

# Han Wang

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4455565/publications.pdf>

Version: 2024-02-01

29  
papers

267  
citations

1039880

9  
h-index

996849

15  
g-index

31  
all docs

31  
docs citations

31  
times ranked

339  
citing authors

#	ARTICLE	IF	CITATIONS
1	Understanding Membrane Protein Drug Targets in Computational Perspective. <i>Current Drug Targets</i> , 2019, 20, 551-564.	1.0	45
2	Deep learning architecture for iris recognition based on optimal Gabor filters and deep belief network. <i>Journal of Electronic Imaging</i> , 2017, 26, 023005.	0.5	36
3	SERS studies on normal epithelial and cancer cells derived from clinical breast cancer specimens. <i>Spectrochimica Acta - Part A: Molecular and Biomolecular Spectroscopy</i> , 2020, 237, 118364.	2.0	20
4	MPLs-Pred: Predicting Membrane Protein-Ligand Binding Sites Using Hybrid Sequence-Based Features and Ligand-Specific Models. <i>International Journal of Molecular Sciences</i> , 2019, 20, 3120.	1.8	16
5	Predicting siRNA efficacy based on multiple selective siRNA representations and their combination at score level. <i>Scientific Reports</i> , 2017, 7, 44836.	1.6	15
6	TMPSS: A Deep Learning-Based Predictor for Secondary Structure and Topology Structure Prediction of Alpha-Helical Transmembrane Proteins. <i>Frontiers in Bioengineering and Biotechnology</i> , 2020, 8, 629937.	2.0	14
7	Research on Single Nucleotide Polymorphisms Interaction Detection from Network Perspective. <i>PLoS ONE</i> , 2015, 10, e0119146.	1.1	14
8	Transmembrane Protein Alignment and Fold Recognition Based on Predicted Topology. <i>PLoS ONE</i> , 2013, 8, e69744.	1.1	13
9	Protein Function Prediction Using Function Associations in Protein-Protein Interaction Network. <i>IEEE Access</i> , 2018, 6, 30892-30902.	2.6	12
10	PsyMuKB: An Integrative De Novo Variant Knowledge Base for Developmental Disorders. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 453-464.	3.0	10
11	Relevance popularity: A term event model based feature selection scheme for text classification. <i>PLoS ONE</i> , 2017, 12, e0174341.	1.1	8
12	Improving transmembrane protein consensus topology prediction using inter-helical interaction. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 2012, 1818, 2679-2686.	1.4	7
13	TMP-SSurface: A Deep Learning-Based Predictor for Surface Accessibility of Transmembrane Protein Residues. <i>Crystals</i> , 2019, 9, 640.	1.0	7
14	OMPcontact: An Outer Membrane Protein Inter-Barrel Residue Contact Prediction Method. <i>Journal of Computational Biology</i> , 2017, 24, 217-228.	0.8	6
15	Prediction of Metal Ion Binding Sites of Transmembrane Proteins. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-11.	0.7	6
16	A Decision-Making Supporting Prediction Method for Breast Cancer Neoadjuvant Chemotherapy. <i>Frontiers in Oncology</i> , 2020, 10, 592556.	1.3	5
17	TMP-SSurface2: A Novel Deep Learning-Based Surface Accessibility Predictor for Transmembrane Protein Sequence. <i>Frontiers in Genetics</i> , 2021, 12, 656140.	1.1	5
18	A Sequential Segment Based Alpha-Helical Transmembrane Protein Alignment Method. <i>International Journal of Biological Sciences</i> , 2018, 14, 901-906.	2.6	4

#	ARTICLE	IF	CITATIONS
19	DMCTOP: Topology Prediction of Alpha-Helical Transmembrane Protein Based on Deep Multi-Scale Convolutional Neural Network. , 2019, , .		4
20	TM-ZC: A Deep Learning-Based Predictor for the Z-Coordinate of Residues in $\hat{\alpha}$ -Helical Transmembrane Proteins. IEEE Access, 2020, 8, 40129-40137.	2.6	4
21	GECluster: a novel protein complex prediction method. Biotechnology and Biotechnological Equipment, 2014, 28, 753-761.	0.5	3
22	A Term Frequency Based Weighting Scheme Using Naïve Bayes for Text Classification. Journal of Computational and Theoretical Nanoscience, 2016, 13, 319-326.	0.4	3
23	A Topology Structure Based Outer Membrane Proteins Segment Alignment Method. Mathematical Problems in Engineering, 2013, 2013, 1-10.	0.6	2
24	An Improved Topology Prediction of Alpha-Helical Transmembrane Protein Based on Deep Multi-Scale Convolutional Neural Network. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2022, 19, 295-304.	1.9	2
25	Computational Identification and Analysis of Ubiquinone-Binding Proteins. Cells, 2020, 9, 520.	1.8	2
26	IMPCContact: An Interhelical Residue Contact Prediction Method. BioMed Research International, 2020, 2020, 1-10.	0.9	2
27	Discover the Binding Domain of Transmembrane Proteins Based on Structural Universality. , 2021, , .		1
28	MRMD-palm: A novel method for the identification of palmitoylated protein. Chemometrics and Intelligent Laboratory Systems, 2021, 210, 104245.	1.8	0
29	SeqTMPPI: Sequence-Based Transmembrane Protein Interaction Prediction. , 2020, , .		0