

Francesco Rao

List of Publications by Citations

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

30
papers

1,467
citations

16
h-index

30
g-index

30
ext. papers

1,575
ext. citations

5
avg, IF

4.53
L-index

| # | Paper | IF | Citations |
|----|--|------|-----------|
| 30 | The protein folding network. <i>Journal of Molecular Biology</i> , 2004 , 342, 299-306 | 6.5 | 322 |
| 29 | Wordom: a program for efficient analysis of molecular dynamics simulations. <i>Bioinformatics</i> , 2007 , 23, 2625-7 | 7.2 | 227 |
| 28 | Wordom: a user-friendly program for the analysis of molecular structures, trajectories, and free energy surfaces. <i>Journal of Computational Chemistry</i> , 2011 , 32, 1183-94 | 3.5 | 187 |
| 27 | Replica exchange molecular dynamics simulations of reversible folding. <i>Journal of Chemical Physics</i> , 2003 , 119, 4035-4042 | 3.9 | 92 |
| 26 | Local modularity measure for network clusterizations. <i>Physical Review E</i> , 2005 , 72, 056107 | 2.4 | 87 |
| 25 | Three-dimensional infrared spectroscopy of isotope-substituted liquid water reveals heterogeneous dynamics. <i>Journal of Physical Chemistry B</i> , 2011 , 115, 6976-84 | 3.4 | 63 |
| 24 | Phi-value analysis by molecular dynamics simulations of reversible folding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005 , 102, 628-33 | 11.5 | 63 |
| 23 | The quest for self-consistency in hydrogen bond definitions. <i>Journal of Chemical Physics</i> , 2013 , 139, 084501 | 5.0 | 57 |
| 22 | Protein dynamics investigated by inherent structure analysis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010 , 107, 9152-7 | 11.5 | 49 |
| 21 | Beyond the binding site: the role of the H-loop and extra-domain structures in PDZ domains. <i>PLoS Computational Biology</i> , 2012 , 8, e1002429 | 5 | 35 |
| 20 | Structural inhomogeneity of water by complex network analysis. <i>Journal of Physical Chemistry B</i> , 2010 , 114, 15598-604 | 3.4 | 34 |
| 19 | Estimation of protein folding probability from equilibrium simulations. <i>Journal of Chemical Physics</i> , 2005 , 122, 184901 | 3.9 | 32 |
| 18 | Uncovering the topology of configuration space networks. <i>Physical Review E</i> , 2007 , 76, 026113 | 2.4 | 29 |
| 17 | Topological dynamics in supramolecular rotors. <i>Nano Letters</i> , 2014 , 14, 4461-8 | 11.5 | 28 |
| 16 | Structure-dynamics relationship in coherent transport through disordered systems. <i>Nature Communications</i> , 2013 , 4, 2296 | 17.4 | 20 |
| 15 | Towards a microscopic description of the free-energy landscape of water. <i>Journal of Chemical Physics</i> , 2012 , 137, 144504 | 3.9 | 18 |
| 14 | Consensus for the Fip35 folding mechanism?. <i>Journal of Chemical Physics</i> , 2013 , 139, 035102 | 3.9 | 16 |

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|----|--|-----|----|
| 13 | Structure and dynamics of water in crowded environments slows down peptide conformational changes. <i>Journal of Chemical Physics</i> , 2014 , 141, 045101 | 3.9 | 15 |
| 12 | Accounting for the kinetics in order parameter analysis: lessons from theoretical models and a disordered peptide. <i>Journal of Chemical Physics</i> , 2012 , 137, 194101 | 3.9 | 14 |
| 11 | Water structure-forming capabilities are temperature shifted for different models. <i>Journal of Physical Chemistry B</i> , 2012 , 116, 7538-43 | 3.4 | 12 |
| 10 | Computational Screening of Rhodopsin Mutations Associated with Retinitis Pigmentosa. <i>Journal of Chemical Theory and Computation</i> , 2009 , 5, 2472-85 | 6.4 | 12 |
| 9 | Network analysis of proton transfer in liquid water. <i>Journal of Chemical Physics</i> , 2014 , 140, 244502 | 3.9 | 11 |
| 8 | Thermodynamics and kinetics of large-time-step molecular dynamics. <i>Journal of Computational Chemistry</i> , 2012 , 33, 475-83 | 3.5 | 10 |
| 7 | Local Transition Gradients Indicating the Global Attributes of Protein Energy Landscapes. <i>Journal of Physical Chemistry Letters</i> , 2010 , 1, 1580-1583 | 6.4 | 10 |
| 6 | A comparative analysis of clustering algorithms: O ₂ migration in truncated hemoglobin I from transition networks. <i>Journal of Chemical Physics</i> , 2015 , 142, 025103 | 3.9 | 9 |
| 5 | Estimation of folding probabilities and phi values from molecular dynamics simulations of reversible Peptide folding. <i>Methods in Molecular Biology</i> , 2007 , 350, 225-49 | 1.4 | 6 |
| 4 | Protein inherent structures by different minimization strategies. <i>Journal of Computational Chemistry</i> , 2011 , 32, 1113-6 | 3.5 | 4 |
| 3 | A hydro-kinetic scheme for the dynamics of hydrogen bonds in water-like fluids. <i>Physical Chemistry Chemical Physics</i> , 2014 , 16, 15510-8 | 3.6 | 3 |
| 2 | Lattice Boltzmann implementation of the three-dimensional Ben-Naim potential for water-like fluids. <i>Journal of Chemical Physics</i> , 2013 , 138, 124105 | 3.9 | 2 |
| 1 | Frequency-domain study of β -relaxation in the random orthogonal model. <i>Philosophical Magazine</i> , 2004 , 84, 1389-1395 | 1.6 | |