

# Han Wang

## List of Publications by Year in descending order

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29  
papers

267  
citations

1039880

9  
h-index

996849

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g-index

31  
all docs

31  
docs citations

31  
times ranked

339  
citing authors

#	ARTICLE	IF	CITATIONS
1	An Improved Topology Prediction of Alpha-Helical Transmembrane Protein Based on Deep Multi-Scale Convolutional Neural Network. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2022, 19, 295-304.	1.9	2
2	MRMD-palm: A novel method for the identification of palmitoylated protein. <i>Chemometrics and Intelligent Laboratory Systems</i> , 2021, 210, 104245.	1.8	0
3	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
4	Prediction of Metal Ion Binding Sites of Transmembrane Proteins. <i>Computational and Mathematical Methods in Medicine</i> , 2021, 2021, 1-11.	0.7	6
5	Discover the Binding Domain of Transmembrane Proteins Based on Structural Universality. , 2021, , .		1
6	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
7	Computational Identification and Analysis of Ubiquinone-Binding Proteins. <i>Cells</i> , 2020, 9, 520.	1.8	2
8	TM-ZC: A Deep Learning-Based Predictor for the Z-Coordinate of Residues in $\alpha$ -Helical Transmembrane Proteins. <i>IEEE Access</i> , 2020, 8, 40129-40137.	2.6	4
9	IMPContact: An Interhelical Residue Contact Prediction Method. <i>BioMed Research International</i> , 2020, 2020, 1-10.	0.9	2
10	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
11	A Decision-Making Supporting Prediction Method for Breast Cancer Neoadjuvant Chemotherapy. <i>Frontiers in Oncology</i> , 2020, 10, 592556.	1.3	5
12	SeqTMPPI: Sequence-Based Transmembrane Protein Interaction Prediction. , 2020, , .		0
13	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
14	DMCTOP: Topology Prediction of Alpha-Helical Transmembrane Protein Based on Deep Multi-Scale Convolutional Neural Network. , 2019, , .		4
15	PsyMuKB: An Integrative De Novo Variant Knowledge Base for Developmental Disorders. <i>Genomics, Proteomics and Bioinformatics</i> , 2019, 17, 453-464.	3.0	10
16	TMP-SSurface: A Deep Learning-Based Predictor for Surface Accessibility of Transmembrane Protein Residues. <i>Crystals</i> , 2019, 9, 640.	1.0	7
17	Understanding Membrane Protein Drug Targets in Computational Perspective. <i>Current Drug Targets</i> , 2019, 20, 551-564.	1.0	45
18	Protein Function Prediction Using Function Associations in Protein-Protein Interaction Network. <i>IEEE Access</i> , 2018, 6, 30892-30902.	2.6	12

#	ARTICLE	IF	CITATIONS
19	A Sequential Segment Based Alpha-Helical Transmembrane Protein Alignment Method. International Journal of Biological Sciences, 2018, 14, 901-906.	2.6	4
20	Deep learning architecture for iris recognition based on optimal Gabor filters and deep belief network. Journal of Electronic Imaging, 2017, 26, 023005.	0.5	36
21	Predicting siRNA efficacy based on multiple selective siRNA representations and their combination at score level. Scientific Reports, 2017, 7, 44836.	1.6	15
22	OMPcontact: An Outer Membrane Protein Inter-Barrel Residue Contact Prediction Method. Journal of Computational Biology, 2017, 24, 217-228.	0.8	6
23	Relevance popularity: A term event model based feature selection scheme for text classification. PLoS ONE, 2017, 12, e0174341.	1.1	8
24	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
25	Research on Single Nucleotide Polymorphisms Interaction Detection from Network Perspective. PLoS ONE, 2015, 10, e0119146.	1.1	14
26	GECluster: a novel protein complex prediction method. Biotechnology and Biotechnological Equipment, 2014, 28, 753-761.	0.5	3
27	A Topology Structure Based Outer Membrane Proteins Segment Alignment Method. Mathematical Problems in Engineering, 2013, 2013, 1-10.	0.6	2
28	Transmembrane Protein Alignment and Fold Recognition Based on Predicted Topology. PLoS ONE, 2013, 8, e69744.	1.1	13
29	Improving transmembrane protein consensus topology prediction using inter-helical interaction. Biochimica Et Biophysica Acta - Biomembranes, 2012, 1818, 2679-2686.	1.4	7