

Ronald D Hills Jr

List of Publications by Year in descending order

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Version: 2024-02-01

18
papers

1,369
citations

687363

13
h-index

839539

18
g-index

20
all docs

20
docs citations

20
times ranked

2000
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 1 | Gut Microbiome: Profound Implications for Diet and Disease. <i>Nutrients</i> , 2019, 11, 1613. | 4.1 | 615 |
| 2 | Insights from Coarse-Grained GÅ•Models for Protein Folding and Dynamics. <i>International Journal of Molecular Sciences</i> , 2009, 10, 889-905. | 4.1 | 228 |
| 3 | Multiscale Coarse-Graining of the Protein Energy Landscape. <i>PLoS Computational Biology</i> , 2010, 6, e1000827. | 3.2 | 116 |
| 4 | Hydrophobic Cooperativity as a Mechanism for Amyloid Nucleation. <i>Journal of Molecular Biology</i> , 2007, 368, 894-901. | 4.2 | 100 |
| 5 | Structure of the inhibitory region of troponin by site directed spin labeling electron paramagnetic resonance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002, 99, 12765-12770. | 7.1 | 61 |
| 6 | Subdomain Competition, Cooperativity, and Topological Frustration in the Folding of CheY. <i>Journal of Molecular Biology</i> , 2008, 382, 485-495. | 4.2 | 51 |
| 7 | Model parameters for simulation of physiological lipids. <i>Journal of Computational Chemistry</i> , 2016, 37, 1112-1118. | 3.3 | 36 |
| 8 | Topological Frustration in Î²-Repeat Proteins: Sequence Diversity Modulates the Conserved Folding Mechanisms of Î²/Î² Sandwich Proteins. <i>Journal of Molecular Biology</i> , 2010, 398, 332-350. | 4.2 | 29 |
| 9 | Mechanism of Binding Site Conformational Switching in the CD44â€™Hyaluronan Proteinâ€™Carbohydrate Binding Interaction. <i>Journal of Molecular Biology</i> , 2011, 406, 631-647. | 4.2 | 28 |
| 10 | Coarse grain lipidâ€™protein molecular interactions and diffusion with MsbA flippase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2012, 80, 2178-2190. | 2.6 | 23 |
| 11 | The Structure of the NXF2/NXT1 Heterodimeric Complex Reveals the Combined Specificity and Versatility of the NTF2-Like Fold. <i>Journal of Molecular Biology</i> , 2012, 415, 649-665. | 4.2 | 22 |
| 12 | Peptide Backbone Sampling Convergence with the Adaptive Biasing Force Algorithm. <i>Journal of Physical Chemistry B</i> , 2013, 117, 518-526. | 2.6 | 20 |
| 13 | Coevolution of Function and the Folding Landscape: Correlation with Density of Native Contacts. <i>Biophysical Journal</i> , 2008, 95, L57-L59. | 0.5 | 18 |
| 14 | Balancing Bond, Nonbond, and GÅ•Like Terms in Coarse Grain Simulations of Conformational Dynamics. <i>Methods in Molecular Biology</i> , 2014, 1084, 123-140. | 0.9 | 7 |
| 15 | Simulation of lipid-protein interactions with the CgProt force field. <i>AIMS Molecular Science</i> , 2017, 4, 352-369. | 0.5 | 6 |
| 16 | Refining amino acid hydrophobicity for dynamics simulation of membrane proteins. <i>PeerJ</i> , 2018, 6, e4230. | 2.0 | 5 |
| 17 | Guide to Popular Diets, Food Choices, and Their Health Outcome. <i>Health Care Current Reviews</i> , 2018, 06, . | 0.1 | 2 |
| 18 | Statin Treatment in Specific Patient Groups: Role for Improved Cardiovascular Risk Markers. <i>Journal of Clinical Medicine</i> , 2020, 9, 3748. | 2.4 | 2 |