

# Alok Sharma

## List of Publications by Year in descending order

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123  
papers

5,048  
citations

94433

37  
h-index

110387

64  
g-index

126  
all docs

126  
docs citations

126  
times ranked

4564  
citing authors

#	ARTICLE	IF	CITATIONS
1	Single-stranded and double-stranded DNA-binding protein prediction using HMM profiles. <i>Analytical Biochemistry</i> , 2021, 612, 113954.	2.4	8
2	OPTICAL+: a frequency-based deep learning scheme for recognizing brain wave signals. <i>PeerJ Computer Science</i> , 2021, 7, e375.	4.5	21
3	Critical assessment of protein intrinsic disorder prediction. <i>Nature Methods</i> , 2021, 18, 472-481.	19.0	187
4	Forecasting the spread of COVID-19 using LSTM network. <i>BMC Bioinformatics</i> , 2021, 22, 316.	2.6	15
5	SPECTRA: a tool for enhanced brain wave signal recognition. <i>BMC Bioinformatics</i> , 2021, 22, 195.	2.6	4
6	DeepFeature: feature selection in nonimage data using convolutional neural network. <i>Briefings in Bioinformatics</i> , 2021, 22, .	6.5	31
7	CluSem: Accurate clustering-based ensemble method to predict motor imagery tasks from multi-channel EEG data. <i>Journal of Neuroscience Methods</i> , 2021, 364, 109373.	2.5	9
8	PupStruct: Prediction of Pupylated Lysine Residues Using Structural Properties of Amino Acids. <i>Genes</i> , 2020, 11, 1431.	2.4	6
9	Prognosis prediction model for conversion from mild cognitive impairment to Alzheimer's disease created by integrative analysis of multi-omics data. <i>Alzheimer's Research and Therapy</i> , 2020, 12, 145.	6.2	33
10	Genome-wide characterization and expression analysis suggested diverse functions of the mechanosensitive channel of small conductance-like (MSL) genes in cereal crops. <i>Scientific Reports</i> , 2020, 10, 16583.	3.3	24
11	Accurately Predicting Glutarylation Sites Using Sequential Bi-Peptide-Based Evolutionary Features. <i>Genes</i> , 2020, 11, 1023.	2.4	17
12	RAM-PGK: Prediction of Lysine Phosphoglycerylation Based on Residue Adjacency Matrix. <i>Genes</i> , 2020, 11, 1524.	2.4	5
13	Accurate prediction of RNA 5-hydroxymethylcytosine modification by utilizing novel position-specific gapped k-mer descriptors. <i>Computational and Structural Biotechnology Journal</i> , 2020, 18, 3528-3538.	4.1	11
14	Mal-Light: Enhancing Lysine Malonylation Sites Prediction Problem Using Evolutionary-based Features. <i>IEEE Access</i> , 2020, 8, 77888-77902.	4.2	12
15	C-iSUMO: A sumoylation site predictor that incorporates intrinsic characteristics of amino acid sequences. <i>Computational Biology and Chemistry</i> , 2020, 87, 107235.	2.3	12
16	Predicting protein-peptide binding sites with a deep convolutional neural network. <i>Journal of Theoretical Biology</i> , 2020, 496, 110278.	1.7	25
17	DeepInsight: A methodology to transform a non-image data to an image for convolution neural network architecture. <i>Scientific Reports</i> , 2019, 9, 11399.	3.3	162
18	Protein secondary structure prediction using neural networks and deep learning: A review. <i>Computational Biology and Chemistry</i> , 2019, 81, 1-8.	2.3	49

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19	A comparison of machine learning classifiers for dementia with Lewy bodies using miRNA expression data. BMC Medical Genomics, 2019, 12, 150.	1.5	22
20	Community assessment to advance computational prediction of cancer drug combinations in a pharmacogenomic screen. Nature Communications, 2019, 10, 2674.	12.8	240
21	Brain wave classification using long short-term memory network based OPTICAL predictor. Scientific Reports, 2019, 9, 9153.	3.3	64
22	EvolStruct-Phogly: incorporating structural properties and evolutionary information from profile bigrams for the phosphoglycerylation prediction. BMC Genomics, 2019, 19, 984.	2.8	17
23	HseSUMO: Sumoylation site prediction using half-sphere exposures of amino acids residues. BMC Genomics, 2019, 19, 982.	2.8	12
24	PyFeat: a Python-based effective feature generation tool for DNA, RNA and protein sequences. Bioinformatics, 2019, 35, 3831-3833.	4.1	80
25	GlyStruct: glycation prediction using structural properties of amino acid residues. BMC Bioinformatics, 2019, 19, 547.	2.6	31
26	Risk prediction models for dementia constructed by supervised principal component analysis using miRNA expression data. Communications Biology, 2019, 2, 77.	4.4	50
27	Discovering MoRFs by trisecting intrinsically disordered protein sequence into terminals and middle regions. BMC Bioinformatics, 2019, 19, 378.	2.6	13
28	Bigram-PGK: phosphoglycerylation prediction using the technique of bigram probabilities of position specific scoring matrix. BMC Molecular and Cell Biology, 2019, 20, 57.	2.0	11
29	A novel one-class classification approach to accurately predict disease-gene association in acute myeloid leukemia cancer. PLoS ONE, 2019, 14, e0226115.	2.5	16
30	OPAL+: Length-Specific MoRF Prediction in Intrinsically Disordered Protein Sequences. Proteomics, 2019, 19, e1800058.	2.2	30
31	Clustering of Small-Sample Single-Cell RNA-Seq Data via Feature Clustering and Selection. Lecture Notes in Computer Science, 2019, , 445-456.	1.3	4
32	Computational Prediction of Lysine Pupylation Sites in Prokaryotic Proteins Using Position Specific Scoring Matrix into Bigram for Feature Extraction. Lecture Notes in Computer Science, 2019, , 488-500.	1.3	1
33	Subject-Specific-Frequency-Band for Motor Imagery EEG Signal Recognition Based on Common Spatial Spectral Pattern. Lecture Notes in Computer Science, 2019, , 712-722.	1.3	9
34	A new parameter tuning approach for enhanced motor imagery EEG signal classification. Medical and Biological Engineering and Computing, 2018, 56, 1861-1874.	2.8	47
35	EvoStruct-Sub: An accurate Gram-positive protein subcellular localization predictor using evolutionary and structural features. Journal of Theoretical Biology, 2018, 443, 138-146.	1.7	31
36	OPAL: prediction of MoRF regions in intrinsically disordered protein sequences. Bioinformatics, 2018, 34, 1850-1858.	4.1	53

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37	MoRFPred-plus: Computational Identification of MoRFs in Protein Sequences using Physicochemical Properties and HMM profiles. <i>Journal of Theoretical Biology</i> , 2018, 437, 9-16.	1.7	43
38	PhoglyStruct: Prediction of phosphoglycerylated lysine residues using structural properties of amino acids. <i>Scientific Reports</i> , 2018, 8, 17923.	3.3	31
39	SumSec: Accurate Prediction of Sumoylation Sites Using Predicted Secondary Structure. <i>Molecules</i> , 2018, 23, 3260.	3.8	13
40	A crowdsourced analysis to identify ab initio molecular signatures predictive of susceptibility to viral infection. <i>Nature Communications</i> , 2018, 9, 4418.	12.8	14
41	Success: evolutionary and structural properties of amino acids prove effective for succinylation site prediction. <i>BMC Genomics</i> , 2018, 19, 923.	2.8	50
42	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.	2.5	51
43	An integrative machine learning approach for prediction of toxicity-related drug safety. <i>Life Science Alliance</i> , 2018, 1, e201800098.	2.8	44
44	Hierarchical Maximum Likelihood Clustering Approach. <i>IEEE Transactions on Biomedical Engineering</i> , 2017, 64, 112-122.	4.2	28
45	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.	1.7	65
46	SucStruct: Prediction of succinylated lysine residues by using structural properties of amino acids. <i>Analytical Biochemistry</i> , 2017, 527, 24-32.	2.4	55
47	CSP-TSM: Optimizing the performance of Riemannian tangent space mapping using common spatial pattern for MI-BCI. <i>Computers in Biology and Medicine</i> , 2017, 91, 231-242.	7.0	61
48	iPHLoc-ES: Identification of bacteriophage protein locations using evolutionary and structural features. <i>Journal of Theoretical Biology</i> , 2017, 435, 229-237.	1.7	29
49	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.	0.9	137
50	2D-EM clustering approach for high-dimensional data through folding feature vectors. <i>BMC Bioinformatics</i> , 2017, 18, 547.	2.6	7
51	HMMBinder: DNA-Binding Protein Prediction Using HMM Profile Based Features. <i>BioMed Research International</i> , 2017, 2017, 1-10.	1.9	41
52	Divisive hierarchical maximum likelihood clustering. <i>BMC Bioinformatics</i> , 2017, 18, 546.	2.6	23
53	An improved discriminative filter bank selection approach for motor imagery EEG signal classification using mutual information. <i>BMC Bioinformatics</i> , 2017, 18, 545.	2.6	94
54	Predicting MoRFs in protein sequences using HMM profiles. <i>BMC Bioinformatics</i> , 2016, 17, 504.	2.6	24

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55	A Deep Learning Approach for Motor Imagery EEG Signal Classification. , 2016, , .		82
56	Improving protein fold recognition and structural class prediction accuracies using physicochemical properties of amino acids. Journal of Theoretical Biology, 2016, 402, 117-128.	1.7	22
57	Decimation filter with Common Spatial Pattern and Fishers Discriminant Analysis for motor imagery classification. , 2016, , .		19
58	Stepwise iterative maximum likelihood clustering approach. BMC Bioinformatics, 2016, 17, 319.	2.6	14
59	Gene masking - a technique to improve accuracy for cancer classification with high dimensionality in microarray data. BMC Medical Genomics, 2016, 9, 74.	1.5	7
60	Protein fold recognition using HMMâ€“HMM alignment and dynamic programming. Journal of Theoretical Biology, 2016, 393, 67-74.	1.7	33
61	Highly accurate sequence-based prediction of half-sphere exposures of amino acid residues in proteins. Bioinformatics, 2016, 32, 843-849.	4.1	79
62	Protein Fold Recognition Using Genetic Algorithm Optimized Voting Scheme and Profile Bigram. Journal of Software, 2016, 11, 756-767.	0.6	23
63	Patient Condition Monitoring Modular Hospital Robot. Journal of Software, 2016, 11, 768-786.	0.6	2
64	Importance of dimensionality reduction in protein fold recognition. , 2015, , .		1
65	Application of cepstrum analysis and linear predictive coding for motor imaginary task classification. , 2015, , .		2
66	Gram-positive and gram-negative subcellular localization using rotation forest and physicochemical-based features. BMC Bioinformatics, 2015, 16, S1.	2.6	26
67	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
68	Ordered Regions of Channel Nucleoporins Nup62, Nup54, and Nup58 Form Dynamic Complexes in Solution. Journal of Biological Chemistry, 2015, 290, 18370-18378.	3.4	18
69	Predict Gram-Positive and Gram-Negative Subcellular Localization via Incorporating Evolutionary Information and Physicochemical Features Into Chou's General PseAAC. IEEE Transactions on Nanobioscience, 2015, 14, 915-926.	3.3	72
70	Probabilistic expression of spatially varied amino acid dimers into general form of Chou's pseudo amino acid composition for protein fold recognition. Journal of Theoretical Biology, 2015, 380, 291-298.	1.7	22
71	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
72	Subcellular localization for Gram positive and Gram negative bacterial proteins using linear interpolation smoothing model. Journal of Theoretical Biology, 2015, 386, 25-33.	1.7	13

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73	Advancing the Accuracy of Protein Fold Recognition by Utilizing Profiles From Hidden Markov Models. IEEE Transactions on Nanobioscience, 2015, 14, 761-772.	3.3	34
74	Linear discriminant analysis for the small sample size problem: an overview. International Journal of Machine Learning and Cybernetics, 2015, 6, 443-454.	3.6	154
75	A deterministic approach to regularized linear discriminant analysis. Neurocomputing, 2015, 151, 207-214.	5.9	34
76	Gram-positive and Gram-negative protein subcellular localization by incorporating evolutionary-based descriptors into Chou's general PseAAC. Journal of Theoretical Biology, 2015, 364, 284-294.	1.7	232
77	Some aspects on geometric and matrix work-hardening characteristics of sintered cold forged copper alloy preforms. Materials Research, 2014, 17, 196-202.	1.3	2
78	Remote patient physical condition monitoring service module for iWARD hospital robots. , 2014, , .		11
79	Growing radial basis function network models. , 2014, , .		3
80	Vision based autonomous path tracking of a mobile robot using fuzzy logic. , 2014, , .		12
81	Genetic algorithm for an optimized weighted voting scheme incorporating k-separated bigram transition probabilities to improve protein fold recognition. , 2014, , .		4
82	A feature selection method using fixed-point algorithm for DNA microarray gene expression data. International Journal of Knowledge-Based and Intelligent Engineering Systems, 2014, 18, 55-59.	1.0	5
83	Proposing a highly accurate protein structural class predictor using segmentation-based features. BMC Genomics, 2014, 15, S2.	2.8	32
84	Predicting backbone $\phi$ 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
85	A Tri-Gram Based Feature Extraction Technique Using Linear Probabilities of Position Specific Scoring Matrix for Protein Fold Recognition. IEEE Transactions on Nanobioscience, 2014, 13, 44-50.	3.3	64
86	A feature selection method using improved regularized linear discriminant analysis. Machine Vision and Applications, 2014, 25, 775-786.	2.7	55
87	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
88	Protein fold recognition by alignment of amino acid residues using kernelized dynamic time warping. Journal of Theoretical Biology, 2014, 354, 137-145.	1.7	30
89	Improving protein fold recognition using the amalgamation of evolutionary-based and structural based information. BMC Bioinformatics, 2014, 15, S12.	2.6	20
90	Evaluation of Sequence Features from Intrinsically Disordered Regions for the Estimation of Protein Function. PLoS ONE, 2014, 9, e89890.	2.5	19

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91	Principal component analysis using QR decomposition. International Journal of Machine Learning and Cybernetics, 2013, 4, 679-683.	3.6	66
92	A strategy to select suitable physicochemical attributes of amino acids for protein fold recognition. BMC Bioinformatics, 2013, 14, 233.	2.6	40
93	A feature extraction technique using bi-gram probabilities of position specific scoring matrix for protein fold recognition. Journal of Theoretical Biology, 2013, 320, 41-46.	1.7	139
94	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
95	A BETWEEN-CLASS OVERLAPPING FILTER-BASED METHOD FOR TRANSCRIPTOME DATA ANALYSIS. Journal of Bioinformatics and Computational Biology, 2012, 10, 1250010.	0.8	22
96	A Filter Based Feature Selection Algorithm Using Null Space of Covariance Matrix for DNA Microarray Gene Expression Data. Current Bioinformatics, 2012, 7, 289-294.	1.5	24
97	IMPROVED PSEUDOINVERSE LINEAR DISCRIMINANT ANALYSIS METHOD FOR DIMENSIONALITY REDUCTION. International Journal of Pattern Recognition and Artificial Intelligence, 2012, 26, 1250002.	1.2	14
98	Null space based feature selection method for gene expression data. International Journal of Machine Learning and Cybernetics, 2012, 3, 269-276.	3.6	62
99	A Top-r Feature Selection Algorithm for Microarray Gene Expression Data. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2012, 9, 754-764.	3.0	152
100	A new perspective to null linear discriminant analysis method and its fast implementation using random matrix multiplication with scatter matrices. Pattern Recognition, 2012, 45, 2205-2213.	8.1	43
101	A two-stage linear discriminant analysis for face-recognition. Pattern Recognition Letters, 2012, 33, 1157-1162.	4.2	27
102	Strategy of finding optimal number of features on gene expression data. Electronics Letters, 2011, 47, 480.	1.0	21
103	Approximate LDA Technique for Dimensionality Reduction in the Small Sample Size Case. Journal of Pattern Recognition Research, 2011, 6, 298-306.	0.9	9
104	Tanimoto Based Similarity Measure for Intrusion Detection System. Journal of Information Security, 2011, 02, 195-201.	0.8	10
105	Improved direct LDA and its application to DNA microarray gene expression data. Pattern Recognition Letters, 2010, 31, 2489-2492.	4.2	31
106	Improved nearest centroid classifier with shrunken distance measure for null LDA method on cancer classification problem. Electronics Letters, 2010, 46, 1251.	1.0	6
107	Regularisation of eigenfeatures by extrapolation of scatter-matrix in face-recognition problem. Electronics Letters, 2010, 46, 682.	1.0	8
108	Solution structure of the Equine Infectious Anemia Virus p9 protein: a rationalization of its different ALIX binding requirements compared to the analogous HIV-p6 protein. BMC Structural Biology, 2009, 9, 74.	2.3	5

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109	A Gradient Linear Discriminant Analysis for Small Sample Sized Problem. Neural Processing Letters, 2008, 27, 17-24.	3.2	32
110	Cancer classification by gradient LDA technique using microarray gene expression data. Data and Knowledge Engineering, 2008, 66, 338-347.	3.4	66
111	Rotational Linear Discriminant Analysis Technique for Dimensionality Reduction. IEEE Transactions on Knowledge and Data Engineering, 2008, 20, 1336-1347.	5.7	36
112	Structural Characterization and Oligomerization of PB1-F2, a Proapoptotic Influenza A Virus Protein. Journal of Biological Chemistry, 2007, 282, 353-363.	3.4	57
113	Intrusion detection using text processing techniques with a kernel based similarity measure. Computers and Security, 2007, 26, 488-495.	6.0	54
114	Detecting masquerades using a combination of Naïve Bayes and weighted RBF approach. Journal in Computer Virology, 2007, 3, 237-245.	1.9	10
115	Fast principal component analysis using fixed-point algorithm. Pattern Recognition Letters, 2007, 28, 1151-1155.	4.2	168
116	Class-dependent PCA, MDC and LDA: A combined classifier for pattern classification. Pattern Recognition, 2006, 39, 1215-1229.	8.1	50
117	Subspace independent component analysis using vector kurtosis. Pattern Recognition, 2006, 39, 2227-2232.	8.1	29
118	Rotational Linear Discriminant Analysis Using Bayes Rule for Dimensionality Reduction. Journal of Computer Science, 2006, 2, 754-757.	0.6	8
119	Splitting Technique Initialization in Local PCA. Journal of Computer Science, 2006, 2, 53-58.	0.6	5
120	Pattern Classification: An Improvement Using Combination of VQ and PCA Based Techniques. American Journal of Applied Sciences, 2005, 2, 1445-1455.	0.2	3
121	Radioactive mineral identification based on FFT Radix-2 algorithm. Electronics Letters, 2004, 40, 536.	1.0	1
122	Evaluation of Matrix and Geometric Strain Hardening of Axial Deformed Sintered Fe-0.75%C Preform. Advanced Materials Research, 0, 911, 143-147.	0.3	0
123	Densification and Corrosion Studies of as-Sintered-Swaged Al Composite Preforms. Advanced Materials Research, 0, 911, 67-71.	0.3	0