

Nguyen-Quoc-Khanh Le

List of Publications by Year in Descending Order

Source: <https://exaly.com/author-pdf/9525446/nguyen-quoc-khanh-le-publications-by-year.pdf>

Version: 2024-04-27

This document has been generated based on the publications and citations recorded by exaly.com. For the latest version of this publication list, visit the link given above.

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	Development and Validation of Clinical Diagnostic Model for Girls with Central Precocious Puberty: Machine-learning Approaches.. <i>PLoS ONE</i> , 2022 , 17, e0261965	3.7	1
63	An AI-based prediction model for drug-drug interactions in osteoporosis and Paget's diseases from SMILES.. <i>Molecular Informatics</i> , 2022 ,	3.8	13
62	Machine Learning Algorithm for Distinguishing Ductal Carcinoma In Situ from Invasive Breast Cancer. <i>Cancers</i> , 2022 , 14, 2437	6.6	0
61	Potential of deep representative learning features to interpret the sequence information in proteomics. <i>Proteomics</i> , 2021 , e2100232	4.8	6
60	Improved Prediction Model of Protein Lysine Crotonylation Sites Using Bidirectional Recurrent Neural Networks. <i>Journal of Proteome Research</i> , 2021 ,	5.6	11
59	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> , 2021 , 107, 533-542	4.6	1
58	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> , 2021 , 13,	6.6	2
57	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> , 2021 , 18, 2189-2197	3	31
56	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> , 2021 , 130, 104212	7	2
55	FAD-BERT: Improved prediction of FAD binding sites using pre-training of deep bidirectional transformers. <i>Computers in Biology and Medicine</i> , 2021 , 131, 104258	7	8
54	Radiomics-based machine learning model for efficiently classifying transcriptome subtypes in glioblastoma patients from MRI. <i>Computers in Biology and Medicine</i> , 2021 , 132, 104320	7	29
53	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> , 2021 , 10,	5.1	2
52	A sequence-based prediction of Kruppel-like factors proteins using XGBoost and optimized features. <i>Gene</i> , 2021 , 787, 145643	3.8	5
51	Risk Score Generated from CT-Based Radiomics Signatures for Overall Survival Prediction in Non-Small Cell Lung Cancer. <i>Cancers</i> , 2021 , 13,	6.6	8
50	Using deep neural networks and biological subwords to detect protein S-sulfenylation sites. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	36
49	A transformer architecture based on BERT and 2D convolutional neural network to identify DNA enhancers from sequence information. <i>Briefings in Bioinformatics</i> , 2021 , 22,	13.4	28
48	Machine Learning-Based Radiomics Signatures for EGFR and KRAS Mutations Prediction in Non-Small-Cell Lung Cancer. <i>International Journal of Molecular Sciences</i> , 2021 , 22,	6.3	13

47	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> , 2021 ,	13.4	1
46	Identifying GPSM Family Members as Potential Biomarkers in Breast Cancer: A Comprehensive Bioinformatics Analysis. <i>Biomedicines</i> , 2021 , 9,	4.8	4
45	Deep transformers and convolutional neural network in identifying DNA N6-methyladenine sites in cross-species genomes.. <i>Methods</i> , 2021 ,	4.6	12
44	TNFPred: identifying tumor necrosis factors using hybrid features based on word embeddings. <i>BMC Medical Genomics</i> , 2020 , 13, 155	3.7	3
43	Using Language Representation Learning Approach to Efficiently Identify Protein Complex Categories in Electron Transport Chain. <i>Molecular Informatics</i> , 2020 , 39, e2000033	3.8	1
42	Using extreme gradient boosting to identify origin of replication in <i>Saccharomyces cerevisiae</i> via hybrid features. <i>Genomics</i> , 2020 , 112, 2445-2451	4.3	29
41	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> , 2020 , 1-17	7.3	3
40	Identification of gene expression signatures for psoriasis classification using machine learning techniques 2020 , 1, 100001		2
39	. <i>IEEE Transactions on Industrial Electronics</i> , 2020 , 67, 9671-9682	8.9	23
38	Radiomic Immunophenotyping of GSEA-Assessed Immunophenotypes of Glioblastoma and Its Implications for Prognosis: A Feasibility Study. <i>Cancers</i> , 2020 , 12,	6.6	7
37	Incorporating convolutional neural networks and sequence graph transform for identifying multilabel protein Lysine PTM sites. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2020 , 206, 104171	3.8	15
36	Machine Learning Model for Identifying Antioxidant Proteins Using Features Calculated from Primary Sequences. <i>Biology</i> , 2020 , 9,	4.9	27
35	XGBoost Improves Classification of MGMT Promoter Methylation Status in IDH1 Wildtype Glioblastoma. <i>Journal of Personalized Medicine</i> , 2020 , 10,	3.6	41
34	A Computational Framework Based on Ensemble Deep Neural Networks for Essential Genes Identification. <i>International Journal of Molecular Sciences</i> , 2020 , 21,	6.3	31
33	DeepETC: A deep convolutional neural network architecture for investigating and classifying electron transport chain complexes. <i>Neurocomputing</i> , 2020 , 375, 71-79	5.4	27
32	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> , 2020 , PP,	3	7
31	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> , 2019 , 194, 103855	3.8	7
30	Using two-dimensional convolutional neural networks for identifying GTP binding sites in Rab proteins. <i>Journal of Bioinformatics and Computational Biology</i> , 2019 , 17, 1950005	1	7

29	Identification of clathrin proteins by incorporating hyperparameter optimization in deep learning and PSSM profiles. <i>Computer Methods and Programs in Biomedicine</i> , 2019 , 177, 81-88	6.9	38
28	Using word embedding technique to efficiently represent protein sequences for identifying substrate specificities of transporters. <i>Analytical Biochemistry</i> , 2019 , 577, 73-81	3.1	15
27	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> , 2019 , 294, 1173-1182	3.1	44
26	In silico screening of sugar alcohol compounds to inhibit viral matrix protein VP40 of Ebola virus. <i>Molecular Biology Reports</i> , 2019 , 46, 3315-3324	2.8	4
25	iMotor-CNN: Identifying molecular functions of cytoskeleton motor proteins using 2D convolutional neural network via Chou's 5-step rule. <i>Analytical Biochemistry</i> , 2019 , 575, 17-26	3.1	43
24	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> , 2019 , 18, 3503-3511	5.6	33
23	Prediction of ATP-binding sites in membrane proteins using a two-dimensional convolutional neural network. <i>Journal of Molecular Graphics and Modelling</i> , 2019 , 92, 86-93	2.8	10
22	ET-GRU: using multi-layer gated recurrent units to identify electron transport proteins. <i>BMC Bioinformatics</i> , 2019 , 20, 377	3.6	32
21	Ensemble of Deep Recurrent Neural Networks for Identifying Enhancers via Dinucleotide Physicochemical Properties. <i>Cells</i> , 2019 , 8,	7.9	12
20	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> , 2019 , 7, 305	5.8	37
19	Computational identification of vesicular transport proteins from sequences using deep gated recurrent units architecture. <i>Computational and Structural Biotechnology Journal</i> , 2019 , 17, 1245-1254	6.8	28
18	SNARE-CNN: a 2D convolutional neural network architecture to identify SNARE proteins from high-throughput sequencing data. <i>PeerJ Computer Science</i> , 2019 , 5, e177	2.7	31
17	iEnhancer-5Step: Identifying enhancers using hidden information of DNA sequences via Chou's 5-step rule and word embedding. <i>Analytical Biochemistry</i> , 2019 , 571, 53-61	3.1	76
16	Application of Computational Biology and Artificial Intelligence Technologies in Cancer Precision Drug Discovery. <i>BioMed Research International</i> , 2019 , 2019, 8427042	3	25
15	Classification of adaptor proteins using recurrent neural networks and PSSM profiles. <i>BMC Genomics</i> , 2019 , 20, 966	4.5	8
14	iEnhancer-ECNN: identifying enhancers and their strength using ensembles of convolutional neural networks. <i>BMC Genomics</i> , 2019 , 20, 951	4.5	20
13	Identifying SNAREs by Incorporating Deep Learning Architecture and Amino Acid Embedding Representation. <i>Frontiers in Physiology</i> , 2019 , 10, 1501	4.6	25
12	Exploiting Two-Layer Support Vector Machine to Predict Protein SUMOylation Sites. <i>Lecture Notes in Networks and Systems</i> , 2019 , 324-332	0.5	

11	DeepEfflux: a 2D convolutional neural network model for identifying families of efflux proteins in transporters. <i>Bioinformatics</i> , 2018 , 34, 3111-3117	7.2	24
10	Classifying the molecular functions of Rab GTPases in membrane trafficking using deep convolutional neural networks. <i>Analytical Biochemistry</i> , 2018 , 555, 33-41	3.1	46
9	Incorporating post translational modification information for enhancing the predictive performance of membrane transport proteins. <i>Computational Biology and Chemistry</i> , 2018 , 77, 251-260	3.6	10
8	Identifying the molecular functions of electron transport proteins using radial basis function networks and biochemical properties. <i>Journal of Molecular Graphics and Modelling</i> , 2017 , 73, 166-178	2.8	26
7	Incorporating deep learning with convolutional neural networks and position specific scoring matrices for identifying electron transport proteins. <i>Journal of Computational Chemistry</i> , 2017 , 38, 2000-2006	3.5	65
6	Incorporating efficient radial basis function networks and significant amino acid pairs for predicting GTP binding sites in transport proteins. <i>BMC Bioinformatics</i> , 2016 , 17, 501	3.6	18
5	Using Deep Learning with Position Specific Scoring Matrices to Identify Efflux Proteins in Membrane and Transport Proteins 2016 ,		1
4	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> , 2016 , 17, 298	3.6	41
3	TNFPred: Identifying tumor necrosis factors using hybrid features based on word embeddings		1
2	Intelligent wavelet fuzzy brain emotional controller using dual function-link network for uncertain nonlinear control systems. <i>Applied Intelligence</i> , 1	4.9	2
1	Automatic Detection of Meniscus Tears Using Backbone Convolutional Neural Networks on Knee MRI. <i>Journal of Magnetic Resonance Imaging</i> ,	5.6	2