Ali Rana Atilgan

List of Publications by Year
in descending order

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85 papers	6,256 citations	201385 27 h-index	98622 67 g-index
91 all docs	91 docs citations	91 times ranked	3663 citing authors

#	Article	IF	Citations
1	Anisotropy of Fluctuation Dynamics of Proteins with an Elastic Network Model. Biophysical Journal, 2001, 80, 505-515.	0.2	1,486
2	Direct evaluation of thermal fluctuations in proteins using a single-parameter harmonic potential. Folding & Design, 1997, 2, 173-181.	4.5	1,243
3	Vibrational Dynamics of Folded Proteins: Significance of Slow and Fast Motions in Relation to Function and Stability. Physical Review Letters, 1998, 80, 2733-2736.	2.9	382
4	Small-World Communication of Residues and Significance for Protein Dynamics. Biophysical Journal, 2004, 86, 85-91.	0.2	295
5	Dynamics of proteins predicted by molecular dynamics simulations and analytical approaches: Application to ?-amylase inhibitor. Proteins: Structure, Function and Bioinformatics, 2000, 40, 512-524.	1.5	260
6	Collective Motions in HIV-1 Reverse Transcriptase: Examination of Flexibility and Enzyme Function. Journal of Molecular Biology, 1999, 285, 1023-1037.	2.0	199
7	Perturbation-Response Scanning Reveals Ligand Entry-Exit Mechanisms of Ferric Binding Protein. PLoS Computational Biology, 2009, 5, e1000544.	1.5	192
8	Nonclassical Behavior of Thinâ€Walled Composite Beams with Closed Cross Sections. Journal of the American Helicopter Society, 1990, 35, 42-50.	0.5	171
9	MD-TASK: a software suite for analyzing molecular dynamics trajectories. Bioinformatics, 2017, 33, 2768-2771.	1.8	142
10	Freeâ€Vibration Analysis of Composite Beams. Journal of the American Helicopter Society, 1991, 36, 36-47.	0.5	141
11	On a simplified strain energy function for geometrically nonlinear behaviour of anisotropic beams. Composites Part B: Engineering, 1992, 2, 513-526.	0.6	139
12	Manipulation of Conformational Change in Proteins by Single-Residue Perturbations. Biophysical Journal, 2010, 99, 933-943.	0.2	139
13	Dynamics of proteins predicted by molecular dynamics simulations and analytical approaches: application to alpha-amylase inhibitor. Proteins: Structure, Function and Bioinformatics, 2000, 40, 512-24.	1.5	134
14	Understanding the recognition of protein structural classes by amino acid composition. Proteins: Structure, Function and Bioinformatics, 1997, 29, 172-185.	1.5	120
15	Identification of kinetically hot residues in proteins. Protein Science, 1998, 7, 2522-2532.	3.1	114
16	A Geometrically Nonlinear Theory of Elastic Plates. Journal of Applied Mechanics, Transactions ASME, 1993, 60, 109-116.	1.1	99
17	Unified nonlinear analysis for nonhomogeneous anisotropic beams withclosed cross sections. AIAA Journal, 1991, 29, 1990-1999.	1.5	65
18	Network-Based Models as Tools Hinting at Nonevident Protein Functionality. Annual Review of Biophysics, 2012, 41, 205-225.	4.5	54

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19	Screened Nonbonded Interactions in Native Proteins Manipulate Optimal Paths for Robust Residue Communication. Biophysical Journal, 2007, 92, 3052-3062.	0.2	53
20	High-Order Epistasis in Catalytic Power of Dihydrofolate Reductase Gives Rise to a Rugged Fitness Landscape in the Presence of Trimethoprim Selection. Molecular Biology and Evolution, 2019, 36, 1533-1550.	3.5	52
21	MODE-TASK: large-scale protein motion tools. Bioinformatics, 2018, 34, 3759-3763.	1.8	45
22	On the strain energy of laminated composite plates. International Journal of Solids and Structures, 1992, 29, 2527-2543.	1.3	41
23	Designing Molecular Dynamics Simulations to Shift Populations of the Conformational States of Calmodulin. PLoS Computational Biology, 2013, 9, e1003366.	1.5	41
24	A trimethoprim derivative impedes antibiotic resistance evolution. Nature Communications, 2021, 12, 2949.	5.8	41
25	Application of the variational-asymptotical method to laminated composite plates. AIAA Journal, 1993, 31, 1674-1683.	1.5	39
26	Elucidating the structural mechanisms for biological activity of the chemokine family. Proteins: Structure, Function and Bioinformatics, 2001, 43, 150-160.	1.5	33
27	Identifying the adaptive mechanism in globular proteins: Fluctuations in densely packed regions manipulate flexible parts. Journal of Chemical Physics, 2000, 113, 4454-4464.	1.2	32
28	Coordination topology and stability for the native and binding conformers of chymotrypsin inhibitor 2. Proteins: Structure, Function and Bioinformatics, 2001, 45, 62-70.	1.5	28
29	Relaxation Kinetics and the Glassiness of Proteins: The Case of Bovine Pancreatic Trypsin Inhibitor. Biophysical Journal, 2002, 83, 699-705.	0.2	28
30	Relaxation Kinetics and the Glassiness of Native Proteins: Coupling of Timescales. Biophysical Journal, 2005, 88, 1570-1576.	0.2	25
31	Nanosecond Motions in Proteins Impose Bounds on the Timescale Distributions of Local Dynamics. Biophysical Journal, 2009, 97, 2080-2088.	0.2	25
32	Increased substrate affinity in the Escherichia coli L28R dihydrofolate reductase mutant causes trimethoprim resistance. Physical Chemistry Chemical Physics, 2017, 19, 11416-11428.	1.3	24
33	Detailed molecular dynamics simulations of human transferrin provide insights into iron release dynamics at serum and endosomal pH. Journal of Biological Inorganic Chemistry, 2015, 20, 705-718.	1.1	23
34	Subtle pH differences trigger single residue motions for moderating conformations of calmodulin. Journal of Chemical Physics, 2011, 135, 155102.	1.2	21
35	Understanding the recognition of protein structural classes by amino acid composition. Proteins: Structure, Function and Bioinformatics, 1997, 29, 172-85.	1.5	20
36	Perturbation response scanning specifies key regions in subtilisin serine protease for both function and stability. Journal of Enzyme Inhibition and Medicinal Chemistry, 2015, 30, 867-873.	2.5	19

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37	Unraveling the Motions behind Enterovirus 71ÂUncoating. Biophysical Journal, 2018, 114, 822-838.	0.2	19
38	Molecular Dynamics Analysis of Coupling between Librational Motions and Isomeric Jumps in Chain Molecules. Macromolecules, 1996, 29, 2510-2514.	2.2	18
39	How orientational order governs collectivity of folded proteins. Proteins: Structure, Function and Bioinformatics, 2010, 78, 3363-3375.	1.5	18
40	Mechanisms by Which Salt Concentration Moderates the Dynamics of Human Serum Transferrin. Journal of Physical Chemistry B, 2017, 121, 4778-4789.	1.2	18
41	Local motifs in proteins combine to generate global functional moves. Briefings in Functional Genomics, 2012, 11, 479-488.	1.3	17
42	Computational approaches for deciphering the equilibrium and kinetic properties of iron transport proteins. Metallomics, 2017, 9, 1513-1533.	1.0	17
43	FbpA iron storage and release are governed by periplasmic microenvironments. Physical Chemistry Chemical Physics, 2017, 19, 6064-6075.	1.3	16
44	State-space prediction model for chaotic time series. Physical Review E, 1998, 58, 2640-2643.	0.8	14
45	In silico mutational studies of <scp>H</scp>sp70 disclose sites with distinct functional attributes. Proteins: Structure, Function and Bioinformatics, 2015, 83, 2077-2090.	1.5	14
46	Assortative Mixing in Close-Packed Spatial Networks. PLoS ONE, 2010, 5, e15551.	1.1	13
47	SPACE-TIME MIXED FINITE ELEMENTS FOR RODS. Journal of Sound and Vibration, 1996, 192, 731-739.	2.1	12
48	Protonation States of Remote Residues Affect Bindingâ€“Release Dynamics of the Ligand but Not the Conformation of Apo Ferric Binding Protein. Journal of Physical Chemistry B, 2014, 118, 11677-11687.	1.2	12
49	How a Vicinal Layer of Solvent Modulates the Dynamics of Proteins. Biophysical Journal, 2008, 94, 79-89.	0.2	11
50	Relating the Structure ofHIV-1 Reverse Transcriptaseto Its Processing Step. Journal of Biomolecular Structure and Dynamics, 2000, 17, 49-55.	2.0	10
51	Calmodulin Readily Switches Conformation upon Protonating High pK_a Acidic Residues. Journal of Physical Chemistry B, 2012, 116, 7145-7153.	1.2	9
52	Dynamic Community Composition Unravels Allosteric Communication in PDZ3. Journal of Physical Chemistry B, 2021, 125, 2266-2276.	1.2	8
53	DYNAMICS OF DISORDERED STRUCTURES: EFFECT OF NON-LINEARITY ON THE LOCALIZATION. Journal of Sound and Vibration, 1997, 205, 372-379.	2.1	7
54	El Farol revisited. Physica A: Statistical Mechanics and Its Applications, 2005, 346, 651-656.	1.2	7

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55	Depth dependent dynamics in the hydration shell of a protein. Journal of Chemical Physics, 2010, 133, 085101.	1.2	7
56	Dynamics of proteins predicted by molecular dynamics simulations and analytical approaches: Application to Î±-amylase inhibitor. , 2000, 40, 512.		7
57	Coupling between different modes in local chain dynamics: a modal correlation analysis. Journal of the Chemical Society, Faraday Transactions, 1995, 91, 2483.	1.7	6
58	Computational strategies for protein conformational ensemble detection. Current Opinion in Structural Biology, 2022, 72, 79-87.	2.6	6
59	COLLECTIVE BEHAVIOR OF EL FAROL ATTENDEES. International Journal of Modeling, Simulation, and Scientific Computing, 2008, 11, 629-639.	0.9	3
60	Designed-in Molecular Interactions Lead to Superior Thermo-mechanical Properties in Nanocomposites. Materials Research Society Symposia Proceedings, 2011, 1304, 1.	0.1	3
61	Correlated fluctuations in polymer networks. Computational and Theoretical Polymer Science, 1998, 8, 55-59.	1.1	2
62	Driving Calmodulin Protein towards Conformational Shift by Changing Ionization States of Select Residues. Journal of Physics: Conference Series, 2012, 402, 012047.	0.3	2
63	N-Terminus of the Third PDZ Domain of PSD-95 Orchestrates Allosteric Communication for Selective Ligand Binding. Journal of Chemical Information and Modeling, 2021, 61, 347-357.	2.5	2
64	Dynamics of proteins predicted by molecular dynamics simulations and analytical approaches: Application to Î±-amylase inhibitor. , 0, .		2
65	Some Remarks on the Stability of Laminated Composite Beams. ZAMM Zeitschrift Fur Angewandte Mathematik Und Mechanik, 1994, 74, 131-133.	0.9	1
66	Statistical mechanics of Fermi-Pasta-Ulam chains with the canonical ensemble. Physical Review E, 1997, 55, 3727-3730.	0.8	1
67	Analogy between Dislocation Mechanics and Aerodynamics. ZAMM Zeitschrift Fur Angewandte Mathematik Und Mechanik, 1997, 77, 631-633.	0.9	1
68	On modifying properties of polymeric melts by nanoscopic particles. Journal of Polymer Science, Part B: Polymer Physics, 2012, 50, 1653-1662.	2.4	1
69	A Coarse-Grained Methodology Identifies Intrinsic Mechanisms That Dissociate Interacting Protein Pairs. Frontiers in Molecular Biosciences, 2020, 7, 210.	1.6	1
70	A Nonlinear Model for the Kinking Behavior of Unidirectional Polymer Matrix Composites. ZAMM Zeitschrift Fur Angewandte Mathematik Und Mechanik, 1998, 78, 212-216.	0.9	0
71	Long-Range Structural Regularities and Collectivity of Folded Proteins. Materials Research Society Symposia Proceedings, 2009, 1227, 30601.	0.1	0
72	Multiple Channels of Structural Relaxations in Functional Proteins. Biophysical Journal, 2009, 96, 72a.	0.2	0

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73	A Coarsened Network Model Reveals Allosteric Machinery. Biophysical Journal, 2009, 96, 5a-6a.	0.2	0
74	Functional Pathways in Proteins Are Uncovered By Strong Disorder. Biophysical Journal, 2010, 98, 27a.	0.2	0
75	Molecular Recognition Mechanism of Calmodulin Examined by Perturbation-Response Scanning. Biophysical Journal, 2011, 100, 534a.	0.2	0
76	Molecular Recognition Mechanisms of Calmodulin Examined by Perturbation-Response Scanning. Materials Research Society Symposia Proceedings, 2011, 1301, 137.	0.1	0
77	Effect of van der Waals Interaction Strength and Nanocluster Size on the Dynamical and Mechanical Properties of 1,4-cis-polybutadiene Melts. Materials Research Society Symposia Proceedings, 2012, 1424, 121.	0.1	0
78	Exploring pH Dependent Landscape Shifts of Proteins. Biophysical Journal, 2012, 102, 450a.	0.2	0
79	Changes in Bond-Orientational Order of Residues are Associated with Shifts in Energy Landscapes. Biophysical Journal, 2012, 102, 445a.	0.2	0
80	Where do Proteins Fit in the Structural Classification of Condensed Matter?. Biophysical Journal, 2012, 102, 250a.	0.2	0
81	Non-Equilibrium Fluctuation Theorems, Redundant Paths in Proteins, and Elucidating Conformational Changes by Single-Residue Perturbations. Biophysical Journal, 2013, 104, 70a.	0.2	0
82	Structural Basis of How Ferric Binding Proteins Utilize pH Differences for Controlled Release of Iron. Biophysical Journal, 2013, 104, 212a.	0.2	0
83	Computational Assessment of Trimethoprim Resistance in Dihydrofolate Reductase. Biophysical Journal, 2016, 110, 47a-48a.	0.2	0
84	Allosteric Communication in PDZ3 is Orchestrated by the Charged N-Terminus. Biophysical Journal, 2021, 120, 189a.	0.2	0
85	Could network structures generated with simple rules imposed on a cubic lattice reproduce the structural descriptors of globular proteins?. Journal of Complex Networks, 2021, 10, .	1.1	0