Peng Chen

List of Publications by Year
in descending order

147 papers	2,909 citations	196777 29 h-index	242451 47 g-index
152 all docs	152 docs citations	152 times ranked	3367 citing authors

#	Article	IF	Citations
1	An automatic system for pest recognition and forecasting. Pest Management Science, 2022, 78, 711-721.	1.7	5
2	A Real-Time Steel Surface Defect Detection Approach With High Accuracy. IEEE Transactions on Instrumentation and Measurement, 2022, 71, 1-10.	2.4	21
3	Transformer Model for Functional Near-Infrared Spectroscopy Classification. IEEE Journal of Biomedical and Health Informatics, 2022, 26, 2559-2569.	3.9	17
4	A two-step ensemble learning for predicting protein hot spot residues from whole protein sequence. Amino Acids, 2022, 54, 765-776.	1.2	3
5	Adaptive feature fusion pyramid network for multi-classes agricultural pest detection. Computers and Electronics in Agriculture, 2022, 195, 106827.	3.7	30
6	Prediction of electron ionization mass spectra based on graph convolutional networks. International Journal of Mass Spectrometry, 2022, 475, 116817.	0.7	5
7	Visual Feature Learning on Video Object and Human Action Detection: A Systematic Review. Micromachines, 2022, 13, 72.	1.4	7
8	Surface Defects Classification of Hot Rolled Strip Based on Few-shot Learning. ISIJ International, 2022, 62, 1222-1226.	0.6	3
9	A General and Scalable Vision Framework for Functional Near-Infrared Spectroscopy Classification. IEEE Transactions on Neural Systems and Rehabilitation Engineering, 2022, 30, 1982-1991.	2.7	6
10	A Convolutional Neural Network System to Discriminate Drug-Target Interactions. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1315-1324.	1.9	17
11	Potential Pathogenic Genes Prioritization Based on Protein Domain Interaction Network Analysis. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 1026-1034.	1.9	13
12	Imbalance Data Processing Strategy for Protein Interaction Sites Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, 18, 985-994.	1.9	25
13	Paper acceptance prediction at the institutional level based on the combination of individual and network features. Scientometrics, 2021, 126, 1581-1597.	1.6	2
14	Prediction Method of Core Dead Stock Column Temperature Based on PCA and Ridge Regression. ISIJ International, 2021, 61, 2785-2791.	0.6	2
15	Prediction of Drug-target Binding Affinity by An Ensemble Lear ning System with Network Fusion Information. Current Bioinformatics, 2021, 16, 1223-1235.	0.7	2
16	A Cascade Graph Convolutional Network for Predicting Protein–Ligand Binding Affinity. International Journal of Molecular Sciences, 2021, 22, 4023.	1.8	18
17	Surface Defects Classification of Hot Rolled Strip Based on Improved Convolutional Neural Network. ISIJ International, 2021, 61, 1579-1583.	0.6	20
18	Compound identification via deep classification model for electron-ionization mass spectrometry. International Journal of Mass Spectrometry, 2021, 463, 116540.	0.7	6

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19	Recognition and counting of wheat mites in wheat fields by a three-step deep learning method. Neurocomputing, 2021, 437, 21-30.	3.5	15
20	Predicting Drug–Target Interactions Based on the Ensemble Models of Multiple Feature Pairs. International Journal of Molecular Sciences, 2021, 22, 6598.	1.8	1
21	S-RPN: Sampling-balanced region proposal network for small crop pest detection. Computers and Electronics in Agriculture, 2021, 187, 106290.	3.7	49
22	Automatic estimation of road visibility in foggy weather based on image feature statistics. Journal of Electronic Imaging, 2021, 30, .	0.5	0
23	Protein-Protein Interaction Sites Prediction Based on an Under-Sampling Strategy and Random Forest Algorithm. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2021, PP, 1-1.	1.9	4
24	Occurrence prediction of cotton pests and diseases by bidirectional long short-term memory networks with climate and atmosphere circulation. Computers and Electronics in Agriculture, 2020, 176, 105612.	3.7	35
25	Predicting Drug-Target Interactions with Electrotopological State Fingerprints and Amphiphilic Pseudo Amino Acid Composition. International Journal of Molecular Sciences, 2020, 21, 5694.	1.8	9
26	High-Yield Biosynthesis of Glucosylglycerol through Coupling Phosphorolysis and Transglycosylation Reactions. Journal of Agricultural and Food Chemistry, 2020, 68, 15249-15256.	2.4	15
27	Application of LSTM for short term fog forecasting based on meteorological elements. Neurocomputing, 2020, 408, 285-291.	3.5	61
28	Apple Leaf Diseases Recognition Based on An Improved Convolutional Neural Network. Sensors, 2020, 20, 3535.	2.1	73
29	Artificially designed routes for the conversion of starch to value-added mannosyl compounds through coupling in vitro and in vivo metabolic engineering strategies. Metabolic Engineering, 2020, 61, 215-224.	3.6	12
30	A Deep Learning-Based Chemical System for QSAR Prediction. IEEE Journal of Biomedical and Health Informatics, 2020, 24, 3020-3028.	3.9	50
31	Developing Computational Model to Predict Protein-Protein Interaction Sites Based on the XGBoost Algorithm. International Journal of Molecular Sciences, 2020, 21, 2274.	1.8	49
32	Crop leaf disease grade identification based on an improved convolutional neural network. Journal of Electronic Imaging, 2020, 29, 1.	0.5	33
33	A Sequence-segment Neighbor Encoding Schema for Protein Hotspot Residue Prediction. Current Bioinformatics, 2020, 15, 445-454.	0.7	9
34	Discrete Haze Level Dehazing Network. , 2020, , .		7
35	Autokinase Activity of Casein Kinase 1 δ/ε Governs the Period of Mammalian Circadian Rhythms. Journal of Biological Rhythms, 2019, 34, 482-496.	1.4	12
36	Urine Sediment Detection Based on Deep Learning. Lecture Notes in Computer Science, 2019, , 543-552.	1.0	2

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37	Identification of Apple Leaf Diseases Based on Convolutional Neural Network. Lecture Notes in Computer Science, 2019, , 553-564.	1.0	12
38	Deep spatial attention hashing network for image retrieval. Journal of Visual Communication and Image Representation, 2019, 63, 102577.	1.7	9
39	Identification of Apple Tree Trunk Diseases Based on Improved Convolutional Neural Network with Fused Loss Functions. Lecture Notes in Computer Science, 2019, , 274-283.	1.0	2
40	Classification of Plant Leaf Diseases Based on Improved Convolutional Neural Network. Sensors, 2019, 19, 4161.	2.1	82
41	In Silico Prediction of Drug-Induced Liver Injury Based on Ensemble Classifier Method. International Journal of Molecular Sciences, 2019, 20, 4106.	1.8	22
42	The Characterization and Modification of a Novel Bifunctional and Robust Alginate Lyase Derived from Marinimicrobium sp. H1. Marine Drugs, 2019, 17, 545.	2.2	38
43	Multi-enzyme systems and recombinant cells for synthesis of valuable saccharides: Advances and perspectives. Biotechnology Advances, 2019, 37, 107406.	6.0	40
44	Automatic Localization and Count of Agricultural Crop Pests Based on an Improved Deep Learning Pipeline. Scientific Reports, 2019, 9, 7024.	1.6	43
45	Vibration and Noise of High Speed Amorphous Alloy Permanent Magnet Synchronous Motor with Different Slot Width. , 2019, , .		0
46	Occurrence prediction of pests and diseases in cotton on the basis of weather factors by long short term memory network. BMC Bioinformatics, 2019, 20, 688.	1.2	30
47	Predicting drug-target interactions from drug structure and protein sequence using novel convolutional neural networks. BMC Bioinformatics, 2019, 20, 689.	1.2	39
48	Semi-supervised prediction of protein interaction sites from unlabeled sample information. BMC Bioinformatics, 2019, 20, 699.	1.2	7
49	dbHDPLS: A database of human disease-related protein-ligand structures. Computational Biology and Chemistry, 2019, 78, 353-358.	1.1	5
50	Ranking Research Institutions Based on the Combination of Individual and Network Features. Lecture Notes in Computer Science, 2019, , 443-454.	1.0	0
51	An Optimization Regression Model for Predicting Average Temperature of Core Dead Stock Column. Lecture Notes in Computer Science, 2019, , 468-478.	1.0	0
52	Real-Time Pedestrian Detection in Monitoring Scene Based on Head Model. Lecture Notes in Computer Science, 2019, , 558-568.	1.0	2
53	A new soft assignment K-means algorithm. , 2018, , .		1
54	Hot spot prediction in protein-protein interactions by an ensemble system. BMC Systems Biology, 2018, 12, 132.	3.0	24

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55	dbMPIKT: a database of kinetic and thermodynamic mutant protein interactions. BMC Bioinformatics, 2018, 19, 455.	1.2	26
56	Cell Counting in Image Based on Ridge Regression. , 2018, , .		0
57	Unbalance Data Processing Strategy for Protein Interaction Sites Prediction. , 2018, , .		0
58	Insect Detection and Classification Based on an Improved Convolutional Neural Network. Sensors, 2018, 18, 4169.	2.1	127
59	Effects of Interconnected Polymer Nanopores Leading to Different Degrees of Confined Polymerization. Macromolecular Chemistry and Physics, 2018, 219, 1800362.	1.1	2
60	Purification and Characterization of a Novel Alginate Lyase from the Marine Bacterium Bacillus sp. Alg07. Marine Drugs, 2018, 16, 86.	2.2	42
61	Multi-level learning features for automatic classification of field crop pests. Computers and Electronics in Agriculture, 2018, 152, 233-241.	3.7	107
62	Protein-protein interface hot spots prediction based on a hybrid feature selection strategy. BMC Bioinformatics, 2018, 19, 14.	1.2	86
63	A spatial filtering approach to environmental emotion perception based on electroencephalography. Medical Engineering and Physics, 2018, 60, 77-85.	0.8	7
64	Prediction of Crop Pests and Diseases in Cotton by Long Short Term Memory Network. Lecture Notes in Computer Science, 2018, , 11-16.	1.0	11
65	Early Stage Identification of Alzheimerâ€™s Disease Using a Two-stage Ensemble Classifier. Current Bioinformatics, 2018, 13, 529-535.	0.7	14
66	Verifying TCM Syndrome Hypothesis Based on Improved Latent Tree Model. Lecture Notes in Computer Science, 2018, , 460-469.	1.0	1
67	Deep Convolutional Neural Network for Fog Detection. Lecture Notes in Computer Science, 2018, , 1-10.	1.0	0
68	Using Novel Convolutional Neural Networks Architecture to Predict Drug-Target Interactions. Lecture Notes in Computer Science, 2018, , 432-437.	1.0	0
69	Similarity-Based Integrated Method for Predicting Drug-Disease Interactions. Lecture Notes in Computer Science, 2018, , 395-400.	1.0	1
70	Cells Counting with Convolutional Neural Network. Lecture Notes in Computer Science, 2018, , 102-111.	1.0	1
71	Chinese Text Detection Using Deep Learning Model and Synthetic Data. Lecture Notes in Computer Science, 2018, , 503-512.	1.0	0
72	Robust object tracking via multi-scale patch based sparse coding histogram. Multimedia Tools and Applications, 2017, 76, 12181-12203.	2.6	6

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73	Functionalization of Biodegradable PLA Nonwoven Fabric as Superoleophilic and Superhydrophobic Material for Efficient Oil Absorption and Oil/Water Separation. ACS Applied Materials & Interfaces, 2017, 9, 5968-5973.	4.0	241
74	Optimization enhanced genetic algorithm-support vector regression for the prediction of compound retention indices in gas chromatography. Neurocomputing, 2017, 240, 183-190.	3.5	20
75	Protein binding hot spots prediction from sequence only by a new ensemble learning method. Amino Acids, 2017, 49, 1773-1785.	1.2	35
76	DrugRPE: Random projection ensemble approach to drug-target interaction prediction. Neurocomputing, 2017, 228, 256-262.	3.5	34
77	Utilization of rotation-invariant uniform LBP histogram distribution and statistics of connected regions in automatic image annotation based on multi-label learning. Neurocomputing, 2017, 228, 11-18.	3.5	21
78	Prediction of Protein Hotspots from Whole Protein Sequences by a Random Projection Ensemble System. International Journal of Molecular Sciences, 2017, 18, 1543.	1.8	18
79	DrugECs: An Ensemble System with Feature Subspaces for Accurate Drug-Target Interaction Prediction. BioMed Research International, 2017, 2017, 1-10.	0.9	12
80	A Machine Vision Method for Automatic Circular Parts Detection Based on Optimization Algorithm. Lecture Notes in Computer Science, 2017, , 600-611.	1.0	2
81	Compound identification using random projection for gas chromatographyâ€"mass spectrometry data. International Journal of Mass Spectrometry, 2016, 407, 16-21.	0.7	6
82	Complete genome sequence and transcriptomic analysis of a novel marine strain Bacillus weihaiensis reveals the mechanism of brown algae degradation. Scientific Reports, 2016, 6, 38248.	1.6	39
83	A regression model for calculating the second dimension retention index in comprehensive two-dimensional gas chromatography time-of-flight mass spectrometry. Journal of Chromatography A, 2016, 1451, 127-134.	1.8	12
84	Synchronous architecture of ring-banded and non-ring-banded morphology within one spherulite based on in situ ring-opening polymerization of cyclic butylene terephthalate oligomers. RSC Advances, 2016, 6, 94524-94530.	1.7	8
85	Accurate Prediction of Protein Hot Spots Residues Based on Gentle AdaBoost Algorithm. Lecture Notes in Computer Science, 2016, , 742-749.	1.0	1
86	Prediction of Hot Spots Based on Physicochemical Features and Relative Accessible Surface Area of Amino Acid Sequence. Lecture Notes in Computer Science, 2016, , 422-431.	1.0	1
87	Effect of sulfonation with concentrated sulfuric acid on the composition and carbonizability of LLDPE fibers. Polymer Bulletin, 2016, 73, 891-908.	1.7	25
88	A Sequence-Based Dynamic Ensemble Learning System for Protein Ligand-Binding Site Prediction. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2016, 13, 901-912.	1.9	32
89	A Feature Selection Scheme for Accurate Identification of Alzheimerâ€™s Disease. Lecture Notes in Computer Science, 2016, , 71-81.	1.0	1
90	Identification of ovarian cancer subtype-specific network modules and candidate drivers through an integrative genomics approach. Oncotarget, 2016, 7, 4298-4309.	0.8	20

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91	Inferring Disease-Related Domain Using Network-Based Method. Lecture Notes in Computer Science, 2016, , 775-783.	1.0	0
92	A hierarchical model for identifying mild cognitive impairment. , 2015, , .		3
93	Correlation between polymerization of cyclic butylene terephthalate (CBT) and crystallization of polymerized CBT. Chinese Journal of Polymer Science (English Edition), 2015, 33, 1104-1113.	2.0	4
94	A Multi-feature Fusion Method for Automatic Multi-label Image Annotation with Weighted Histogram Integral and Closure Regions Counting. Lecture Notes in Computer Science, 2015, , 323-330.	1.0	2
95	Automatic classification for field crop insects via multiple-task sparse representation and multiple-kernel learning. Computers and Electronics in Agriculture, 2015, 119, 123-132.	3.7	120
96	Sequence-Based Random Projection Ensemble Approach to Identify Hotspot Residues from Whole Protein Sequence. Lecture Notes in Computer Science, 2015, , 379-389.	1.0	1
97	A Random Projection Ensemble Approach to Drug-Target Interaction Prediction. Lecture Notes in Computer Science, 2015, , 693-699.	1.0	1
98	Multi-scale patch-based sparse appearance model for robust object tracking. Machine Vision and Applications, 2014, 25, 1859-1876.	1.7	6
99	SPARSE REPRESENTATION-BASED APPROACH FOR UNSUPERVISED FEATURE SELECTION. International Journal of Pattern Recognition and Artificial Intelligence, 2014, 28, 1450006.	0.7	2
100	Interaction Relation Ontology Learning. Journal of Computational Biology, 2014, 21, 80-88.	0.8	2
101	PPI-IRO: a two-stage method for protein-protein interaction extraction based on interaction relation ontology. International Journal of Data Mining and Bioinformatics, 2014, 10, 98.	0.1	0
102	A General Route Towards Defect and Pore Engineering in Graphene. Small, 2014, 10, 2280-2284.	5.2	46
103	Collaborative object tracking model with local sparse representation. Journal of Visual Communication and Image Representation, 2014, 25, 423-434.	1.7	21
104	Influences of high aspect ratio carbon nanotube network on normal stress difference measurements and extrusion behaviors for isotactic polypropylene nanocomposite melts. RSC Advances, 2014, 4, 1246-1255.	1.7	20
105	LigandRFs: random forest ensemble to identify ligand-binding residues from sequence information alone. BMC Bioinformatics, 2014, 15, S4.	1.2	51
106	Prediction of peptide drift time in ion mobility mass spectrometry from sequence-based features. BMC Bioinformatics, 2013, 14, S9.	1.2	9
107	Living lamellar crystal initiating polymerization and brittleness mechanism investigations based on crystallization during the ring-opening of cyclic butylene terephthalate oligomers. Polymer Chemistry, 2013, 4, 1648.	1.9	9
108	Solution crystallization behavior of linear and star-shaped poly(ethylene) Tj ETQq0 0 0 rgBT /Overlock 10 Tf 50 67 Td (glycol)-b-poly(É›-ca 2013, 31, 1717-1724.	2.0	8

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109	Synthesis and characterization of triblock copolymer PLA-b-PBT-b-PLA and its effect on the crystallization of PLA. RSC Advances, 2013, 3, 18464.	1.7	23
110	Accurate prediction of hot spot residues through physicochemical characteristics of amino acid sequences. Proteins: Structure, Function and Bioinformatics, 2013, 81, 1351-1362.	1.5	43
111	Crystallization behavior, thermal and mechanical properties of PHBV/graphene nanosheet composites. Chinese Journal of Polymer Science (English Edition), 2013, 31, 670-678.	2.0	38
112	Multiple instance learning tracking method with local sparse representation. IET Computer Vision, 2013, 7, 320-334.	1.3	11
113	Current Status of Machine Learning-Based Methods for Identifying Protein-Protein Interaction Sites. Current Bioinformatics, 2013, 8, 177-182.	0.7	8
114	Consensus of Sample-Balanced Classifiers for Identifying Ligand-Binding Residue by Co-evolutionary Physicochemical Characteristics of Amino Acids. Communications in Computer and Information Science, 2013, , 206-212.	0.4	0
115	Detection of Outlier Residues for Improving Interface Prediction in Protein Heterocomplexes. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 1155-1165.	1.9	22
116	Agricultural Ontology Based Feature Optimization for Agricultural Text Clustering. Journal of Integrative Agriculture, 2012, 11, 752-759.	1.7	6
117	Online EM Algorithm for Background Subtraction. Procedia Engineering, 2012, 29, 164-169.	1.2	6
118	Protein Interface Residues Prediction Based on Amino Acid Properties Only. Lecture Notes in Computer Science, 2012, , 448-452.	1.0	2
119	Relationship between tensile properties and ballistic performance of poly(ethylene naphthalate) woven and nonwoven fabrics. Journal of Applied Polymer Science, 2012, 125, 2271-2280.	1.3	9
120	Chitin nanocrystals grafted with poly(3-hydroxybutyrate-co-3-hydroxyvalerate) and their effects on thermal behavior of PHBV. Carbohydrate Polymers, 2012, 87, 784-789.	5.1	65
121	Web entity extraction based on entity attribute classification. , 2011, , .		0
122	A dynamic subspace learning method for tumor classification using microarray gene expression data. , 2011, , .		4
123	Inferring Protein-Protein Interactions Using a Hybrid Genetic Algorithm/Support Vector Machine Method. Protein and Peptide Letters, 2010, 17, 1079-1084.	0.4	9
124	Radial Basis Function Neural Network Ensemble for Predicting Protein-Protein Interaction Sites in Heterocomplexes. Protein and Peptide Letters, 2010, 17, 1111-1116.	0.4	26
125	Prediction of inter-residue contact clusters from hydrophobic cores. International Journal of Data Mining and Bioinformatics, 2010, 4, 722.	0.1	2
126	DomSVR: domain boundary prediction with support vector regression from sequence information alone. Amino Acids, 2010, 39, 713-726.	1.2	23

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127	Sequence-based identification of interface residues by an integrative profile combining hydrophobic and evolutionary information. BMC Bioinformatics, 2010, 11, 402.	1.2	40
128	Prediction of protein long-range contacts using an ensemble of genetic algorithm classifiers with sequence profile centers. BMC Structural Biology, 2010, 10, S2.	2.3	16
129	IRCDB: A Database of Inter-residues Contacts in Protein Chains. , 2009, , .		0
130	DomSVR: Domain Boundary Prediction with Support Vector Regression and Evolutionary Information. , 2009, , .		1
131	PROTEIN FOLD CLASSIFICATION WITH GENETIC ALGORITHMS AND FEATURE SELECTION. Journal of Bioinformatics and Computational Biology, 2009, 07, 773-788.	0.3	6
132	Suppressed coalescence of dispersed viscous poly(methyl methacrylate) phase in polystyrene matrix by glass beads. Journal of Polymer Science, Part B: Polymer Physics, 2009, 47, 25-35.	2.4	10
133	Prediction of protein long-range contacts using GaMC approach with sequence profile centers. , 2009, , .		0
134	Prediction of Inter-residue Contact Clusters from Hydrophobic Cores. , 2008, 2008, 703-708.		6
135	Predicting contact map using Radial Basis Function Neural Network with Conformational Energy Function. International Journal of Bioinformatics Research and Applications, 2008, 4, 123.	0.1	8
136	Predicting Key Long-Range Interaction Sites by B-Factors. Protein and Peptide Letters, 2008, 15, 478-483.	0.4	14
137	Predicting contact map using radial basis function neural network with conformational energy function. International Journal of Bioinformatics Research and Applications, 2008, 4, 123-36.	0.1	4
138	Prediction of Protein B-Factors Using Multi-Class Bounded SVM. Protein and Peptide Letters, 2007, 14, 185-190.	0.4	24
139	Prediction of Long-range Contacts from Sequence Profile. Neural Networks (IJCNN), International Joint Conference on, 2007, , .	0.0	3
140	Noticeable viscosity reduction of polycarbonate melts caused jointly by nano-silica filling and TLCP fibrillation. Polymer Engineering and Science, 2007, 47, 757-764.	1.5	16
141	Predicting protein interaction sites from residue spatial sequence profile and evolution rate. FEBS Letters, 2006, 580, 380-384.	1.3	141
142	Effect of glass bead packing on the fibrillation of liquid-crystalline polymer in polycarbonate. Journal of Polymer Science, Part B: Polymer Physics, 2006, 44, 1020-1030.	2.4	16
143	Predicting Protein-Protein Interaction Sites using Radial Basis Function Neural Networks. , 2006, , .		5
144	Long-Range Interaction Analysis using Principal Component Analysis. , 2006, , .		0

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145	Increased flow property of polycarbonate by adding hollow glass beads. Polymer Engineering and Science, 2005, 45, 1119-1131.	1.5	32
146	Prediction of contact map integrated PNN with conformational energy. , 0, , .		1
147	Predicting protein-protein interactions based on protein-domain relationships. , 0, , .		3