Abdul Sattar

List of Publications by Year
in descending order

126 papers	2,689 citations	257429 24 h-index	223791 46 g-index
132 all docs	132 docs citations	132 times ranked	2314 citing authors

#	Article	IF	Citations
1	Improving prediction of secondary structure, local backbone angles and solvent accessible surface area of proteins by iterative deep learning. Scientific Reports, 2015, 5, 11476.	3.3	290
2	Gram-positive and Gram-negative protein subcellular localization by incorporating evolutionary-based descriptors into Chou×³s general PseAAC. Journal of Theoretical Biology, 2015, 364, 284-294.	1.7	232
3	SPIDER2: A Package to Predict Secondary Structure, Accessible Surface Area, and Main-Chain Torsional Angles by Deep Neural Networks. Methods in Molecular Biology, 2017, 1484, 55-63.	0.9	137
4	Predicting backbone Cα angles and dihedrals from protein sequences by stacked sparse auto-encoder deep neural network. Journal of Computational Chemistry, 2014, 35, 2040-2046.	3.3	133
5	Local search with edge weighting and configuration checking heuristics for minimum vertex cover. Artificial Intelligence, 2011, 175, 1672-1696.	5.8	123
6	EASE-MM: Sequence-Based Prediction of Mutation-Induced Stability Changes with Feature-Based Multiple Models. Journal of Molecular Biology, 2016, 428, 1394-1405.	4.2	101
7	Highly accurate sequence-based prediction of half-sphere exposures of amino acid residues in proteins. Bioinformatics, 2016, 32, 843-849.	4.1	79
8	PSSM-Suc: Accurately predicting succinylation using position specific scoring matrix into bigram for feature extraction. Journal of Theoretical Biology, 2017, 425, 97-102.	1.7	65
9	SucStruct: Prediction of succinylated lysine residues by using structural properties of amino acids. Analytical Biochemistry, 2017, 527, 24-32.	2.4	55
10	A Combination of Feature Extraction Methods with an Ensemble of Different Classifiers for Protein Structural Class Prediction Problem. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 564-575.	3.0	53
11	DDIG-in: detecting disease-causing genetic variations due to frameshifting indels and nonsense mutations employing sequence and structural properties at nucleotide and protein levels. Bioinformatics, 2015, 31, 1599-1606.	4.1	52
12	Improving succinylation prediction accuracy by incorporating the secondary structure via helix, strand and coil, and evolutionary information from profile bigrams. PLoS ONE, 2018, 13, e0191900.	2.5	51
13	Success: evolutionary and structural properties of amino acids prove effective for succinylation site prediction. BMC Genomics, 2018, 19, 923.	2.8	50
14	Scatter search for mixed blocking flowshop scheduling. Expert Systems With Applications, 2017, 79, 20-32.	7.6	47
15	Twin Removal in Genetic Algorithms for Protein Structure Prediction Using Low-Resolution Model. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2011, 8, 234-245.	3.0	46
16	Efficient Toxicity Prediction via Simple Features Using Shallow Neural Networks and Decision Trees. ACS Omega, 2019, 4, 1874-1888.	3.5	46
17	Extended HP Model for Protein Structure Prediction. Journal of Computational Biology, 2009, 16, 85-103.	1.6	41
18	A comparative study on network alignment techniques. Expert Systems With Applications, 2020, 140, 112883.	7.6	40

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19	Model Checking Temporal Logics of Knowledge Via OBDDs1. Computer Journal, 2007, 50, 403-420.	2.4	36
20	A Segmentation-Based Method to Extract Structural and Evolutionary Features for Protein Fold Recognition. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 510-519.	3.0	34
21	A trust management architecture for hierarchical wireless sensor networks. , 2010, , .		33
22	Proposing a highly accurate protein structural class predictor using segmentation-based features. BMC Genomics, 2014, 15, S2.	2.8	32
23	INDu: An Interval & Duration Network. Lecture Notes in Computer Science, 1999, , 291-303.	1.3	32
24	Protein folding prediction in 3D FCC HP lattice model using genetic algorithm. , 2007, , .		30
25	An Enhanced Genetic Algorithm for <italic>Ab Initio</italic> Protein Structure Prediction. IEEE Transactions on Evolutionary Computation, 2016, 20, 627-644.	10.0	29
26	A Dynamic Trust Establishment and Management Framework for Wireless Sensor Networks. , 2010, , .		27
27	Gram-positive and gram-negative subcellular localization using rotation forest and physicochemical-based features. BMC Bioinformatics, 2015, 16, S1.	2.6	26
28	Kangaroo: An Efficient Constraint-Based Local Search System Using Lazy Propagation. Lecture Notes in Computer Science, 2011, , 645-659.	1.3	24
29	An evolutionary hyper-heuristic to optimise deep belief networks for image reconstruction. Applied Soft Computing Journal, 2020, 97, 105510.	7.2	22
30	Constraint guided accelerated search for mixed blocking permutation flowshop scheduling. Computers and Operations Research, 2019, 102, 102-120.	4.0	21
31	Quantitative Toxicity Prediction via Meta Ensembling of Multitask Deep Learning Models. ACS Omega, 2021, 6, 12306-12317.	3.5	21
32	Enhancing Protein Fold Prediction Accuracy Using Evolutionary and Structural Features. Lecture Notes in Computer Science, 2013, , 196-207.	1.3	21
33	Genetic Algorithm inAb Initio Protein Structure Prediction Using Low Resolution Model: A Review. Studies in Computational Intelligence, 2009, , 317-342.	0.9	20
34	A New Genetic Algorithm for Simplified Protein Structure Prediction. Lecture Notes in Computer Science, 2012, , 107-119.	1.3	19
35	Artificial intelligence in health â€" the three big challenges. Australasian Medical Journal, 2013, 6, 315-317.	0.1	18
36	Enhancing protein backbone angle prediction by using simpler models of deep neural networks. Scientific Reports, 2020, 10, 19430.	3.3	18

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37	A Constraint-Based Autonomous 3D Camera System. Constraints, 2008, 13, 180-205.	0.7	17
38	Modelling and solving temporal reasoning as propositional satisfiability. Artificial Intelligence, 2008, 172, 1752-1782.	5.8	17
39	A mixture of physicochemical and evolutionary-based feature extraction approaches for protein fold recognition. International Journal of Data Mining and Bioinformatics, 2015, 11, 115.	0.1	17
40	CardioTox net: a robust predictor for hERG channel blockade based on deep learning meta-feature ensembles. Journal of Cheminformatics, 2021, 13, 60.	6.1	17
41	DFS-generated pathways in GA crossover for protein structure prediction. Neurocomputing, 2010, 73, 2308-2316.	5.9	16
42	Scheduling blocking flowshops with setup times via constraint guided and accelerated local search. Computers and Operations Research, 2019, 109, 64-76.	4.0	16
43	Guided macro-mutation in a graded energy based genetic algorithm for protein structure prediction. Computational Biology and Chemistry, 2016, 61, 162-177.	2.3	15
44	Feature-based multiple models improve classification of mutation-induced stability changes. BMC Genomics, 2014, 15, S6.	2.8	14
45	Memory-based local search for simplified protein structure prediction. , 2012, , .		13
46	The road not taken: retreat and diverge in local search for simplified protein structure prediction. BMC Bioinformatics, 2013, 14, S19.	2.6	13
47	Spiral search: a hydrophobic-core directed local search for simplified PSP on 3D FCC lattice. BMC Bioinformatics, 2013, 14, S16.	2.6	13
48	Using crucial literals to select better theories. Computational Intelligence, 1991, 7, 11-22.	3.2	12
49	Trust Management Scheme for Mobile Ad-Hoc Networks. , 2010, , .		12
50	Trust Formalization in Mobile Ad-Hoc Networks. , 2010, , .		12
51	A Node-based Trust Management Scheme for Mobile Ad-Hoc Networks. , 2010, , .		12
52	Querying now-relative data. Journal of Intelligent Information Systems, 2013, 41, 285-311.	3.9	12
53	How Good Are Simplified Models for Protein Structure Prediction?. Advances in Bioinformatics, 2014, 2014, 1-9.	5.7	12
54	HseSUMO: Sumoylation site prediction using half-sphere exposures of amino acids residues. BMC Genomics, 2019, 19, 982.	2.8	12

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55	Toxicity Prediction by Multimodal Deep Learning. Lecture Notes in Computer Science, 2019, , 142-152.	1.3	12
56	Exploring Potential Discriminatory Information Embedded in PSSM to Enhance Protein Structural Class Prediction Accuracy. Lecture Notes in Computer Science, 2013, , 208-219.	1.3	12
57	Advanced indexing technique for temporal data. Computer Science and Information Systems, 2010, 7, 679-703.	1.0	12
58	An implicit approach to deal with periodically repeated medical data. Artificial Intelligence in Medicine, 2012, 55, 149-162.	6.5	11
59	Sequence-only evolutionary and predicted structural features for the prediction of stability changes in protein mutants. BMC Bioinformatics, 2013, 14, S6.	2.6	11
60	A Comprehensive Approach to â€˜Nowâ€™ in Temporal Relational Databases: Semantics and Representation. IEEE Transactions on Knowledge and Data Engineering, 2016, 28, 2538-2551.	5.7	11
61	Using prediction to improve elective surgery scheduling. Australasian Medical Journal, 2013, 6, 287-289.	0.1	10
62	Towards sequence-based prediction of mutation-induced stability changes in unseen non-homologous proteins. BMC Genomics, 2014, 15, S4.	2.8	10
63	Tailoring customer order scheduling search algorithms. Computers and Operations Research, 2019, 108, 155-165.	4.0	10
64	On Fibring Semantics for BDI Logics. Lecture Notes in Computer Science, 2002, , 198-210.	1.3	10
65	Random-walk. , 2012, , .		9
66	A fusion of data analysis and non-monotonic reasoning to restore missed RFID readings. , 2009, , .		8
67	An efficient encoding for simplified protein structure prediction using genetic algorithms. , 2013, , .		8
68	Mixing Energy Models in Genetic Algorithms for On-Lattice Protein Structure Prediction. BioMed Research International, 2013, 2013, 1-15.	1.9	7
69	Towards an Efficient SAT Encoding for Temporal Reasoning. Lecture Notes in Computer Science, 2006, , 421-436.	1.3	7
70	Protein Fold Recognition Using an Overlapping Segmentation Approach and a Mixture of Feature Extraction Models. Lecture Notes in Computer Science, 2013, , 32-43.	1.3	7
71	Constraint-Based Local Search for Golomb Rulers. Lecture Notes in Computer Science, 2015, , 322-331.	1.3	7
72	Local Search for Maximum Vertex Weight Clique on Large Sparse Graphs with Efficient Data Structures. Lecture Notes in Computer Science, 2016, , 255-267.	1.3	7

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73	The POINT approach to represent now in bitemporal databases. Journal of Intelligent Information Systems, 2009, 32, 297-323.	3.9	6
74	A complete first-order temporal BDI logic for forest multi-agent systems. Knowledge-Based Systems, 2012, 27, 343-351.	7.1	6
75	A local search embedded genetic algorithm for simplified protein structure prediction. , 2013, , .		6
76	Local Search with Noisy Strategy for Minimum Vertex Cover in Massive Graphs. Lecture Notes in Computer Science, 2016, , 283-294.	1.3	6
77	Constraint guided search for aircraft sequencing. Expert Systems With Applications, 2019, 118, 440-458.	7.6	6
78	Verification of Multi-agent Systems Via Bounded Model Checking. Lecture Notes in Computer Science, 2006, , 69-78.	1.3	6
79	Correcting Missing Data Anomalies with Clausal Defeasible Logic. Lecture Notes in Computer Science, 2010, , 149-163.	1.3	6
80	Protein Fold Recognition Using Segmentation-Based Feature Extraction Model. Lecture Notes in Computer Science, 2013, , 345-354.	1.3	6
81	An Efficient Algorithm for Solving Dynamic Complex DCOP Problems. , 2009, , .		5
82	Let's Trust Users It is Their Search. , 2010, , .		5
83	Genetic algorithm feature-based resampling for protein structure prediction. , 2010, , .		5
84	Adaptive Clause Weight Redistribution. Lecture Notes in Computer Science, 2006, , 229-243.	1.3	5
85	Ensemble of Diversely Trained Support Vector Machines for Protein Fold Recognition. Lecture Notes in Computer Science, 2013, , 335-344.	1.3	5
86	Probabilistic Belief Revision via Imaging. Lecture Notes in Computer Science, 2014, , 694-707.	1.3	5
87	Secondary structure specific simpler prediction models for protein backbone angles. BMC Bioinformatics, 2022, 23, 6.	2.6	5
88	Verification of Authentication Protocols for Epistemic Goals via SAT Compilation. Journal of Computer Science and Technology, 2006, 21, 932-943.	1.5	4
89	Advances in artifical intelligence research in health. Australasian Medical Journal, 2012, 5, 475-477.	0.1	4
90	Refining Genetic Algorithm twin removal for high-resolution protein structure prediction. , 2012, , .		4

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91	Multiagent Based Scheduling of Elective Surgery. Lecture Notes in Computer Science, 2012, , 74-89.	1.3	4
92	Levels of Modalities for BDI Logic. , 2008, , .		3
93	Evolutionary Learning Based Iterated Local Search for Google Machine Reassignment Problems. Lecture Notes in Computer Science, 2017, , 409-421.	1.3	3
94	A scatter search algorithm for time-dependent prize-collecting arc routing problems. Computers and Operations Research, 2021, 134, 105392.	4.0	3
95	Variable Granularity Space Filling Curve for Indexing Multidimensional Data. Lecture Notes in Computer Science, 2011, , 111-124.	1.3	3
96	Stochastic Local Search Based Channel Assignment in Wireless Mesh Networks. Lecture Notes in Computer Science, 2013, , 832-847.	1.3	3
97	An Intelligent Approach to Surgery Scheduling. Lecture Notes in Computer Science, 2012, , 535-550.	1.3	3
98	Detecting intrusions within RFID systems through non-monotonic reasoning cleaning. , 2010, , .		2
99	An intelligent approach to handle False-Positive Radio Frequency Identification Anomalies. Intelligent Data Analysis, 2011, 15, 931-954.	0.9	2
100	A Parallel Framework for Multipoint Spiral Search in <i>ab Initio</i> Protein Structure Prediction. Advances in Bioinformatics, 2014, 2014, 1-17.	5.7	2
101	A General Approach to Represent and Query Now-Relative Medical Data in Relational Databases. Lecture Notes in Computer Science, 2015, , 327-331.	1.3	2
102	Multi-neighbourhood Great Deluge for Google Machine Reassignment Problem. Lecture Notes in Computer Science, 2017, , 706-715.	1.3	2
103	Constraint based local search for flowshops with sequence-dependent setup times. Engineering Applications of Artificial Intelligence, 2021, 102, 104264.	8.1	2
104	On the KL Divergence of Probability Mixtures for Belief Contraction. Lecture Notes in Computer Science, 2015, , 249-255.	1.3	2
105	DFS Based Partial Pathways in GA for Protein Structure Prediction. Lecture Notes in Computer Science, 2008, , 41-53.	1.3	2
106	Constraint-Based Evolutionary Local Search for Protein Structures with Secondary Motifs. Lecture Notes in Computer Science, 2014, , 333-344.	1.3	2
107	Solving Sum and Product Riddle via BDD-Based Model Checking. , 2008, , .		1
108	X-CleLo: intelligent deterministic RFID data and event transformer. Personal and Ubiquitous Computing, 2012, 16, 259-269.	2.8	1

#	ARTICLE	IF	CITATIONS
109	Collaborative Parallel Local Search for Simplified Protein Structure Prediction. , 2013, , .		1
110	Constraint-directed search for all-interval series. Constraints, 2017, 22, 403-431.	0.7	1
111	A Novel Integrated Classifier for Handling Data Warehouse Anomalies. Lecture Notes in Computer Science, 2011, , 98-110.	1.3	1
112	A Method to Avoid Duplicative Flipping in Local Search for SAT. Lecture Notes in Computer Science, 2012, , 218-229.	1.3	1
113	Probabilistic Belief Contraction: Considerations on Epistemic Entrenchment, Probability Mixtures and KL Divergence. Lecture Notes in Computer Science, 2015, , 109-122.	1.3	1
114	Levels of modality for BDI Logic. Journal of Applied Logic, 2011, 9, 250-273.	1.1	0
115	A casual model for fluctuating sugar levels in diabetic patients. Australasian Medical Journal, 2012, 5, 497-502.	0.1	0
116	AI@NICTA. AI Magazine, 2012, 33, 115.	1.6	0
117	An intensional approach for periodic data in relational databases. Journal of Intelligent Information Systems, 2013, 41, 151-186.	3.9	0
118	Constraint-Guided Local Search for Single Mixed-Operation Runway. Lecture Notes in Computer Science, 2018, , 329-341.	1.3	0
119	Makespan preserving flowshop reengineering via blocking constraints. Computers and Operations Research, 2019, 112, 104755.	4.0	0
120	Improving Protein Backbone Angle Prediction Using Hidden Markov Models in Deep Learning. Lecture Notes in Computer Science, 2021, , 239-251.	1.3	0
121	Fibred BDI Logics: Completeness Preservation in the Presence of Interaction Axioms. Lecture Notes in Computer Science, 2011, , 63-74.	1.3	0
122	Towards Real Intelligent Web Exploration. Lecture Notes in Computer Science, 2012, , 411-422.	1.3	0
123	Diversify Intensification Phases in Local Search for SAT with a New Probability Distribution. Lecture Notes in Computer Science, 2013, , 166-177.	1.3	0
124	Amino Acids Pattern-Biased Spiral Search for Protein Structure Prediction. Lecture Notes in Computer Science, 2014, , 143-156.	1.3	0
125	Deterministic Tournament Selection in Local Search for Maximum Edge Weight Clique onÂLarge Sparse Graphs. Lecture Notes in Computer Science, 2017, , 353-364.	1.3	0
126	Exploiting Setup Time Constraints in Local Search for Flowshop Scheduling. Lecture Notes in Computer Science, 2019, , 379-392.	1.3	0