

# Nguyen-Quoc-Khanh Le

## List of Publications by Citations

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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.

64

papers

1,182

citations

24

h-index

31

g-index

79

ext. papers

1,885

ext. citations

4.6

avg, IF

5.94

L-index

#	Paper	IF	Citations
64	iEnhancer-5Step: Identifying enhancers using hidden information of DNA sequences via Chou's 5-step rule and word embedding. <i>Analytical Biochemistry</i> , <b>2019</b> , 571, 53-61	3.1	76
63	Incorporating deep learning with convolutional neural networks and position specific scoring matrices for identifying electron transport proteins. <i>Journal of Computational Chemistry</i> , <b>2017</b> , 38, 2000-2006	3.5	65
62	Classifying the molecular functions of Rab GTPases in membrane trafficking using deep convolutional neural networks. <i>Analytical Biochemistry</i> , <b>2018</b> , 555, 33-41	3.1	46
61	iN6-methylat (5-step): identifying DNA N-methyladenine sites in rice genome using continuous bag of nucleobases via Chou's 5-step rule. <i>Molecular Genetics and Genomics</i> , <b>2019</b> , 294, 1173-1182	3.1	44
60	iMotor-CNN: Identifying molecular functions of cytoskeleton motor proteins using 2D convolutional neural network via Chou's 5-step rule. <i>Analytical Biochemistry</i> , <b>2019</b> , 575, 17-26	3.1	43
59	XGBoost Improves Classification of MGMT Promoter Methylation Status in IDH1 Wildtype Glioblastoma. <i>Journal of Personalized Medicine</i> , <b>2020</b> , 10,	3.6	41
58	Prediction of FAD binding sites in electron transport proteins according to efficient radial basis function networks and significant amino acid pairs. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 298	3.6	41
57	Identification of clathrin proteins by incorporating hyperparameter optimization in deep learning and PSSM profiles. <i>Computer Methods and Programs in Biomedicine</i> , <b>2019</b> , 177, 81-88	6.9	38
56	Classifying Promoters by Interpreting the Hidden Information of DNA Sequences via Deep Learning and Combination of Continuous FastText N-Grams. <i>Frontiers in Bioengineering and Biotechnology</i> , <b>2019</b> , 7, 305	5.8	37
55	Using deep neural networks and biological subwords to detect protein S-sulfenylation sites. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	36
54	Fertility-GRU: Identifying Fertility-Related Proteins by Incorporating Deep-Gated Recurrent Units and Original Position-Specific Scoring Matrix Profiles. <i>Journal of Proteome Research</i> , <b>2019</b> , 18, 3503-3511	5.6	33
53	ET-GRU: using multi-layer gated recurrent units to identify electron transport proteins. <i>BMC Bioinformatics</i> , <b>2019</b> , 20, 377	3.6	32
52	SNARE-CNN: a 2D convolutional neural network architecture to identify SNARE proteins from high-throughput sequencing data. <i>PeerJ Computer Science</i> , <b>2019</b> , 5, e177	2.7	31
51	Prediction of FMN Binding Sites in Electron Transport Chains Based on 2-D CNN and PSSM Profiles. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2021</b> , 18, 2189-2197	3	31
50	A Computational Framework Based on Ensemble Deep Neural Networks for Essential Genes Identification. <i>International Journal of Molecular Sciences</i> , <b>2020</b> , 21,	6.3	31
49	Using extreme gradient boosting to identify origin of replication in <i>Saccharomyces cerevisiae</i> via hybrid features. <i>Genomics</i> , <b>2020</b> , 112, 2445-2451	4.3	29
48	Radiomics-based machine learning model for efficiently classifying transcriptome subtypes in glioblastoma patients from MRI. <i>Computers in Biology and Medicine</i> , <b>2021</b> , 132, 104320	7	29

47	Computational identification of vesicular transport proteins from sequences using deep gated recurrent units architecture. <i>Computational and Structural Biotechnology Journal</i> , <b>2019</b> , 17, 1245-1254	6.8	28
46	A transformer architecture based on BERT and 2D convolutional neural network to identify DNA enhancers from sequence information. <i>Briefings in Bioinformatics</i> , <b>2021</b> , 22,	13.4	28
45	Machine Learning Model for Identifying Antioxidant Proteins Using Features Calculated from Primary Sequences. <i>Biology</i> , <b>2020</b> , 9,	4.9	27
44	DeepETC: A deep convolutional neural network architecture for investigating and classifying electron transport chain complexes. <i>Neurocomputing</i> , <b>2020</b> , 375, 71-79	5.4	27
43	Identifying the molecular functions of electron transport proteins using radial basis function networks and biochemical properties. <i>Journal of Molecular Graphics and Modelling</i> , <b>2017</b> , 73, 166-178	2.8	26
42	Application of Computational Biology and Artificial Intelligence Technologies in Cancer Precision Drug Discovery. <i>BioMed Research International</i> , <b>2019</b> , 2019, 8427042	3	25
41	Identifying SNAREs by Incorporating Deep Learning Architecture and Amino Acid Embedding Representation. <i>Frontiers in Physiology</i> , <b>2019</b> , 10, 1501	4.6	25
40	DeepEfflux: a 2D convolutional neural network model for identifying families of efflux proteins in transporters. <i>Bioinformatics</i> , <b>2018</b> , 34, 3111-3117	7.2	24
39	. <i>IEEE Transactions on Industrial Electronics</i> , <b>2020</b> , 67, 9671-9682	8.9	23
38	iEnhancer-ECNN: identifying enhancers and their strength using ensembles of convolutional neural networks. <i>BMC Genomics</i> , <b>2019</b> , 20, 951	4.5	20
37	Incorporating efficient radial basis function networks and significant amino acid pairs for predicting GTP binding sites in transport proteins. <i>BMC Bioinformatics</i> , <b>2016</b> , 17, 501	3.6	18
36	Using word embedding technique to efficiently represent protein sequences for identifying substrate specificities of transporters. <i>Analytical Biochemistry</i> , <b>2019</b> , 577, 73-81	3.1	15
35	Incorporating convolutional neural networks and sequence graph transform for identifying multilabel protein Lysine PTM sites. <i>Chemometrics and Intelligent Laboratory Systems</i> , <b>2020</b> , 206, 104171	3.8	15
34	An AI-based prediction model for drug-drug interactions in osteoporosis and Paget's diseases from SMILES.. <i>Molecular Informatics</i> , <b>2022</b> ,	3.8	13
33	Machine Learning-Based Radiomics Signatures for EGFR and KRAS Mutations Prediction in Non-Small-Cell Lung Cancer. <i>International Journal of Molecular Sciences</i> , <b>2021</b> , 22,	6.3	13
32	Ensemble of Deep Recurrent Neural Networks for Identifying Enhancers via Dinucleotide Physicochemical Properties. <i>Cells</i> , <b>2019</b> , 8,	7.9	12
31	Deep transformers and convolutional neural network in identifying DNA N6-methyladenine sites in cross-species genomes.. <i>Methods</i> , <b>2021</b> ,	4.6	12
30	Improved Prediction Model of Protein Lysine Crotonylation Sites Using Bidirectional Recurrent Neural Networks. <i>Journal of Proteome Research</i> , <b>2021</b> ,	5.6	11

29	Prediction of ATP-binding sites in membrane proteins using a two-dimensional convolutional neural network. <i>Journal of Molecular Graphics and Modelling</i> , <b>2019</b> , 92, 86-93	2.8	10
28	Incorporating post translational modification information for enhancing the predictive performance of membrane transport proteins. <i>Computational Biology and Chemistry</i> , <b>2018</b> , 77, 251-260	3.6	10
27	FAD-BERT: Improved prediction of FAD binding sites using pre-training of deep bidirectional transformers. <i>Computers in Biology and Medicine</i> , <b>2021</b> , 131, 104258	7	8
26	Risk Score Generated from CT-Based Radiomics Signatures for Overall Survival Prediction in Non-Small Cell Lung Cancer. <i>Cancers</i> , <b>2021</b> , 13,	6.6	8
25	Classification of adaptor proteins using recurrent neural networks and PSSM profiles. <i>BMC Genomics</i> , <b>2019</b> , 20, 966	4.5	8
24	A sequence-based approach for identifying recombination spots in <i>Saccharomyces cerevisiae</i> by using hyper-parameter optimization in FastText and support vector machine. <i>Chemometrics and Intelligent Laboratory Systems</i> , <b>2019</b> , 194, 103855	3.8	7
23	Using two-dimensional convolutional neural networks for identifying GTP binding sites in Rab proteins. <i>Journal of Bioinformatics and Computational Biology</i> , <b>2019</b> , 17, 1950005	1	7
22	Radiomic Immunophenotyping of GSEA-Assessed Immunophenotypes of Glioblastoma and Its Implications for Prognosis: A Feasibility Study. <i>Cancers</i> , <b>2020</b> , 12,	6.6	7
21	Use Chou's 5-steps rule with different word embedding types to boost performance of electron transport protein prediction model. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , <b>2020</b> , PP,	3	7
20	Potential of deep representative learning features to interpret the sequence information in proteomics. <i>Proteomics</i> , <b>2021</b> , e2100232	4.8	6
19	A sequence-based prediction of Kruppel-like factors proteins using XGBoost and optimized features. <i>Gene</i> , <b>2021</b> , 787, 145643	3.8	5
18	In silico screening of sugar alcohol compounds to inhibit viral matrix protein VP40 of Ebola virus. <i>Molecular Biology Reports</i> , <b>2019</b> , 46, 3315-3324	2.8	4
17	Identifying GPSM Family Members as Potential Biomarkers in Breast Cancer: A Comprehensive Bioinformatics Analysis. <i>Biomedicines</i> , <b>2021</b> , 9,	4.8	4
16	TNFPred: identifying tumor necrosis factors using hybrid features based on word embeddings. <i>BMC Medical Genomics</i> , <b>2020</b> , 13, 155	3.7	3
15	Self-Organizing Double Function-Link Fuzzy Brain Emotional Control System Design for Uncertain Nonlinear Systems. <i>IEEE Transactions on Systems, Man, and Cybernetics: Systems</i> , <b>2020</b> , 1-17	7.3	3
14	Development and Validation of an Efficient MRI Radiomics Signature for Improving the Predictive Performance of 1p/19q Co-Deletion in Lower-Grade Gliomas. <i>Cancers</i> , <b>2021</b> , 13,	6.6	2
13	Identification of gene expression signatures for psoriasis classification using machine learning techniques <b>2020</b> , 1, 100001		2
12	Incorporating a transfer learning technique with amino acid embeddings to efficiently predict N-linked glycosylation sites in ion channels. <i>Computers in Biology and Medicine</i> , <b>2021</b> , 130, 104212	7	2

11	A Multiparametric MRI-Based Radiomics Analysis to Efficiently Classify Tumor Subregions of Glioblastoma: A Pilot Study in Machine Learning. <i>Journal of Clinical Medicine</i> , <b>2021</b> , 10,	5.1	2
10	Intelligent wavelet fuzzy brain emotional controller using dual function-link network for uncertain nonlinear control systems. <i>Applied Intelligence</i> , 1	4.9	2
9	Automatic Detection of Meniscus Tears Using Backbone Convolutional Neural Networks on Knee MRI. <i>Journal of Magnetic Resonance Imaging</i> ,	5.6	2
8	Using Language Representation Learning Approach to Efficiently Identify Protein Complex Categories in Electron Transport Chain. <i>Molecular Informatics</i> , <b>2020</b> , 39, e2000033	3.8	1
7	Development and Validation of Clinical Diagnostic Model for Girls with Central Precocious Puberty: Machine-learning Approaches.. <i>PLoS ONE</i> , <b>2022</b> , 17, e0261965	3.7	1
6	Using k-mer embeddings learned from a Skip-gram based neural network for building a cross-species DNA N6-methyladenine site prediction model. <i>Plant Molecular Biology</i> , <b>2021</b> , 107, 533-542	4.6	1
5	TNFPred: Identifying tumor necrosis factors using hybrid features based on word embeddings		1
4	Using Deep Learning with Position Specific Scoring Matrices to Identify Efflux Proteins in Membrane and Transport Proteins <b>2016</b> ,		1
3	mCNN-ETC: identifying electron transporters and their functional families by using multiple windows scanning techniques in convolutional neural networks with evolutionary information of protein sequences. <i>Briefings in Bioinformatics</i> , <b>2021</b> ,	13.4	1
2	Machine Learning Algorithm for Distinguishing Ductal Carcinoma In Situ from Invasive Breast Cancer. <i>Cancers</i> , <b>2022</b> , 14, 2437	6.6	0
1	Exploiting Two-Layer Support Vector Machine to Predict Protein SUMOylation Sites. <i>Lecture Notes in Networks and Systems</i> , <b>2019</b> , 324-332	0.5	