

# Xiuquan Du

## List of Publications by Year in descending order

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46  
papers

1,029  
citations

471509

17  
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434195

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g-index

46  
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46  
docs citations

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times ranked

1347  
citing authors

#	ARTICLE	IF	CITATIONS
1	Constraint-Based Unsupervised Domain Adaptation Network for Multi-Modality Cardiac Image Segmentation. <i>IEEE Journal of Biomedical and Health Informatics</i> , 2022, 26, 67-78.	6.3	7
2	DFpin: Deep learning-based protein-binding site prediction with feature-based non-redundancy from RNA level. <i>Computers in Biology and Medicine</i> , 2022, 142, 105216.	7.0	8
3	Two-stage segmentation network with feature aggregation and multi-level attention mechanism for multi-modality heart images. <i>Computerized Medical Imaging and Graphics</i> , 2022, 97, 102054.	5.8	6
4	DeepBtoD: Improved RNA-binding proteins prediction via integrated deep learning. <i>Journal of Bioinformatics and Computational Biology</i> , 2022, 20, 2250006.	0.8	2
5	Using Chou's 5-Step Rule to Predict DNA-Protein Binding with Multi-scale Complementary Feature. <i>Journal of Proteome Research</i> , 2021, 20, 1639-1656.	3.7	3
6	Incomplete data ensemble classification using imputation-revision framework with local spatial neighborhood information. <i>Applied Soft Computing Journal</i> , 2021, 99, 106905.	7.2	8
7	Prediction of DNA binding proteins using local features and long-term dependencies with primary sequences based on deep learning. <i>PeerJ</i> , 2021, 9, e11262.	2.0	17
8	TSU-net: Two-stage multi-scale cascade and multi-field fusion U-net for right ventricular segmentation. <i>Computerized Medical Imaging and Graphics</i> , 2021, 93, 101971.	5.8	9
9	econvRBP: Improved ensemble convolutional neural networks for RNA binding protein prediction directly from sequence. <i>Methods</i> , 2020, 181-182, 15-23.	3.8	5
10	DeepCQ: Deep multi-task conditional quantification network for estimation of left ventricle parameters. <i>Computer Methods and Programs in Biomedicine</i> , 2020, 184, 105288.	4.7	7
11	Generative image inpainting for link prediction. <i>Applied Intelligence</i> , 2020, 50, 4482-4494.	5.3	2
12	An integrated deep learning framework for joint segmentation of blood pool and myocardium. <i>Medical Image Analysis</i> , 2020, 62, 101685.	11.6	14
13	Simultaneous left atrium anatomy and scar segmentations via deep learning in multiview information with attention. <i>Future Generation Computer Systems</i> , 2020, 107, 215-228.	7.5	73
14	Automatic segmentation of left ventricle using parallel end-to-end deep convolutional neural networks framework. <i>Knowledge-Based Systems</i> , 2020, 204, 106210.	7.1	13
15	Segmentation and visualization of left atrium through a unified deep learning framework. <i>International Journal of Computer Assisted Radiology and Surgery</i> , 2020, 15, 589-600.	2.8	7
16	ConvsPPIS: Identifying Protein-protein Interaction Sites by an Ensemble Convolutional Neural Network with Feature Graph. <i>Current Bioinformatics</i> , 2020, 15, 368-378.	1.5	35
17	An integration of deep learning with feature embedding for protein-protein interaction prediction. <i>PeerJ</i> , 2019, 7, e7126.	2.0	62
18	MsDBP: Exploring DNA-Binding Proteins by Integrating Multiscale Sequence Information via Chou's Five-Step Rule. <i>Journal of Proteome Research</i> , 2019, 18, 3119-3132.	3.7	72

#	ARTICLE	IF	CITATIONS
19	Cardiac-DeepLED: Automatic Pixel-Level Deep Segmentation for Cardiac Bi-Ventricle Using Improved End-to-End Encoder-Decoder Network. IEEE Journal of Translational Engineering in Health and Medicine, 2019, 7, 1-10.	3.7	33
20	A Parameter-Free Cleaning Method for SMOTE in Imbalanced Classification. IEEE Access, 2019, 7, 23537-23548.	4.2	45
21	Direct Segmentation-Based Full Quantification for Left Ventricle via Deep Multi-Task Regression Learning Network. IEEE Journal of Biomedical and Health Informatics, 2019, 23, 942-948.	6.3	27
22	An end-to-end joint learning framework of artery-specific coronary calcium scoring in non-contrast cardiac CT. Computing (Vienna/New York), 2019, 101, 667-678.	4.8	9
23	A three-way decision ensemble method for imbalanced data oversampling. International Journal of Approximate Reasoning, 2019, 107, 1-16.	3.3	34
24	A novel machine-learning algorithm to estimate the position and size of myocardial infarction for MRI sequence. Computing (Vienna/New York), 2019, 101, 653-665.	4.8	7
25	Deep Regression Segmentation for Cardiac Bi-Ventricle MR Images. IEEE Access, 2018, 6, 3828-3838.	4.2	39
26	DeepMVF-RBP: Deep Multi-view Fusion Representation Learning for RNA-binding Proteins Prediction. , 2018, , .		7
27	Classifying Incomplete Gene-Expression Data: Ensemble Learning with Non-Pre-Imputation Feature Filtering and Best-First Search Technique. International Journal of Molecular Sciences, 2018, 19, 3398.	4.1	1
28	Direct delineation of myocardial infarction without contrast agents using a joint motion feature learning architecture. Medical Image Analysis, 2018, 50, 82-94.	11.6	96
29	Correlated Regression Feature Learning for Automated Right Ventricle Segmentation. IEEE Journal of Translational Engineering in Health and Medicine, 2018, 6, 1-10.	3.7	19
30	DeepSS: Exploring Splice Site Motif Through Convolutional Neural Network Directly From DNA Sequence. IEEE Access, 2018, 6, 32958-32978.	4.2	25
31	Multiview Two-Task Recursive Attention Model for Left Atrium and Atrial Scars Segmentation. Lecture Notes in Computer Science, 2018, , 455-463.	1.3	23
32	Identification and Analysis of Cancer Diagnosis Using Probabilistic Classification Vector Machines with Feature Selection. Current Bioinformatics, 2018, 13, 625-632.	1.5	22
33	Beat-to-Beat Blood Pressure and Two-dimensional (axial and radial) Motion of the Carotid Artery Wall: Physiological Evaluation of Arterial Stiffness. Scientific Reports, 2017, 7, 42254.	3.3	16
34	DeepPPI: Boosting Prediction of Protein-Protein Interactions with Deep Neural Networks. Journal of Chemical Information and Modeling, 2017, 57, 1499-1510.	5.4	181
35	Prediction of Splice Site using Support Vector Machine with Feature Selection. , 2017, , .		2
36	Analysis and Prediction of Exon Skipping Events from RNA-Seq with Sequence Information Using Rotation Forest. International Journal of Molecular Sciences, 2017, 18, 2691.	4.1	3

#	ARTICLE	IF	CITATIONS
37	Complexity Analysis of Electroencephalogram Dynamics in Patients with Parkinson's Disease. Parkinson's Disease, 2017, 2017, 1-9.	1.1	36
38	Prediction of protein-protein interaction sites by means of ensemble learning and weighted feature descriptor. Journal of Biological Research, 2016, 23, 10.	2.1	7
39	Prediction of Protein-Protein Interaction By Metasample-Based Sparse Representation. Mathematical Problems in Engineering, 2015, 2015, 1-7.	1.1	0
40	A novel feature extraction scheme for prediction of protein-protein interaction sites. Molecular BioSystems, 2015, 11, 475-485.	2.9	3
41	A Novel Feature Extraction Scheme with Ensemble Coding for Protein-Protein Interaction Prediction. International Journal of Molecular Sciences, 2014, 15, 12731-12749.	4.1	26
42	Identification and Analysis of Driver Missense Mutations Using Rotation Forest with Feature Selection. BioMed Research International, 2014, 2014, 1-7.	1.9	1
43	Inferring protein-protein interactions from sequence using sequence order information. , 2010, , .		1
44	Identifying Protein-Protein Interaction Sites Using Covering Algorithm. International Journal of Molecular Sciences, 2009, 10, 2190-2202.	4.1	2
45	Improved Prediction of Protein Binding Sites from Sequences Using Genetic Algorithm. Protein Journal, 2009, 28, 273-280.	1.6	13
46	Prediction of Protein-Protein Interaction Sites Using Granularity Computing of Quotient Space Theory. , 2008, , .		1