

# Jing He

## List of Publications by Year in descending order

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73  
papers

1,098  
citations

623574

14  
h-index

434063

31  
g-index

74  
all docs

74  
docs citations

74  
times ranked

567  
citing authors

| #  | ARTICLE   | IF  | CITATIONS |
|----|---|-----|-----------|
| 1  | 3D reconstruction from cryo-EM projection images using two spherical embeddings. <i>Communications Biology</i> , 2022, 5, 304.  | 2.0 | 3         |
| 2  | Interpreting Cytoskeletal Filaments in Cryo-Electron Tomograms with Shape-Constrained Deconvolution. <i>Microscopy and Microanalysis</i> , 2021, 27, 72-73.                             | 0.2 | 0         |
| 3  | Tracing Filaments in Simulated and Experimental 3D Cryo-Electron Tomography Maps Using a Fast Dynamic Programming Algorithm. <i>Microscopy and Microanalysis</i> , 2021, 27, 3236-3237. | 0.2 | 1         |
| 4  | A Tool for Segmentation of Secondary Structures in 3D Cryo-EM Density Map Components Using Deep Convolutional Neural Networks. <i>Frontiers in Bioinformatics</i> , 2021, 1, .          | 1.0 | 12        |
| 5  | Combining Cryo-EM Density Map and Residue Contact for Protein Secondary Structure Topologies. <i>Molecules</i> , 2021, 26, 7049.  | 1.7 | 0         |
| 6  | TomoSim: Simulation of Filamentous Cryo-Electron Tomograms. , 2021, , .   |     | 5         |
| 7  | Correction of Missing-Wedge Artifacts in Filamentous Tomograms by Template-Based Constrained Deconvolution. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2626-2633.  | 2.5 | 9         |
| 8  | A cryo-tomography-based volumetric model of the actin core of mouse vestibular hair cell stereocilia lacking plastin 1. <i>Journal of Structural Biology</i> , 2020, 210, 107461.       | 1.3 | 14        |
| 9  | Outlier Profiles of Atomic Structures Derived from X-ray Crystallography and from Cryo-Electron Microscopy. <i>Molecules</i> , 2020, 25, 1540.  | 1.7 | 1         |
| 10 | Cylindrical Similarity Measurement for Helices in Medium-Resolution Cryo-Electron Microscopy Density Maps. <i>Journal of Chemical Information and Modeling</i> , 2020, 60, 2644-2650.   | 2.5 | 12        |
| 11 | Combine Cryo-EM Density Map and Residue Contact for Protein Structure Prediction. , 2020, , .   |     | 0         |
| 12 | Using Curriculum Learning in Pattern Recognition of 3-dimensional Cryo-electron Microscopy Density Maps. , 2020, , .  |     | 2         |
| 13 | A Histogram-based Outlier Profile for Atomic Structures Derived from Cryo-Electron Microscopy. , 2019, , .  |     | 2         |
| 14 | Quantification of Twist from the Central Lines of $\beta^2$ -Strands. <i>Journal of Computational Biology</i> , 2018, 25, 114-120.  | 0.8 | 1         |
| 15 | <i>Special Issue</i>Preface: The 9th Computational Structural Bioinformatics Workshop. <i>Journal of Computational Biology</i> , 2018, 25, 1-2.   | 0.8 | 2         |
| 16 | Using Combined Features to Analyze Atomic Structures derived from Cryo-EM Density Maps. , 2018, , .   |     | 1         |
| 17 | Exploratory Studies Detecting Secondary Structures in Medium Resolution 3D Cryo-EM Images Using Deep Convolutional Neural Networks. , 2018, , .   |     | 4         |
| 18 | An Investigation of Atomic Structures Derived from X-ray Crystallography and Cryo-Electron Microscopy Using Distal Blocks of Side-Chains. <i>Molecules</i> , 2018, 23, 610.             | 1.7 | 4         |

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|----|--|-----|-----------|
| 19 | Tracing Actin Filament Bundles in Three-Dimensional Electron Tomography Density Maps of Hair Cell Stereocilia. <i>Molecules</i> , 2018, 23, 882.   | 1.7 | 15        |
| 20 | A Pattern Recognition Tool for Medium-Resolution Cryo-EM Density Maps and Low-Resolution Cryo-ET Density Maps. <i>Lecture Notes in Computer Science</i> , 2018, , 233-238.   | 1.0 | 1         |
| 21 | An Effective Computational Method Incorporating Multiple Secondary Structure Predictions in Topology Determination for Cryo-EM Images. <i>IEEE/ACM Transactions on Computational Biology and Bioinformatics</i> , 2017, 14, 578-586. | 1.9 | 19        |
| 22 | Preface: Selected Articles from 2015 Computational Structural Bioinformatics Workshop. <i>Journal of Computational Biology</i> , 2017, 24, 1-1.  | 0.8 | 4         |
| 23 | Comparing an Atomic Model or Structure to a Corresponding Cryo-electron Microscopy Image at the Central Axis of a Helix. <i>Journal of Computational Biology</i> , 2017, 24, 52-67.  | 0.8 | 8         |
| 24 | Detection of Protein Secondary Structure Patterns from 3D Cryo-TEM Maps at Medium Resolution - Combining the Best of SSETracer and VolTrac. <i>Microscopy and Microanalysis</i> , 2017, 23, 242-243.                                 | 0.2 | 1         |
| 25 | Analysis of Å-Å-strand Twist from the 3-dimensional Image of a Protein. , 2017, , .  |     | 0         |
| 26 | Modeling Beta-Traces for Beta-Barrels from Cryo-EM Density Maps. <i>BioMed Research International</i> , 2017, 2017, 1-9.   | 0.9 | 11        |
| 27 | An Iterative BÄ©zier Method for Fitting Beta-sheet Component of a Cryo-EM Density Map. <i>Computational and Mathematical Biophysics</i> , 2017, 5, 31-39.  | 0.6 | 0         |
| 28 | Constrained cyclic coordinate descent for cryo-EM images at medium resolutions: beyond the protein loop closure problem. <i>Robotica</i> , 2016, 34, 1777-1790.  | 1.3 | 13        |
| 29 | Challenges in matching secondary structures in cryo-EM: An exploration. , 2016, 2016, 1714-1719.   |     | 1         |
| 30 | Deep convolutional neural networks for detecting secondary structures in protein density maps from cryo-electron microscopy. , 2016, 2016, 41-46.  |     | 47        |
| 31 | Selecting near-native structures from decoys using maximal cliques. , 2016, , .  |     | 0         |
| 32 | Numerical geometry of map and model assessment. <i>Journal of Structural Biology</i> , 2015, 192, 255-261.   | 1.3 | 18        |
| 33 | Comparison of an atomic model and its cryo-EM image at the central axis of a helix. , 2015, 2015, 1253-1259.   |     | 1         |
| 34 | Deriving Protein Backbone Using Traces Extracted from Density Maps at Medium Resolutions. <i>Lecture Notes in Computer Science</i> , 2015, , 1-11.   | 1.0 | 1         |
| 35 | The 7th Computational Structural Bioinformatics Workshop. <i>Journal of Computational Biology</i> , 2015, 22, 785-786.   | 0.8 | 0         |
| 36 | A Dynamic Programming Algorithm for Finding the Optimal Placement of a Secondary Structure Topology in Cryo-EM Data. <i>Journal of Computational Biology</i> , 2015, 22, 837-843.  | 0.8 | 10        |

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|----|---|-----|-----------|
| 37 | Detection of Secondary Structures from 3D Protein Images of Medium Resolutions and its Challenges. Lecture Notes in Computer Science, 2015, , 147-155.  | 1.0 | 1         |
| 38 | Combining image processing and modeling to generate traces of beta-strands from cryo-EM density images of beta-barrels. , 2014, 2014, 3941-4.   |     | 2         |
| 39 | Orientations of beta-strand traces and near maximum twist. , 2014, , .  |     | 3         |
| 40 | Construction of protein backbone pieces using segment-based FBCCD and Cryo-EM skeleton. , 2014, , .   |     | 0         |
| 41 | Tracing Beta Strands Using StrandTwister from Cryo-EM Density Maps at Medium Resolutions. Structure, 2014, 22, 1665-1676.   | 1.6 | 39        |
| 42 | A distanceâ€•and orientationâ€•dependent energy function of amino acid key blocks. Biopolymers, 2014, 101, 681-692.   | 1.2 | 7         |
| 43 | Solving the Secondary Structure Matching Problem in Cryo-EM De Novo Modeling Using a Constrained $\text{K}$ -Shortest Path Graph Algorithm. IEEE/ACM Transactions on Computational Biology and Bioinformatics. 2014, 11, 419-430. | 1.9 | 33        |
| 44 | The 6th Computational Structural Bioinformatics Workshop. BMC Structural Biology, 2013, 13, 11.   | 2.3 | 1         |
| 45 | Estimating loop length from CryoEM images at medium resolutions. BMC Structural Biology, 2013, 13, S5.  | 2.3 | 4         |
| 46 | A Constrained K-shortest Path Algorithm to Rank the Topologies of the Protein Secondary Structure Elements Detected in CryoEM Volume Maps. , 2013, , .  |     | 2         |
| 47 | Beta-sheet Detection and Representation from Medium Resolution Cryo-EM Density Maps. , 2013, , .  |     | 35        |
| 48 | Intensity-Based Skeletonization of CryoEM Gray-Scale Images Using a True Segmentation-Free Algorithm. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2013, 10, 1289-1298.                                     | 1.9 | 17        |
| 49 | Building the initial chain of the proteins through de novo modeling of the cryo-electron microscopy volume data at the medium resolutions. , 2012, , .  |     | 17        |
| 50 | CryoEM skeleton length estimation using a decimated curve. , 2012, , .  |     | 1         |
| 51 | IMPROVED EFFICIENCY IN CRYO-EM SECONDARY STRUCTURE TOPOLOGY DETERMINATION FROM INACCURATE DATA. Journal of Bioinformatics and Computational Biology, 2012, 10, 1242006.   | 0.3 | 12        |
| 52 | A Machine Learning Approach for the Identification of Protein Secondary Structure Elements from Electron Cryoâ€•Microscopy Density Maps. Biopolymers, 2012, 97, 698-708.  | 1.2 | 87        |
| 53 | A Constraint Dynamic Graph Approach to Identify the Secondary Structure Topology from cryoEM Density Data in Presence of Errors. , 2011, , .  |     | 1         |
| 54 | From Isotropic to Anisotropic Side Chain Representations: Comparison of Three Models for Residue Contact Estimation. PLoS ONE, 2011, 6, e19238.   | 1.1 | 17        |

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|----|---|-----|-----------|
| 55 | A distance and orientation dependent potential energy function with cluster energy. , 2011, , .   |     | 0         |
| 56 | RANKING VALID TOPOLOGIES OF THE SECONDARY STRUCTURE ELEMENTS USING A CONSTRAINT GRAPH. Journal of Bioinformatics and Computational Biology, 2011, 09, 415-430.                                    | 0.3 | 33        |
| 57 | Structure prediction for the helical skeletons detected from the low resolution protein density map. BMC Bioinformatics, 2010, 11, S44.   | 1.2 | 17        |
| 58 | Understanding on the residue contact network using the log-normal cluster model and the multilevel wheel diagram. Biopolymers, 2010, 93, 904-916.   | 1.2 | 7         |
| 59 | The 3rd Computational Structural Bioinformatics Workshop. BMC Structural Biology, 2010, 10, 11.   | 2.3 | 0         |
| 60 | Effect of sidechain anisotropy on residue contact determination. , 2009, , .  |     | 0         |
| 61 | Reduction of the secondary structure topological space through direct estimation of the contact energy formed by the secondary structures. BMC Bioinformatics, 2009, 10, S40.                     | 1.2 | 5         |
| 62 | Native secondary structure topology has near minimum contact energy among all possible geometrically constrained topologies. Proteins: Structure, Function and Bioinformatics, 2009, 77, 159-173. | 1.5 | 17        |
| 63 | An effective convergence independent loop closure method using Forward-Backward Cyclic Coordinate Descent. International Journal of Data Mining and Bioinformatics, 2009, 3, 346.                 | 0.1 | 12        |
| 64 | DERIVING TOPOLOGY AND SEQUENCE ALIGNMENT FOR THE HELIX SKELETON IN LOW-RESOLUTION PROTEIN DENSITY MAPS. Journal of Bioinformatics and Computational Biology, 2008, 06, 183-201.                   | 0.3 | 16        |
| 65 | Incorporating constraints from low resolution density map in ab initio structure prediction using Rosetta. , 2007, , .  |     | 1         |
| 66 | A Constraint Logic Programming approach to associate 1D and 3D structural components for large protein complexes. International Journal of Data Mining and Bioinformatics, 2007, 1, 352.          | 0.1 | 1         |
| 67 | An approximate robotics algorithm to assemble a loop between two helices. , 2007, , .   |     | 1         |
| 68 | DERIVING PROTEIN STRUCTURE TOPOLOGY FROM THE HELIX SKELETON IN LOW RESOLUTION DENSITY MAP USING ROSETTA. , 2007, , .  |     | 3         |
| 69 | USING THE LENGTH CONSTRAINTS OF HELIX TO EVALUATE PROTEIN SECONDARY STRUCTURE PREDICTION FOR HELIX. , 2005, , .   |     | 0         |
| 70 | A Parallel Algorithm for Helix Mapping Between 3D and 1D Protein Structure Using the Length Constraints. Lecture Notes in Computer Science, 2004, , 746-756.                                      | 1.0 | 11        |
| 71 | Finding and using local symmetry in identifying lower domain movements in hexon subunits of the herpes simplex virus type 1 B capsid. Journal of Molecular Biology, 2001, 309, 903-914.           | 2.0 | 20        |
| 72 | Seeing the Herpesvirus Capsid at 8.5&nbsp;&Aring;&nbsp;&nbsp;. Science, 2000, 288, 877-880.   | 6.0 | 298       |

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|----|--|-----|-----------|
| 73 | Assembly of VP26 in herpes simplex virus-1 inferred from structures of wild-type and recombinant capsids. <i>Nature Structural and Molecular Biology</i> , 1995, 2, 1026-1030. | 3.6 | 152       |