Nurit Haspel

List of Publications by Year
in descending order

51 papers	958 citations	516561 16 h-index	454834 30 g-index
55 all docs	55 docs citations	55 times ranked	1156 citing authors

#	Article	IF	Citations
1	Active and Inactive Cdc42 Differ in Their Insert Region Conformational Dynamics. Biophysical Journal, 2021, 120, 306-318.	0.2	20
2	Integrating Rigidity Analysis into the Exploration of Protein Conformational Pathways Using RRT* and MC. Molecules, 2021, 26, 2329.	1.7	1
3	Protein hormone fragmentation in intercellular signaling: hormones as nested information systems. Biology of Reproduction, 2021, 104, 887-901.	1.2	5
4	Patch-DCA: improved protein interface prediction by utilizing structural information and clustering DCA scores. Bioinformatics, 2020, 36, 1460-1467.	1.8	10
5	Efficient Exploration of Protein Conformational Pathways using RRT* and MC. , 2020, , .		3
6	Fusion Transcript Detection from RNA-Seq using Jaccard Distance. , 2020, , .		3
7	Integrating Co-Evolutionary Information in Monte Carlo Based Method for Proteins Trajectory Simulation. , 2019, , .		3
8	Predicting the Effect of Single and Multiple Mutations on Protein Structural Stability. Molecules, 2018, 23, 251.	1.7	31
9	Preface: Selected Articles from 2015 Computational Structural Bioinformatics Workshop. Journal of Computational Biology, 2017, 24, 1-1.	0.8	4
10	A Protocol for the Design of Protein and Peptide Nanostructure Self-Assemblies Exploiting Synthetic Amino Acids. Methods in Molecular Biology, 2017, 1529, 323-352.	0.4	2
11	Introduction to selected papers from the 8th International Conference on Bioinformatics and Computational Biology (BICOB 2016). Journal of Bioinformatics and Computational Biology, 2017, 15, 1702002.	0.3	0
12	Machine Learning Approaches for Predicting Protein Complex Similarity. Journal of Computational Biology, 2017, 24, 40-51.	0.8	1
13	Methods for Detecting Critical Residues in Proteins. Methods in Molecular Biology, 2017, 1498, 227-242.	0.4	3
14	Detecting chromosomal structural variation using jaccard distance and parallel architecture. , 2017, , .		4
15	Detecting intermediate protein conformations using algebraic topology. BMC Bioinformatics, 2017, 18, 502.	1.2	10
16	Detecting intermediate protein conformations using algebraic topology. , 2016, , .		0
17	Introduction to the selected papers from the 7th International Conference on Bioinformatics and Computational Biology (BICoB 2015). Journal of Bioinformatics and Computational Biology, 2016, 14, 1602002.	0.3	0
18	Accurate refinement of docked protein complexes using evolutionary information and deep learning. Journal of Bioinformatics and Computational Biology, 2016, 14, 1642002.	0.3	16

#	Article	IF	Citations
19	A new DP algorithm for comparing gene expression data using geometric similarity. , 2015, , .		0
20	Accurate Prediction of Docked Protein Structure Similarity. Journal of Computational Biology, 2015, 22, 892-904.	0.8	5
21	The 7th Computational Structural Bioinformatics Workshop. Journal of Computational Biology, 2015, 22, 785-786.	0.8	0
22	TIDE: Inter-chromosomal translocation and insertion detection using embeddings. , 2014, , .		3
23	Molecular characterization of l-phenylalanine terminated poly(l-lactide) conjugates. RSC Advances, 2014, 4, 23231.	1.7	11
24	Sequence dependence of C-end rule peptides in binding and activation of neuropilin-1 receptor. Journal of Structural Biology, 2013, 182, 78-86.	1.3	58
25	An Evolutionary Conservation & Rigidity Analysis Machine Learning Approach for Detecting Critical Protein Residues. , 2013, , .		6
26	Multi-Resolution Rigidity-Based Sampling of Protein Conformational Paths. , 2013, , .		8
27	AN EVOLUTIONARY CONSERVATION-BASED METHOD FOR REFINING AND RERANKING PROTEIN COMPLEX STRUCTURES. Journal of Bioinformatics and Computational Biology, 2012, 10, 1242002.	0.3	19
28	Combining conservation and rigidity methods to detect critical residues in proteins. , 2012, , .		0
29	An evolutionary-guided iterative refinement approach for protein multimers. , 2012, , .		0
30	Refining multimeric protein complexes using conservation, electrostatics and probabilistic selection. , 2012, , .		2
31	GUIDING PROTEIN DOCKING WITH GEOMETRIC AND EVOLUTIONARY INFORMATION. Journal of Bioinformatics and Computational Biology, 2012, 10, 1242008.	0.3	11
32	Towards a hybrid method for detecting critical protein residues. , 2012, , .		1
33	Conformational Exploration of Two Peptides and Their Hybrid Polymer Conjugates: Potentialities As Self-Aggregating Materials. Journal of Physical Chemistry B, 2012, 116, 13941-13952.	1.2	7
34	THE 5TH INTERNATIONAL CONFERENCE ON BIO-INSPIRED MODELS OF NETWORK, INFORMATION AND COMPUTING SYSTEMS (BIONETICS 2010) SPECIAL TRACK ON BIOINFORMATICS. Journal of Bioinformatics and Computational Biology, 2011, 09, v-vii.	0.3	0
35	Tracing conformational changes in proteins. BMC Structural Biology, 2010, 10, S1.	2.3	61
36	Multiâ€scale characterization of the energy landscape of proteins with application to the C3D/Efbâ€C complex. Proteins: Structure, Function and Bioinformatics, 2010, 78, 1004-1014.	1.5	5

#	Article	IF	Citations
37	Tracing conformational changes in proteins. , 2009, , .		1
38	Protein Segments with Conformationally Restricted Amino Acids Can Control Supramolecular Organization at the Nanoscale. Journal of Chemical Information and Modeling, 2009, 49, 1623-1629.	2.5	14
39	Electrostatic contributions drive the interaction between Staphylococcus aureus protein Efbâ€C and its complement target C3d. Protein Science, 2008, 17, 1894-1906.	3.1	34
40	Novel insights into target specificities and molecular mechanisms for two potent complement evasion proteins from Staphylococcus aureus. Molecular Immunology, 2008, 45, 4114-4115.	1.0	0
41	Stability of Tubular Structures Based on Î²-Helical Proteins:â€‰ Self-Assembled versus Polymerized Nanoconstructs and Wild-Type versus Mutated Sequences. Biomacromolecules, 2007, 8, 3135-3146.	2.6	10
42	Changing the Charge Distribution of Î²-Helical-Based Nanostructures Can Provide the Conditions for Charge Transfer. Biophysical Journal, 2007, 93, 245-253.	0.2	18
43	Principles of nanostructure design with protein building blocks. Proteins: Structure, Function and Bioinformatics, 2007, 68, 1-12.	1.5	51
44	De Novo Tubular Nanostructure Design Based on Self-Assembly of Î²-Helical Protein Motifs. Structure, 2006, 14, 1137-1148.	1.6	41
45	Concepts and schemes for the re-engineering of physical protein modules: generating nanodevices via targeted replacements with constrained amino acids. Physical Biology, 2006, 3, S54-S62.	0.8	20
46	A Comparative Study of Amyloid Fibril Formation by Residues 15â€“19 of the Human Calcitonin Hormone: A Single Î²-Sheet Model with a Small Hydrophobic Core. Journal of Molecular Biology, 2005, 345, 1213-1227.	2.0	71
47	Side chain interactions determine the amyloid organization: a single layer Â-sheet molecular structure of the calcitonin peptide segment 15â€“19. Physical Biology, 2004, 1, 89-99.	0.8	19
48	The Stability and Dynamics of the Human Calcitonin Amyloid Peptide DFNKF. Biophysical Journal, 2004, 87, 146-158.	0.2	46
49	Reducing the computational complexity of protein folding via fragment folding and assembly. Protein Science, 2003, 12, 1177-1187.	3.1	48
50	Hierarchical protein folding pathways: A computational study of protein fragments. Proteins: Structure, Function and Bioinformatics, 2003, 51, 203-215.	1.5	29
51	Taking geometry to its edge: Fast unbound rigid (and hinge-bent) docking. Proteins: Structure, Function and Bioinformatics, 2003, 52, 107-112.	1.5	238