Abdul Sattar

List of Publications by Citations

131 papers	2,004 citations	22 h-index	41 g-index
132 ext. papers	2,344 ext. citations	2.6 avg, IF	5 L-index

#	Paper	IF	Citations
131	Improving prediction of secondary structure, local backbone angles, and solvent accessible surface area of proteins by iterative deep learning. *Scientific Reports*, **2015**, 5, 11476	4.9	227
130	Gram-positive and Gram-negative protein subcellular localization by incorporating evolutionary-based descriptors into Chou?s general PseAAC. *Journal of Theoretical Biology*, **2015**, 364, 284-94	2.3	206
129	Predicting backbone Cα angles and dihedrals from protein sequences by stacked sparse auto-encoder deep neural network. *Journal of Computational Chemistry*, **2014**, 35, 2040-6	3.5	110
128	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	1.4	89
127	Local search with edge weighting and configuration checking heuristics for minimum vertex cover. *Artificial Intelligence*, **2011**, 175, 1672-1696	3.6	88
126	EASE-MM: Sequence-Based Prediction of Mutation-Induced Stability Changes with Feature-Based Multiple Models. *Journal of Molecular Biology*, **2016**, 428, 1394-1405	6.5	72
125	Highly accurate sequence-based prediction of half-sphere exposures of amino acid residues in proteins. *Bioinformatics*, **2016**, 32, 843-9	7.2	65
124	SucStruct: Prediction of succinylated lysine residues by using structural properties of amino acids. *Analytical Biochemistry*, **2017**, 527, 24-32	3.1	46
123	PSSM-Suc: Accurately predicting succinylation using position specific scoring matrix into bigram for feature extraction. *Journal of Theoretical Biology*, **2017**, 425, 97-102	2.3	44
122	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, 1599-606	7.2	44
121	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, 564-75	3	41
120	Success: evolutionary and structural properties of amino acids prove effective for succinylation site prediction. *BMC Genomics*, **2018**, 19, 923	4.5	40
119	Twin removal in genetic algorithms for protein structure prediction using low-resolution model. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2011**, 8, 234-45	3	39
118	Scatter search for mixed blocking flowshop scheduling. *Expert Systems With Applications*, **2017**, 79, 20-32	7.8	37
117	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	3.7	35
116	Extended HP model for protein structure prediction. *Journal of Computational Biology*, **2009**, 16, 85-103	1.7	32
115	Model Checking Temporal Logics of Knowledge Via OBDDs1. *Computer Journal*, **2007**, 50, 403-420	1.3	32

114	Proposing a highly accurate protein structural class predictor using segmentation-based features. *BMC Genomics*, **2014**, 15 Suppl 1, S2	4.5	30
113	A Segmentation-Based Method to Extract Structural and Evolutionary Features for Protein Fold Recognition. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **2014**, 11, 510-9	3	30
112	INDu: An Interval & Duration Network. *Lecture Notes in Computer Science*, **1999**, 291-303	0.9	27
111	Efficient Toxicity Prediction via Simple Features Using Shallow Neural Networks and Decision Trees. *ACS Omega*, **2019**, 4, 1874-1888	3.9	26
110	A trust management architecture for hierarchical wireless sensor networks **2010**,		22
109	A comparative study on network alignment techniques. *Expert Systems With Applications*, **2020**, 140, 112883	7.8	22
108	. *IEEE Transactions on Evolutionary Computation*, **2016**, 20, 627-644	15.6	21
107	Gram-positive and Gram-negative subcellular localization using rotation forest and physicochemical-based features. *BMC Bioinformatics*, **2015**, 16 Suppl 4, S1	3.6	21
106	Protein folding prediction in 3D FCC HP lattice model using genetic algorithm **2007**,		20
105	Genetic Algorithm inAb Initio Protein Structure Prediction Using Low Resolution Model: A Review. *Studies in Computational Intelligence*, **2009**, 317-342	0.8	18
104	A Dynamic Trust Establishment and Management Framework for Wireless Sensor Networks **2010**,		17
103	Kangaroo: An Efficient Constraint-Based Local Search System Using Lazy Propagation. *Lecture Notes in Computer Science*, **2011**, 645-659	0.9	16
102	Enhancing Protein Fold Prediction Accuracy Using Evolutionary and Structural Features. *Lecture Notes in Computer Science*, **2013**, 196-207	0.9	16
101	A mixture of physicochemical and evolutionary-based feature extraction approaches for protein fold recognition. *International Journal of Data Mining and Bioinformatics*, **2015**, 11, 115-38	0.5	14
100	Spiral search: a hydrophobic-core directed local search for simplified PSP on 3D FCC lattice. *BMC Bioinformatics*, **2013**, 14 Suppl 2, S16	3.6	13
99	Constraint guided accelerated search for mixed blocking permutation flowshop scheduling. *Computers and Operations Research*, **2019**, 102, 102-120	4.6	13
98	Artificial intelligence in health - the three big challenges. *Australasian Medical Journal*, **2013**, 6, 315-7	2	12
97	Memory-based local search for simplified protein structure prediction **2012**,		12

96	A Constraint-Based Autonomous 3D Camera System. *Constraints*, **2008**, 13, 180-205	0.3	12
95	Modelling and solving temporal reasoning as propositional satisfiability. *Artificial Intelligence*, **2008**, 172, 1752-1782	3.6	12
94	Guided macro-mutation in a graded energy based genetic algorithm for protein structure prediction. *Computational Biology and Chemistry*, **2016**, 61, 162-77	3.6	11
93	**2010**,		11
92	DFS-generated pathways in GA crossover for protein structure prediction. *Neurocomputing*, **2010**, 73, 2308-2316	5.4	11
91	Exploring Potential Discriminatory Information Embedded in PSSM to Enhance Protein Structural Class Prediction Accuracy. *Lecture Notes in Computer Science*, **2013**, 208-219	0.9	11
90	Parallel Late Acceptance Hill-Climbing Algorithm for the Google Machine Reassignment Problem. *Lecture Notes in Computer Science*, **2016**, 163-174	0.9	11
89	An evolutionary hyper-heuristic to optimise deep belief networks for image reconstruction. *Applied Soft Computing Journal*, **2020**, 97, 105510	7.5	11
88	Feature-based multiple models improve classification of mutation-induced stability changes. *BMC Genomics*, **2014**, 15 Suppl 4, S6	4.5	10
87	The road not taken: retreat and diverge in local search for simplified protein structure prediction. *BMC Bioinformatics*, **2013**, 14 Suppl 2, S19	3.6	10
86	**2010**,		10
85	A New Genetic Algorithm for Simplified Protein Structure Prediction. *Lecture Notes in Computer Science*, **2012**, 107-119	0.9	10
84	Advanced indexing technique for temporal data. *Computer Science and Information Systems*, **2010**, 7, 679-703	0.8	10
83	Scheduling blocking flowshops with setup times via constraint guided and accelerated local search. *Computers and Operations Research*, **2019**, 109, 64-76	4.6	9
82	Sequence-only evolutionary and predicted structural features for the prediction of stability changes in protein mutants. *BMC Bioinformatics*, **2013**, 14 Suppl 2, S6	3.6	9
81	How good are simplified models for protein structure prediction?. *Advances in Bioinformatics*, **2014**, 2014, 867179	5.5	9
80	An implicit approach to deal with periodically repeated medical data. *Artificial Intelligence in Medicine*, **2012**, 55, 149-62	7.4	9
79	Using crucial literals to select better theories. *Computational Intelligence*, **1991**, 7, 11-22	2.5	9

78	*. IEEE Transactions on Knowledge and Data Engineering*, **2016**, 28, 2538-2551	4.2	9
77	Querying now-relative data. *Journal of Intelligent Information Systems*, **2013**, 41, 285-311	2.1	8
76	Random-walk **2012**,		8
75	Towards sequence-based prediction of mutation-induced stability changes in unseen non-homologous proteins. *BMC Genomics*, **2014**, 15 Suppl 1, S4	4.5	7
74	An efficient encoding for simplified protein structure prediction using genetic algorithms **2013**,		7
73	Using prediction to improve elective surgery scheduling. *Australasian Medical Journal*, **2013**, 6, 287-9	2	7
72	Toxicity Prediction by Multimodal Deep Learning. *Lecture Notes in Computer Science*, **2019**, 142-152	0.9	7
71	On Fibring Semantics for BDI Logics. *Lecture Notes in Computer Science*, **2002**, 198-210	0.9	7
70	HseSUMO: Sumoylation site prediction using half-sphere exposures of amino acids residues. *BMC Genomics*, **2019**, 19, 982	4.5	6
69	Tailoring customer order scheduling search algorithms. *Computers and Operations Research*, **2019**, 108, 155-165	4.6	6
68	Mixing energy models in genetic algorithms for on-lattice protein structure prediction. *BioMed Research International*, **2013**, 2013, 924137	3	6
67	Trust Formalization in Mobile Ad-Hoc Networks **2010**,		6
66	Protein Fold Recognition Using an Overlapping Segmentation Approach and a Mixture of Feature Extraction Models. *Lecture Notes in Computer Science*, **2013**, 32-43	0.9	6
65	Constraint-Based Local Search for Golomb Rulers. *Lecture Notes in Computer Science*, **2015**, 322-331	0.9	6
64	Local Search for Maximum Vertex Weight Clique on Large Sparse Graphs with Efficient Data Structures. *Lecture Notes in Computer Science*, **2016**, 255-267	0.9	6
63	Enhancing protein backbone angle prediction by using simpler models of deep neural networks. *Scientific Reports*, **2020**, 10, 19430	4.9	6
62	A complete first-order temporal BDI logic for forest multi-agent systems. *Knowledge-Based Systems*, **2012**, 27, 343-351	7.3	5
61	The POINT approach to represent now in bitemporal databases. *Journal of Intelligent Information Systems*, **2009**, 32, 297-323	2.1	5

60	Correcting Missing Data Anomalies with Clausal Defeasible Logic. *Lecture Notes in Computer Science*, **2010**, 149-163	0.9	5
59	Protein Fold Recognition Using Segmentation-Based Feature Extraction Model. *Lecture Notes in Computer Science*, **2013**, 345-354	0.9	5
58	Local Search with Noisy Strategy for Minimum Vertex Cover in Massive Graphs. *Lecture Notes in Computer Science*, **2016**, 283-294	0.9	4
57	A local search embedded genetic algorithm for simplified protein structure prediction **2013**,		4
56	A fusion of data analysis and non-monotonic reasoning to restore missed RFID readings **2009**,		4
55	An Efficient Algorithm for Solving Dynamic Complex DCOP Problems **2009**,		4
54	Probabilistic Belief Revision via Imaging. *Lecture Notes in Computer Science*, **2014**, 694-707	0.9	4
53	Quantitative Toxicity Prediction via Meta Ensembling of Multitask Deep Learning Models. *ACS Omega*, **2021**, 6, 12306-12317	3.9	4
52	Verification of Multi-agent Systems Via Bounded Model Checking. *Lecture Notes in Computer Science*, **2006**, 69-78	0.9	4
51	Advances in artificial intelligence research in health. *Australasian Medical Journal*, **2012**, 5, 475-7	2	3
50	**2010**,		3
49	Indexing Temporal Data with Virtual Structure. *Lecture Notes in Computer Science*, **2010**, 591-594	0.9	3
48	Multiagent Based Scheduling of Elective Surgery. *Lecture Notes in Computer Science*, **2012**, 74-89	0.9	3
47	Ensemble of Diversely Trained Support Vector Machines for Protein Fold Recognition. *Lecture Notes in Computer Science*, **2013**, 335-344	0.9	3
46	Stochastic Local Search Based Channel Assignment in Wireless Mesh Networks. *Lecture Notes in Computer Science*, **2013**, 832-847	0.9	3
45	Constraint guided search for aircraft sequencing. *Expert Systems With Applications*, **2019**, 118, 440-458	7.8	3
44	Adaptive Clause Weight Redistribution. *Lecture Notes in Computer Science*, **2006**, 229-243	0.9	3
43	Towards an Efficient SAT Encoding for Temporal Reasoning. *Lecture Notes in Computer Science*, **2006**, 421-436	0.9	3

42	A General Approach to Represent and Query Now-Relative Medical Data in Relational Databases. *Lecture Notes in Computer Science*, **2015**, 327-331	0.9	2
41	Evolutionary Learning Based Iterated Local Search for Google Machine Reassignment Problems. *Lecture Notes in Computer Science*, **2017**, 409-421	0.9	2
40	Multi-neighbourhood Great Deluge for Google Machine Reassignment Problem. *Lecture Notes in Computer Science*, **2017**, 706-715	0.9	2
39	Refining Genetic Algorithm twin removal for high-resolution protein structure prediction **2012**,		2
38	Genetic algorithm feature-based resampling for protein structure prediction **2010**,		2
37	Detecting intrusions within RFID systems through non-monotonic reasoning cleaning **2010**,		2
36	Levels of Modalities for BDI Logic **2008**,		2
35	Verification of Authentication Protocols for Epistemic Goals via SAT Compilation. *Journal of Computer Science and Technology*, **2006**, 21, 932-943	1.7	2
34	DFS Based Partial Pathways in GA for Protein Structure Prediction. *Lecture Notes in Computer Science*, **2008**, 41-53	0.9	2
33	On the KL Divergence of Probability Mixtures for Belief Contraction. *Lecture Notes in Computer Science*, **2015**, 249-255	0.9	2
32	Variable Granularity Space Filling Curve for Indexing Multidimensional Data. *Lecture Notes in Computer Science*, **2011**, 111-124	0.9	2
31	Reasoning with Levels of Modalities in BDI Logic. *Lecture Notes in Computer Science*, **2009**, 410-415	0.9	2
30	Constraint-Based Evolutionary Local Search for Protein Structures with Secondary Motifs. *Lecture Notes in Computer Science*, **2014**, 333-344	0.9	2
29	CardioTox net: a robust predictor for hERG channel blockade based on deep learning meta-feature ensembles. *Journal of Cheminformatics*, **2021**, 13, 60	8.6	2
28	Constraint-directed search for all-interval series. *Constraints*, **2017**, 22, 403-431	0.3	1
27	Mixed Neighbourhood Local Search for Customer Order Scheduling Problem. *Lecture Notes in Computer Science*, **2018**, 296-309	0.9	1
26	A Parallel Framework for Multipoint Spiral Search in ab Initio Protein Structure Prediction. *Advances in Bioinformatics*, **2014**, 2014, 985968	5.5	1
25	Collaborative Parallel Local Search for Simplified Protein Structure Prediction **2013**,		1

#			
24	An intelligent approach to handle False-Positive Radio Frequency Identification Anomalies. *Intelligent Data Analysis*, **2011**, 15, 931-954	1.1	1
23	Solving Sum and Product Riddle via BDD-Based Model Checking **2008**,		1
22	Secondary structure specific simpler prediction models for protein backbone angles.. *BMC Bioinformatics*, **2022**, 23, 6	3.6	1
21	Probabilistic Belief Contraction: Considerations on Epistemic Entrenchment, Probability Mixtures and KL Divergence. *Lecture Notes in Computer Science*, **2015**, 109-122	0.9	1
20	A Method to Avoid Duplicative Flipping in Local Search for SAT. *Lecture Notes in Computer Science*, **2012**, 218-229	0.9	1
19	A scatter search algorithm for time-dependent prize-collecting arc routing problems. *Computers and Operations Research*, **2021**, 134, 105392	4.6	1
18	An Intelligent Approach to Surgery Scheduling. *Lecture Notes in Computer Science*, **2012**, 535-550	0.9	0
17	Constraint based local search for flowshops with sequence-dependent setup times. *Engineering Applications of Artificial Intelligence*, **2021**, 102, 104264	7.2	0
16	Makespan preserving flowshop reengineering via blocking constraints. *Computers and Operations Research*, **2019**, 112, 104755	4.6	
15	An intensional approach for periodic data in relational databases. *Journal of Intelligent Information Systems*, **2013**, 41, 151-186	2.1	
14	AI@NICTA. *AI Magazine*, **2012**, 33, 115	6.1	
13	X-CleLo: intelligent deterministic RFID data and event transformer. *Personal and Ubiquitous Computing*, **2012**, 16, 259-269	2.1	
12	Levels of modality for BDI Logic. *Journal of Applied Logic*, **2011**, 9, 250-273		
11	A causal model for fluctuating sugar levels in diabetes patients. *Australasian Medical Journal*, **2012**, 5, 497-502	2	
10	Improving Protein Backbone Angle Prediction Using Hidden Markov Models in Deep Learning. *Lecture Notes in Computer Science*, **2021**, 239-251	0.9	
9	Exploiting Setup Time Constraints in Local Search for Flowshop Scheduling. *Lecture Notes in Computer Science*, **2019**, 379-392	0.9	
8	Deterministic Tournament Selection in Local Search for Maximum Edge Weight Clique on Large Sparse Graphs. *Lecture Notes in Computer Science*, **2017**, 353-364	0.9	
7	A Novel Integrated Classifier for Handling Data Warehouse Anomalies. *Lecture Notes in Computer Science*, **2011**, 98-110	0.9	

LIST OF PUBLICATIONS

6	Fibred BDI Logics: Completeness Preservation in the Presence of Interaction Axioms. *Lecture Notes in Computer Science*, **2011**, 63-74	0.9
5	Towards Real Intelligent Web Exploration. *Lecture Notes in Computer Science*, **2012**, 411-422	0.9
4	Diversify Intensification Phases in Local Search for SAT with a New Probability Distribution. *Lecture Notes in Computer Science*, **2013**, 166-177	0.9
3	Amino Acids Pattern-Biased Spiral Search for Protein Structure Prediction. *Lecture Notes in Computer Science*, **2014**, 143-156	0.9
2	Constraint-Guided Local Search for Single Mixed-Operation Runway. *Lecture Notes in Computer Science*, **2018**, 329-341	0.9
1	Tailoring Contact Based Scoring Functions for Protein Structure Prediction. *Lecture Notes in Computer Science*, **2022**, 155-168	0.9