

Jing He

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/5864887/publications.pdf>

Version: 2024-02-01

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	Seeing the Herpesvirus Capsid at 8.5Å. Science, 2000, 288, 877-880.	6.0	298
2	Assembly of VP26 in herpes simplex virus-1 inferred from structures of wild-type and recombinant capsids. Nature Structural and Molecular Biology, 1995, 2, 1026-1030.	3.6	152
3	A Machine Learning Approach for the Identification of Protein Secondary Structure Elements from Electron Cryo-EM Microscopy Density Maps. Biopolymers, 2012, 97, 698-708.	1.2	87
4	Deep convolutional neural networks for detecting secondary structures in protein density maps from cryo-electron microscopy. , 2016, 2016, 41-46.		47
5	Tracing Beta Strands Using StrandTwister from Cryo-EM Density Maps at Medium Resolutions. Structure, 2014, 22, 1665-1676.	1.6	39
6	Beta-sheet Detection and Representation from Medium Resolution Cryo-EM Density Maps. , 2013, , .		35
7	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
8	Solving the Secondary Structure Matching Problem in Cryo-EM De Novo Modeling Using a Constrained $\text{Shortest Path Graph Algorithm}$. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2014, 11, 419-430.	1.9	33
9	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
10	An Effective Computational Method Incorporating Multiple Secondary Structure Predictions in Topology Determination for Cryo-EM Images. IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2017, 14, 578-586.	1.9	19
11	Numerical geometry of map and model assessment. Journal of Structural Biology, 2015, 192, 255-261.	1.3	18
12	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
13	Structure prediction for the helical skeletons detected from the low resolution protein density map. BMC Bioinformatics, 2010, 11, S44.	1.2	17
14	From Isotropic to Anisotropic Side Chain Representations: Comparison of Three Models for Residue Contact Estimation. PLoS ONE, 2011, 6, e19238.	1.1	17
15	Building the initial chain of the proteins through de novo modeling of the cryo-electron microscopy volume data at the medium resolutions. , 2012, , .		17
16	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
17	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
18	Tracing Actin Filament Bundles in Three-Dimensional Electron Tomography Density Maps of Hair Cell Stereocilia. Molecules, 2018, 23, 882.	1.7	15

#	ARTICLE	IF	CITATIONS
19	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
20	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
21	An effective convergence independent loop closure method using Forward-Backward Cyclic Coordinate Descent. <i>International Journal of Data Mining and Bioinformatics</i> , 2009, 3, 346.	0.1	12
22	IMPROVED EFFICIENCY IN CRYO-EM SECONDARY STRUCTURE TOPOLOGY DETERMINATION FROM INACCURATE DATA. <i>Journal of Bioinformatics and Computational Biology</i> , 2012, 10, 1242006.	0.3	12
23	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
24	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
25	Modeling Beta-Traces for Beta-Barrels from Cryo-EM Density Maps. <i>BioMed Research International</i> , 2017, 2017, 1-9.	0.9	11
26	A Parallel Algorithm for Helix Mapping Between 3D and 1D Protein Structure Using the Length Constraints. <i>Lecture Notes in Computer Science</i> , 2004, , 746-756.	1.0	11
27	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
28	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
29	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
30	Understanding on the residue contact network using the log-normal cluster model and the multilevel wheel diagram. <i>Biopolymers</i> , 2010, 93, 904-916.	1.2	7
31	A distance- and orientation-dependent energy function of amino acid key blocks. <i>Biopolymers</i> , 2014, 101, 681-692.	1.2	7
32	Reduction of the secondary structure topological space through direct estimation of the contact energy formed by the secondary structures. <i>BMC Bioinformatics</i> , 2009, 10, S40.	1.2	5
33	TomoSim: Simulation of Filamentous Cryo-Electron Tomograms. , 2021, , .		5
34	Estimating loop length from CryoEM images at medium resolutions. <i>BMC Structural Biology</i> , 2013, 13, S5.	2.3	4
35	Preface: Selected Articles from 2015 Computational Structural Bioinformatics Workshop. <i>Journal of Computational Biology</i> , 2017, 24, 1-1.	0.8	4
36	Exploratory Studies Detecting Secondary Structures in Medium Resolution 3D Cryo-EM Images Using Deep Convolutional Neural Networks. , 2018, , .		4

#	ARTICLE	IF	CITATIONS
37	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
38	Orientations of beta-strand traces and near maximum twist. , 2014, , .		3
39	DERIVING PROTEIN STRUCTURE TOPOLOGY FROM THE HELIX SKELETON IN LOW RESOLUTION DENSITY MAP USING ROSETTA. , 2007, , .		3
40	3D reconstruction from cryo-EM projection images using two spherical embeddings. <i>Communications Biology</i> , 2022, 5, 304.	2.0	3
41	A Constrained K-shortest Path Algorithm to Rank the Topologies of the Protein Secondary Structure Elements Detected in CryoEM Volume Maps. , 2013, , .		2
42	Combining image processing and modeling to generate traces of beta-strands from cryo-EM density images of beta-barrels. , 2014, 2014, 3941-4.		2
43	<i>Special Issue</i> Preface: The 9th Computational Structural Bioinformatics Workshop. <i>Journal of Computational Biology</i> , 2018, 25, 1-2.	0.8	2
44	A Histogram-based Outlier Profile for Atomic Structures Derived from Cryo-Electron Microscopy. , 2019, , .		2
45	Using Curriculum Learning in Pattern Recognition of 3-dimensional Cryo-electron Microscopy Density Maps. , 2020, , .		2
46	Incorporating constraints from low resolution density map in ab initio structure prediction using Rosetta. , 2007, , .		1
47	A Constraint Logic Programming approach to associate 1D and 3D structural components for large protein complexes. <i>International Journal of Data Mining and Bioinformatics</i> , 2007, 1, 352.	0.1	1
48	An approximate robotics algorithm to assemble a loop between two helices. , 2007, , .		1
49	A Constraint Dynamic Graph Approach to Identify the Secondary Structure Topology from cryoEM Density Data in Presence of Errors. , 2011, , .		1
50	CryoEM skeleton length estimation using a decimated curve. , 2012, , .		1
51	The 6th Computational Structural Bioinformatics Workshop. <i>BMC Structural Biology</i> , 2013, 13, 11.	2.3	1
52	Comparison of an atomic model and its cryo-EM image at the central axis of a helix. , 2015, 2015, 1253-1259.		1
53	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
54	Challenges in matching secondary structures in cryo-EM: An exploration. , 2016, 2016, 1714-1719.		1

#	ARTICLE	IF	CITATIONS
55	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
56	Quantification of Twist from the Central Lines of $\hat{\nu}^2$ -Strands. <i>Journal of Computational Biology</i> , 2018, 25, 114-120.	0.8	1
57	Using Combined Features to Analyze Atomic Structures derived from Cryo-EM Density Maps. , 2018, , .		1
58	Outlier Profiles of Atomic Structures Derived from X-ray Crystallography and from Cryo-Electron Microscopy. <i>Molecules</i> , 2020, 25, 1540.	1.7	1
59	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
60	Detection of Secondary Structures from 3D Protein Images of Medium Resolutions and its Challenges. <i>Lecture Notes in Computer Science</i> , 2015, , 147-155.	1.0	1
61	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
62	Effect of sidechain anisotropy on residue contact determination. , 2009, , .		0
63	The 3rd Computational Structural Bioinformatics Workshop. <i>BMC Structural Biology</i> , 2010, 10, 11.	2.3	0
64	A distance and orientation dependent potential energy function with cluster energy. , 2011, , .		0
65	Construction of protein backbone pieces using segment-based FBCCD and Cryo-EM skeleton. , 2014, , .		0
66	The 7th Computational Structural Bioinformatics Workshop. <i>Journal of Computational Biology</i> , 2015, 22, 785-786.	0.8	0
67	Selecting near-native structures from decoys using maximal cliques. , 2016, , .		0
68	Analysis of $\hat{\nu}^2$ -strand Twist from the 3-dimensional Image of a Protein. , 2017, , .		0
69	An Iterative BÃ©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
70	Interpreting Cytoskeletal Filaments in Cryo-Electron Tomograms with Shape-Constrained Deconvolution. <i>Microscopy and Microanalysis</i> , 2021, 27, 72-73.	0.2	0
71	USING THE LENGTH CONSTRAINTS OF HELIX TO EVALUATE PROTEIN SECONDARY STRUCTURE PREDICTION FOR HELIX. , 2005, , .		0
72	Combine Cryo-EM Density Map and Residue Contact for Protein Structure Prediction. , 2020, , .		0

#	ARTICLE	IF	CITATIONS
73	Combining Cryo-EM Density Map and Residue Contact for Protein Secondary Structure Topologies. Molecules, 2021, 26, 7049.	1.7	0