

Abdul Sattar

List of Publications by Year in Descending Order

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Version: 2024-04-28

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

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	Secondary structure specific simpler prediction models for protein backbone angles.. <i>BMC Bioinformatics</i> , 2022 , 23, 6	3.6	1
130	Tailoring Contact Based Scoring Functions for Protein Structure Prediction. <i>Lecture Notes in Computer Science</i> , 2022 , 155-168	0.9	
129	Improving Protein Backbone Angle Prediction Using Hidden Markov Models in Deep Learning. <i>Lecture Notes in Computer Science</i> , 2021 , 239-251	0.9	
128	Quantitative Toxicity Prediction via Meta Ensembling of Multitask Deep Learning Models. <i>ACS Omega</i> , 2021 , 6, 12306-12317	3.9	4
127	Constraint based local search for flowshops with sequence-dependent setup times. <i>Engineering Applications of Artificial Intelligence</i> , 2021 , 102, 104264	7.2	0
126	CardioTox net: a robust predictor for hERG channel blockade based on deep learning meta-feature ensembles. <i>Journal of Cheminformatics</i> , 2021 , 13, 60	8.6	2
125	A scatter search algorithm for time-dependent prize-collecting arc routing problems. <i>Computers and Operations Research</i> , 2021 , 134, 105392	4.6	1
124	A comparative study on network alignment techniques. <i>Expert Systems With Applications</i> , 2020 , 140, 112883	7.8	22
123	Enhancing protein backbone angle prediction by using simpler models of deep neural networks. <i>Scientific Reports</i> , 2020 , 10, 19430	4.9	6
122	An evolutionary hyper-heuristic to optimise deep belief networks for image reconstruction. <i>Applied Soft Computing Journal</i> , 2020 , 97, 105510	7.5	11
121	Efficient Toxicity Prediction via Simple Features Using Shallow Neural Networks and Decision Trees. <i>ACS Omega</i> , 2019 , 4, 1874-1888	3.9	26
120	Scheduling blocking flowshops with setup times via constraint guided and accelerated local search. <i>Computers and Operations Research</i> , 2019 , 109, 64-76	4.6	9
119	HseSUMO: Sumoylation site prediction using half-sphere exposures of amino acids residues. <i>BMC Genomics</i> , 2019 , 19, 982	4.5	6
118	Tailoring customer order scheduling search algorithms. <i>Computers and Operations Research</i> , 2019 , 108, 155-165	4.6	6
117	Makespan preserving flowshop reengineering via blocking constraints. <i>Computers and Operations Research</i> , 2019 , 112, 104755	4.6	
116	Exploiting Setup Time Constraints in Local Search for Flowshop Scheduling. <i>Lecture Notes in Computer Science</i> , 2019 , 379-392	0.9	
115	Toxicity Prediction by Multimodal Deep Learning. <i>Lecture Notes in Computer Science</i> , 2019 , 142-152	0.9	7

114	Constraint guided search for aircraft sequencing. <i>Expert Systems With Applications</i> , 2019 , 118, 440-458	7.8	3
113	Constraint guided accelerated search for mixed blocking permutation flowshop scheduling. <i>Computers and Operations Research</i> , 2019 , 102, 102-120	4.6	13
112	Success: evolutionary and structural properties of amino acids prove effective for succinylation site prediction. <i>BMC Genomics</i> , 2018 , 19, 923	4.5	40
111	Mixed Neighbourhood Local Search for Customer Order Scheduling Problem. <i>Lecture Notes in Computer Science</i> , 2018 , 296-309	0.9	1
110	Improving succinylation prediction accuracy by incorporating the secondary structure via helix, strand and coil, and evolutionary information from profile bigrams. <i>PLoS ONE</i> , 2018 , 13, e0191900	3.7	35
109	Constraint-Guided Local Search for Single Mixed-Operation Runway. <i>Lecture Notes in Computer Science</i> , 2018 , 329-341	0.9	
108	Scatter search for mixed blocking flowshop scheduling. <i>Expert Systems With Applications</i> , 2017 , 79, 20-32	7.8	37
107	PSSM-Suc: Accurately predicting succinylation using position specific scoring matrix into bigram for feature extraction. <i>Journal of Theoretical Biology</i> , 2017 , 425, 97-102	2.3	44
106	SucStruct: Prediction of succinylated lysine residues by using structural properties of amino acids. <i>Analytical Biochemistry</i> , 2017 , 527, 24-32	3.1	46
105	Constraint-directed search for all-interval series. <i>Constraints</i> , 2017 , 22, 403-431	0.3	1
104	Evolutionary Learning Based Iterated Local Search for Google Machine Reassignment Problems. <i>Lecture Notes in Computer Science</i> , 2017 , 409-421	0.9	2
103	Multi-neighbourhood Great Deluge for Google Machine Reassignment Problem. <i>Lecture Notes in Computer Science</i> , 2017 , 706-715	0.9	2
102	SPIDER2: A Package to Predict Secondary Structure, Accessible Surface Area, and Main-Chain Torsional Angles by Deep Neural Networks. <i>Methods in Molecular Biology</i> , 2017 , 1484, 55-63	1.4	89
101	Deterministic Tournament Selection in Local Search for Maximum Edge Weight Clique on Large Sparse Graphs. <i>Lecture Notes in Computer Science</i> , 2017 , 353-364	0.9	
100	Local Search with Noisy Strategy for Minimum Vertex Cover in Massive Graphs. <i>Lecture Notes in Computer Science</i> , 2016 , 283-294	0.9	4
99	EASE-MM: Sequence-Based Prediction of Mutation-Induced Stability Changes with Feature-Based Multiple Models. <i>Journal of Molecular Biology</i> , 2016 , 428, 1394-1405	6.5	72
98	. <i>IEEE Transactions on Evolutionary Computation</i> , 2016 , 20, 627-644	15.6	21
97	Guided macro-mutation in a graded energy based genetic algorithm for protein structure prediction. <i>Computational Biology and Chemistry</i> , 2016 , 61, 162-77	3.6	11

96	Highly accurate sequence-based prediction of half-sphere exposures of amino acid residues in proteins. <i>Bioinformatics</i> , 2016 , 32, 843-9	7.2	65
95	Local Search for Maximum Vertex Weight Clique on Large Sparse Graphs with Efficient Data Structures. <i>Lecture Notes in Computer Science</i> , 2016 , 255-267	0.9	6
94	. <i>IEEE Transactions on Knowledge and Data Engineering</i> , 2016 , 28, 2538-2551	4.2	9
93	Parallel Late Acceptance Hill-Climbing Algorithm for the Google Machine Reassignment Problem. <i>Lecture Notes in Computer Science</i> , 2016 , 163-174	0.9	11
92	DDIG-in: detecting disease-causing genetic variations due to frameshifting indels and nonsense mutations employing sequence and structural properties at nucleotide and protein levels. <i>Bioinformatics</i> , 2015 , 31, 1599-606	7.2	44
91	A General Approach to Represent and Query Now-Relative Medical Data in Relational Databases. <i>Lecture Notes in Computer Science</i> , 2015 , 327-331	0.9	2
90	Improving prediction of secondary structure, local backbone angles, and solvent accessible surface area of proteins by iterative deep learning. <i>Scientific Reports</i> , 2015 , 5, 11476	4.9	227
89	Gram-positive and Gram-negative protein subcellular localization by incorporating evolutionary-based descriptors into Chou's general PseAAC. <i>Journal of Theoretical Biology</i> , 2015 , 364, 284-94	2.3	206
88	Gram-positive and Gram-negative subcellular localization using rotation forest and physicochemical-based features. <i>BMC Bioinformatics</i> , 2015 , 16 Suppl 4, S1	3.6	21
87	A mixture of physicochemical and evolutionary-based feature extraction approaches for protein fold recognition. <i>International Journal of Data Mining and Bioinformatics</i> , 2015 , 11, 115-38	0.5	14
86	Constraint-Based Local Search for Golomb Rulers. <i>Lecture Notes in Computer Science</i> , 2015 , 322-331	0.9	6
85	On the KL Divergence of Probability Mixtures for Belief Contraction. <i>Lecture Notes in Computer Science</i> , 2015 , 249-255	0.9	2
84	Probabilistic Belief Contraction: Considerations on Epistemic Entrenchment, Probability Mixtures and KL Divergence. <i>Lecture Notes in Computer Science</i> , 2015 , 109-122	0.9	1
83	Towards sequence-based prediction of mutation-induced stability changes in unseen non-homologous proteins. <i>BMC Genomics</i> , 2014 , 15 Suppl 1, S4	4.5	7
82	Proposing a highly accurate protein structural class predictor using segmentation-based features. <i>BMC Genomics</i> , 2014 , 15 Suppl 1, S2	4.5	30
81	Predicting backbone C α angles and dihedrals from protein sequences by stacked sparse auto-encoder deep neural network. <i>Journal of Computational Chemistry</i> , 2014 , 35, 2040-6	3.5	110
80	Feature-based multiple models improve classification of mutation-induced stability changes. <i>BMC Genomics</i> , 2014 , 15 Suppl 4, S6	4.5	10
79	A Segmentation-Based Method to Extract Structural and Evolutionary Features for Protein Fold Recognition. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2014 , 11, 510-9	3	30

78	How good are simplified models for protein structure prediction?. <i>Advances in Bioinformatics</i> , 2014 , 2014, 867179	5.5	9
77	A Parallel Framework for Multipoint Spiral Search in ab Initio Protein Structure Prediction. <i>Advances in Bioinformatics</i> , 2014 , 2014, 985968	5.5	1
76	Amino Acids Pattern-Biased Spiral Search for Protein Structure Prediction. <i>Lecture Notes in Computer Science</i> , 2014 , 143-156	0.9	
75	Constraint-Based Evolutionary Local Search for Protein Structures with Secondary Motifs. <i>Lecture Notes in Computer Science</i> , 2014 , 333-344	0.9	2
74	Probabilistic Belief Revision via Imaging. <i>Lecture Notes in Computer Science</i> , 2014 , 694-707	0.9	4
73	A local search embedded genetic algorithm for simplified protein structure prediction 2013 ,		4
72	Sequence-only evolutionary and predicted structural features for the prediction of stability changes in protein mutants. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 2, S6	3.6	9
71	The road not taken: retreat and diverge in local search for simplified protein structure prediction. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 2, S19	3.6	10
70	Spiral search: a hydrophobic-core directed local search for simplified PSP on 3D FCC lattice. <i>BMC Bioinformatics</i> , 2013 , 14 Suppl 2, S16	3.6	13
69	Querying now-relative data. <i>Journal of Intelligent Information Systems</i> , 2013 , 41, 285-311	2.1	8
68	An intensional approach for periodic data in relational databases. <i>Journal of Intelligent Information Systems</i> , 2013 , 41, 151-186	2.1	
67	A combination of feature extraction methods with an ensemble of different classifiers for protein structural class prediction problem. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2013 , 10, 564-75	3	41
66	An efficient encoding for simplified protein structure prediction using genetic algorithms 2013 ,		7
65	Using prediction to improve elective surgery scheduling. <i>Australasian Medical Journal</i> , 2013 , 6, 287-9	2	7
64	Mixing energy models in genetic algorithms for on-lattice protein structure prediction. <i>BioMed Research International</i> , 2013 , 2013, 924137	3	6
63	Artificial intelligence in health - the three big challenges. <i>Australasian Medical Journal</i> , 2013 , 6, 315-7	2	12
62	Collaborative Parallel Local Search for Simplified Protein Structure Prediction 2013 ,		1
61	Protein Fold Recognition Using an Overlapping Segmentation Approach and a Mixture of Feature Extraction Models. <i>Lecture Notes in Computer Science</i> , 2013 , 32-43	0.9	6

60	Ensemble of Diversely Trained Support Vector Machines for Protein Fold Recognition. <i>Lecture Notes in Computer Science, 2013</i> , 335-344	0.9	3
59	Protein Fold Recognition Using Segmentation-Based Feature Extraction Model. <i>Lecture Notes in Computer Science, 2013</i> , 345-354	0.9	5
58	Enhancing Protein Fold Prediction Accuracy Using Evolutionary and Structural Features. <i>Lecture Notes in Computer Science, 2013</i> , 196-207	0.9	16
57	Exploring Potential Discriminatory Information Embedded in PSSM to Enhance Protein Structural Class Prediction Accuracy. <i>Lecture Notes in Computer Science, 2013</i> , 208-219	0.9	11
56	Stochastic Local Search Based Channel Assignment in Wireless Mesh Networks. <i>Lecture Notes in Computer Science, 2013</i> , 832-847	0.9	3
55	Diversify Intensification Phases in Local Search for SAT with a New Probability Distribution. <i>Lecture Notes in Computer Science, 2013</i> , 166-177	0.9	
54	A complete first-order temporal BDI logic for forest multi-agent systems. <i>Knowledge-Based Systems</i> , 2012 , 27, 343-351	7.3	5
53	An implicit approach to deal with periodically repeated medical data. <i>Artificial Intelligence in Medicine, 2012</i> , 55, 149-62	7.4	9
52	Refining Genetic Algorithm twin removal for high-resolution protein structure prediction 2012 ,		2
51	AI@NICTA. <i>AI Magazine, 2012</i> , 33, 115	6.1	
50	X-CleLo: intelligent deterministic RFID data and event transformer. <i>Personal and Ubiquitous Computing, 2012</i> , 16, 259-269	2.1	
49	Random-walk 2012 ,		8
48	A New Genetic Algorithm for Simplified Protein Structure Prediction. <i>Lecture Notes in Computer Science, 2012</i> , 107-119	0.9	10
47	Advances in artificial intelligence research in health. <i>Australasian Medical Journal, 2012</i> , 5, 475-7	2	3
46	A causal model for fluctuating sugar levels in diabetes patients. <i>Australasian Medical Journal, 2012</i> , 5, 497-502	2	
45	Memory-based local search for simplified protein structure prediction 2012 ,		12
44	Multiagent Based Scheduling of Elective Surgery. <i>Lecture Notes in Computer Science, 2012</i> , 74-89	0.9	3
43	A Method to Avoid Duplicative Flipping in Local Search for SAT. <i>Lecture Notes in Computer Science, 2012</i> , 218-229	0.9	1

42	An Intelligent Approach to Surgery Scheduling. <i>Lecture Notes in Computer Science</i> , 2012 , 535-550	0.9	0
41	Towards Real Intelligent Web Exploration. <i>Lecture Notes in Computer Science</i> , 2012 , 411-422	0.9	
40	Levels of modality for BDI Logic. <i>Journal of Applied Logic</i> , 2011 , 9, 250-273		
39	An intelligent approach to handle False-Positive Radio Frequency Identification Anomalies. <i>Intelligent Data Analysis</i> , 2011 , 15, 931-954	1.1	1
38	Twin removal in genetic algorithms for protein structure prediction using low-resolution model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2011 , 8, 234-45	3	39
37	Local search with edge weighting and configuration checking heuristics for minimum vertex cover. <i>Artificial Intelligence</i> , 2011 , 175, 1672-1696	3.6	88
36	Variable Granularity Space Filling Curve for Indexing Multidimensional Data. <i>Lecture Notes in Computer Science</i> , 2011 , 111-124	0.9	2
35	Kangaroo: An Efficient Constraint-Based Local Search System Using Lazy Propagation. <i>Lecture Notes in Computer Science</i> , 2011 , 645-659	0.9	16
34	A Novel Integrated Classifier for Handling Data Warehouse Anomalies. <i>Lecture Notes in Computer Science</i> , 2011 , 98-110	0.9	
33	Fibred BDI Logics: Completeness Preservation in the Presence of Interaction Axioms. <i>Lecture Notes in Computer Science</i> , 2011 , 63-74	0.9	
32	A trust management architecture for hierarchical wireless sensor networks 2010 ,		22
31	A Dynamic Trust Establishment and Management Framework for Wireless Sensor Networks 2010 ,		17
30	2010 ,		10
29	Trust Formalization in Mobile Ad-Hoc Networks 2010 ,		6
28	2010 ,		11
27	Genetic algorithm feature-based resampling for protein structure prediction 2010 ,		2
26	Detecting intrusions within RFID systems through non-monotonic reasoning cleaning 2010 ,		2
25	2010 ,		3

24	DFS-generated pathways in GA crossover for protein structure prediction. <i>Neurocomputing</i> , 2010 , 73, 2308-2316	5.4	11
23	Advanced indexing technique for temporal data. <i>Computer Science and Information Systems</i> , 2010 , 7, 679-703	0.8	10
22	Correcting Missing Data Anomalies with Clausal Defeasible Logic. <i>Lecture Notes in Computer Science</i> , 2010 , 149-163	0.9	5
21	Indexing Temporal Data with Virtual Structure. <i>Lecture Notes in Computer Science</i> , 2010 , 591-594	0.9	3
20	Extended HP model for protein structure prediction. <i>Journal of Computational Biology</i> , 2009 , 16, 85-103	1.7	32
19	A fusion of data analysis and non-monotonic reasoning to restore missed RFID readings 2009 ,		4
18	The POINT approach to represent now in bitemporal databases. <i>Journal of Intelligent Information Systems</i> , 2009 , 32, 297-323	2.1	5
17	An Efficient Algorithm for Solving Dynamic Complex DCOP Problems 2009 ,		4
16	Genetic Algorithm in Ab Initio Protein Structure Prediction Using Low Resolution Model: A Review. <i>Studies in Computational Intelligence</i> , 2009 , 317-342	0.8	18
15	Reasoning with Levels of Modalities in BDI Logic. <i>Lecture Notes in Computer Science</i> , 2009 , 410-415	0.9	2
14	Solving Sum and Product Riddle via BDD-Based Model Checking 2008 ,		1
13	Levels of Modalities for BDI Logic 2008 ,		2
12	A Constraint-Based Autonomous 3D Camera System. <i>Constraints</i> , 2008 , 13, 180-205	0.3	12
11	Modelling and solving temporal reasoning as propositional satisfiability. <i>Artificial Intelligence</i> , 2008 , 172, 1752-1782	3.6	12
10	DFS Based Partial Pathways in GA for Protein Structure Prediction. <i>Lecture Notes in Computer Science</i> , 2008 , 41-53	0.9	2
9	Model Checking Temporal Logics of Knowledge Via OBDDs1. <i>Computer Journal</i> , 2007 , 50, 403-420	1.3	32
8	Protein folding prediction in 3D FCC HP lattice model using genetic algorithm 2007 ,		20
7	Verification of Authentication Protocols for Epistemic Goals via SAT Compilation. <i>Journal of Computer Science and Technology</i> , 2006 , 21, 932-943	1.7	2

6	Adaptive Clause Weight Redistribution. <i>Lecture Notes in Computer Science</i> , 2006 , 229-243	0.9	3
5	Towards an Efficient SAT Encoding for Temporal Reasoning. <i>Lecture Notes in Computer Science</i> , 2006 , 421-436	0.9	3
4	Verification of Multi-agent Systems Via Bounded Model Checking. <i>Lecture Notes in Computer Science</i> , 2006 , 69-78	0.9	4
3	On Fibring Semantics for BDI Logics. <i>Lecture Notes in Computer Science</i> , 2002 , 198-210	0.9	7
2	INDu: An Interval & Duration Network. <i>Lecture Notes in Computer Science</i> , 1999 , 291-303	0.9	27
1	Using crucial literals to select better theories. <i>Computational Intelligence</i> , 1991 , 7, 11-22	2.5	9