014, 24, 1064-1074.	5.5	317
79	Predicting vulnerability to sleep deprivation using diffusion model parameters. Journal of Sleep Research, 2014, 23, 576-584.	3.2	24
80	SparseHC: A Memory-efficient Online Hierarchical Clustering Algorithm. Procedia Computer Science, 2014, 29, 8-19.	2.0	26
81	Ensemble Positive Unlabeled Learning for Disease Gene Identification. PLoS ONE, 2014, 9, e97079.	2.5	78
82	Binding Affinity Prediction for Protein-Ligand Complexes Based on $\langle i \rangle^2 \langle /i \rangle$ Contacts and B Factor. Journal of Chemical Information and Modeling, 2013, 53, 3076-3085.	5.4	53
83	Using causality modeling and Fuzzy Lattice Reasoning algorithm for predicting blood glucose. Expert Systems With Applications, 2013, 40, 7354-7366.	7.6	21
84	Review of tandem repeat search tools: a systematic approach to evaluating algorithmic performance. Briefings in Bioinformatics, 2013, 14, 67-81.	6.5	85
85	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
86	CovalentDock Cloud: a web server for automated covalent docking. Nucleic Acids Research, 2013, 41, W329-W332.	14.5	27
87	Automatic glaucoma diagnosis through medical imaging informatics. Journal of the American Medical Informatics Association: JAMIA, 2013, 20, 1021-1027.	4.4	29
88	Meta-analysis of Genomic and Proteomic Features to Predict Synthetic Lethality of Yeast and Human Cancer. , 2013, , .		5
89	Improved Time Complexities for Learning Boolean Networks. Entropy, 2013, 15, 3762-3795.	2.2	3
90	Identifying protein complexes from heterogeneous biological data. Proteins: Structure, Function and Bioinformatics, 2013, 81, 2023-2033.	2.6	18

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91	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
92	Beta Atomic Contacts: Identifying Critical Specific Contacts in Protein Binding Interfaces. <i>PLoS ONE</i> , 2013, 8, e59737.	2.5	6
93	Benchmarking Human Protein Complexes to Investigate Drug-Related Systems and Evaluate Predicted Protein Complexes. <i>PLoS ONE</i> , 2013, 8, e53197.	2.5	14
94	Automatic Diagnosis of Pathological Myopia from Heterogeneous Biomedical Data. <i>PLoS ONE</i> , 2013, 8, e65736.	2.5	23
95	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
96	Feature Selection for Computer-Aided Angle Closure Glaucoma Mechanism Detection. <i>Journal of Medical Imaging and Health Informatics</i> , 2012, 2, 438-444.	0.3	7
97	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
98	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
99	Preface: Computational Systems-Biology and Bioinformatics. <i>Procedia Computer Science</i> , 2012, 11, 1-3.	2.0	0
100	Comparison of Structure-based Tools for the Prediction of Ligand Binding Site Residues in Apo-structures. <i>Procedia Computer Science</i> , 2012, 11, 115-126.	2.0	3
101	Identify Predictive SNP groups in Genome Wide Association Study: A Sparse Learning Approach. <i>Procedia Computer Science</i> , 2012, 11, 107-114.	2.0	3
102	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
103	A ranking-based method to predict protein function in terms of gene ontology. , 2011, , .		0
104	Analyzing Trends of Hospital Length of Stay Using Phase-Type Distributions. , 2011, , .		0
105	Inferring Gene-Phenotype Associations via Global Protein Complex Network Propagation. <i>PLoS ONE</i> , 2011, 6, e21502.	2.5	83
106	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
107	Construction of co-complex score matrix for protein complex prediction from AP-MS data. <i>Bioinformatics</i> , 2011, 27, i159-i166.	4.1	34
108	A Feature Subset Selection Method Based On High-Dimensional Mutual Information. <i>Entropy</i> , 2011, 13, 860-901.	2.2	29

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109	Feasibility Structure Modeling: An Effective Chaperone for Constrained Memetic Algorithms. IEEE Transactions on Evolutionary Computation, 2010, 14, 740-758.	10.0	79
110	Integrating diverse biological and computational sources for reliable protein-protein interactions. BMC Bioinformatics, 2010, 11, S8.	2.6	12
111	Computational approaches for detecting protein complexes from protein interaction networks: a survey. BMC Genomics, 2010, 11, S3.	2.8	284
112	Outcomes of gene association analysis of cancer microarray data are impacted by pre-processing algorithms. , 2010, , .		1
113	Structural analysis of (TCR—)HLA/peptide complexes: An initial study. , 2010, , .		0
114	Bioinformatics approaches in tuberculosis vaccination strategies by whole genome sequence. , 2010, , .		0
115	A possible mutation that enables H1N1 influenza a virus to escape antibody recognition. , 2010, , .		1
116	High Performance Protein Sequence Database Scanning on the Cell Broadband Engine. Scientific Programming, 2009, 17, 97-111.	0.7	5
117	Brief Overview of Bioinformatics Activities in Singapore. PLoS Computational Biology, 2009, 5, e1000508.	3.2	7
118	A core-attachment based method to detect protein complexes in PPI networks. BMC Bioinformatics, 2009, 10, 169.	2.6	319
119	Using survival models to analyze the effects of social attributes on length of stay of stroke patients. , 2009, , .		3
120	Semantic Labeling to Identify Reliable Interactions in the Protein Interaction Network. , 2008, , .		0
121	Extracting Protein-Protein Interactions from MEDLINE using the Hidden Vector State model. International Journal of Bioinformatics Research and Applications, 2008, 4, 64.	0.2	8
122	Semi-supervised Learning of the Hidden Vector State Model for Protein-Protein Interactions Extraction. , 2007, , .		0
123	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
124	Prediction of supertype-specific HLA class I binding peptides using support vector machines. Journal of Immunological Methods, 2007, 320, 143-154.	1.4	41
125	Genetic studies of diseases. Cellular and Molecular Life Sciences, 2007, 64, 1739-1751.	5.4	32
126	Dynamic algorithm for inferring qualitative models of Gene Regulatory Networks. International Journal of Data Mining and Bioinformatics, 2006, 1, 111.	0.1	8

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127	Functional Prediction of Snake Neurotoxins. , 2006, , .		0
128	Informative MicroRNA Expression Patterns for Cancer Classification. Lecture Notes in Computer Science, 2006, , 143-154.	1.3	3
129	u-Genome: a database on genome design in unicellular genomes. In Silico Biology, 2005, 5, 611-5.	0.9	4
130	The pattern classification based on the nearest feature midpoints. , 2004, , .		5
131	The safety issues of medical robotics. Reliability Engineering and System Safety, 2001, 73, 183-192.	8.9	67
132	Computer-assisted transurethral laser resection of the prostate (CALRP): theoretical and experimental motion plan. IEEE Transactions on Biomedical Engineering, 2001, 48, 1125-1133.	4.2	12
133	Experimental study of transurethral robotic laser resection of the prostate using the LaserTrode lightguide. Journal of Biomedical Optics, 2001, 6, 244.	2.6	18
134	Outlining the prostate boundary using the harmonics method. Medical and Biological Engineering and Computing, 1998, 36, 768-771.	2.8	34