

# Jaswinder Singh

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/2623548/publications.pdf>

Version: 2024-02-01

14  
papers

513  
citations

1040056

9  
h-index

1199594

12  
g-index

16  
all docs

16  
docs citations

16  
times ranked

374  
citing authors

#	ARTICLE	IF	CITATIONS
1	SPOT-Contact-LM: improving single-sequence-based prediction of protein contact map using a transformer language model. <i>Bioinformatics</i> , 2022, 38, 1888-1894.	4.1	25
2	Probing RNA structures and functions by solvent accessibility: an overview from experimental and computational perspectives. <i>Briefings in Bioinformatics</i> , 2022, 23, .	6.5	13
3	Reaching alignment-profile-based accuracy in predicting protein secondary and tertiary structural properties without alignment. <i>Scientific Reports</i> , 2022, 12, 7607.	3.3	14
4	Predicting RNA distance-based contact maps by integrated deep learning on physics-inferred secondary structure and evolutionary-derived mutational coupling. <i>Bioinformatics</i> , 2022, 38, 3900-3910.	4.1	14
5	Single-sequence and profile-based prediction of RNA solvent accessibility using dilated convolutional neural network. <i>Bioinformatics</i> , 2021, 36, 5169-5176.	4.1	21
6	Improved RNA secondary structure and tertiary base-pairing prediction using evolutionary profile, mutational coupling and two-dimensional transfer learning. <i>Bioinformatics</i> , 2021, 37, 2589-2600.	4.1	47
7	RNA Backbone Torsion and Pseudotorsion Angle Prediction Using Dilated Convolutional Neural Networks. <i>Journal of Chemical Information and Modeling</i> , 2021, 61, 2610-2622.	5.4	12
8	RNAcmap: a fully automatic pipeline for predicting contact maps of RNAs by evolutionary coupling analysis. <i>Bioinformatics</i> , 2021, 37, 3494-3500.	4.1	27
9	SPOT-1D-Single: improving the single-sequence-based prediction of protein secondary structure, backbone angles, solvent accessibility and half-sphere exposures using a large training set and ensembled deep learning. <i>Bioinformatics</i> , 2021, 37, 3464-3472.	4.1	22
10	SPOT-1D2: Improving Protein Secondary Structure Prediction using High Sequence Identity Training Set and an Ensemble of Recurrent and Residual-convolutional Neural Networks. , 2021, , .		1
11	RNA secondary structure prediction using an ensemble of two-dimensional deep neural networks and transfer learning. <i>Nature Communications</i> , 2019, 10, 5407.	12.8	214
12	Single-sequence-based prediction of protein secondary structures and solvent accessibility by deep whole-sequence learning. <i>Journal of Computational Chemistry</i> , 2018, 39, 2210-2216.	3.3	84
13	The effect of thin insulating layers on surface fields from a 433MHz transmitter inside the human body. , 2018, , .		1
14	Detecting Proline and Non-Proline Cis Isomers in Protein Structures from Sequences Using Deep Residual Ensemble Learning. <i>Journal of Chemical Information and Modeling</i> , 2018, 58, 2033-2042.	5.4	13