

Hugo Sanabria

List of Publications by Year in descending order

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68
papers

1,484
citations

430754

18
h-index

360920

35
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74
all docs

74
docs citations

74
times ranked

2002
citing authors

#	ARTICLE	IF	CITATIONS
1	Unraveling multi-state molecular dynamics in single-molecule FRET experiments. I. Theory of FRET-lines. <i>Journal of Chemical Physics</i> , 2022, 156, 141501.	1.2	23
2	Unraveling protein's structural dynamics: from configurational dynamics to ensemble switching guides functional mesoscale assemblies. <i>Current Opinion in Structural Biology</i> , 2021, 66, 129-138.	2.6	18
3	Sequence and Structure Based Approach for Automated FRET Network Design. <i>Biophysical Journal</i> , 2021, 120, 188a.	0.2	0
4	Ensemble Switching of the DNA-Binding Domain of Human FoxP1. <i>Biophysical Journal</i> , 2021, 120, 18a.	0.2	0
5	Structural Dynamics of the Heterodimerization Between the DNA-Binding Domains from Human FoxP1 and FoP2 Transcription Factors. <i>Biophysical Journal</i> , 2021, 120, 127a.	0.2	0
6	Ensemble switching unveils a kinetic rheostat mechanism of the eukaryotic thiamine pyrophosphate riboswitch. <i>Rna</i> , 2021, 27, 771-790.	1.6	15
7	Out-of-Equilibrium Biophysical Chemistry: The Case for Multidimensional, Integrated Single-Molecule Approaches. <i>Journal of Physical Chemistry B</i> , 2021, 125, 10404-10418.	1.2	9
8	Integrative structural dynamics probing of the conformational heterogeneity in synaptosomal-associated protein 25. <i>Cell Reports Physical Science</i> , 2021, 2, 100616.	2.8	9
9	Structural Dynamics of Glutamate Signaling Systems by smFRET. <i>Biophysical Journal</i> , 2020, 119, 1929-1936.	0.2	6
10	Expansion Upon Binding Guides p27 Binding to Cdk2/cyclinA. <i>Biophysical Journal</i> , 2020, 118, 371a.	0.2	0
11	Interdomain Dynamics Underlie Function and Regulation of Postsynaptic Density Protein 95. <i>Biophysical Journal</i> , 2020, 118, 336a.	0.2	0
12	Intrinsically Disordered Regions of the DNA-Binding Domain of Human FoxP1 Facilitate Domain Swapping. <i>Journal of Molecular Biology</i> , 2020, 432, 5411-5429.	2.0	12
13	Dynamic Organization in the Supertertiary Structure of PDZ3-SH3-GuK Core Supramodule of PSD-95 Scaffold Protein. <i>Biophysical Journal</i> , 2020, 118, 206a.	0.2	0
14	Automated and optimally FRET-assisted structural modeling. <i>Nature Communications</i> , 2020, 11, 5394.	5.8	39
15	Specific Conformational Dynamics and Expansion Underpin a Multi-Step Mechanism for Specific Binding of p27 with Cdk2/Cyclin A. <i>Journal of Molecular Biology</i> , 2020, 432, 2998-3017.	2.0	26
16	Resolving dynamics and function of transient states in single enzyme molecules. <i>Nature Communications</i> , 2020, 11, 1231.	5.8	71
17	The correlation between phase transition and photoluminescence properties of CsPbX ₃ (X) Tj ETQq1 1,0.784314 rgBT /Cv	2.2	27
18	Quantitative Fluorescence Quenching by Aromatic Amino Acids. <i>Biophysical Journal</i> , 2020, 118, 472a.	0.2	0

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19	Connection between Electrostatic Interactions and Binding Affinity of Dynein and Microtubules. Biophysical Journal, 2019, 116, 409a.	0.2	0
20	Multiparameter fluorescence spectroscopy of single molecules. , 2019, , 269-333.		5
21	Automated and Optimally FRET-Assisted Structural Modeling. Biophysical Journal, 2019, 116, 333a.	0.2	1
22	Probing Structural States in Fast Exchanging Proteins by FRET and Computational Methods. Biophysical Journal, 2019, 116, 469a.	0.2	0
23	Effects of Local and Global Dynamics on the Supertertiary Organization of Postsynaptic Density Protein 95. Biophysical Journal, 2019, 116, 188a-189a.	0.2	0
24	Integrative Dynamic Structural Biology with Fluorescence Spectroscopy. Biophysical Journal, 2019, 116, 469a-470a.	0.2	0
25	Spontaneous Switching among Conformational Ensembles in Intrinsically Disordered Proteins. Biomolecules, 2019, 9, 114.	1.8	41
26	Dynamic anticipation by Cdk2/Cyclin A-bound p27 mediates signal integration in cell cycle regulation. Nature Communications, 2019, 10, 1676.	5.8	71
27	Secondary Structure Predictions and Determination of Folding Pathways for TPP Riboswitch. Biophysical Journal, 2019, 116, 354a.	0.2	0
28	Manipulating Charge Transfer from Core to Shell in CdSe/CdS/Au Heterojunction Quantum Dots. ACS Applied Materials & Interfaces, 2019, 11, 48551-48555.	4.0	7
29	Transient Interactions in Multidomain Proteins Identified by FRET. Biophysical Journal, 2018, 114, 565a.	0.2	0
30	Single Molecule Study of Long-Range Electrostatic Binding Affinity of Cytoplasmic Dynein's Microtubule Binding Domain. Biophysical Journal, 2018, 114, 512a.	0.2	0
31	Identifying weak interdomain interactions that stabilize the supertertiary structure of the N-terminal tandem PDZ domains of PSD-95. Nature Communications, 2018, 9, 3724.	5.8	41
32	Precision and accuracy of single-molecule FRET measurementsâ€”a multi-laboratory benchmark study. Nature Methods, 2018, 15, 669-676.	9.0	350
33	Fluorescence Evidences for Non-Homogeneity and Residual Structure of Denatured States. Biophysical Journal, 2017, 112, 57a.	0.2	0
34	Dynamic Equilibrium of the TPP Riboswitch as Observed by MFD Fret. Biophysical Journal, 2017, 112, 368a.	0.2	0
35	Submillisecond Dynamics of the NMDA Receptor. Biophysical Journal, 2017, 112, 37a.	0.2	0
36	Calcium Calmodulin Regulates Zinc Mediated Changes in the Structure, Self-Association, and Activity of CaMKII. Biophysical Journal, 2017, 112, 444a-445a.	0.2	0

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37	A Multiscalar Framework describes Fluorescence and FRET of Fluctuating Molecular Species and Resolves Kinetic Networks. <i>Biophysical Journal</i> , 2017, 112, 133a-134a.	0.2	1
38	Cytoskeletal-like Filaments of Ca ²⁺ -Calmodulin-Dependent Protein Kinase II Are Formed in a Regulated and Zn ²⁺ -Dependent Manner. <i>Biochemistry</i> , 2017, 56, 2149-2160.	1.2	7
39	High Precision FRET at Single-molecule Level for Biomolecule Structure Determination. <i>Journal of Visualized Experiments</i> , 2017, , .	0.2	15
40	Conformational Selection and Submillisecond Dynamics of the Ligand-binding Domain of the N-Methyl-d-aspartate Receptor. <i>Journal of Biological Chemistry</i> , 2016, 291, 16175-16185.	1.6	34
41	Sub-Millisecond Unfolding Kinetic Spectra Reveals Intermediate Transitions. <i>Biophysical Journal</i> , 2016, 110, 180a-181a.	0.2	0
42	smFRET and DEER Distance Measurements as Applied to Disordered and Structured Proteins. <i>Biophysical Journal</i> , 2016, 110, 559a.	0.2	2
43	Resolving the Heterogeneity of the Ensemble of Unfolded States by a Combination of Fluorescence Spectroscopic Methods. <i>Biophysical Journal</i> , 2016, 110, 390a.	0.2	0
44	Intra and Interdomain Motions of the NMDA Receptor using Single Molecule FRET. <i>Biophysical Journal</i> , 2016, 110, 288a.	0.2	0
45	Tuning of Structure-Function Relationships by Macromolecular Crowding. <i>Biophysical Journal</i> , 2015, 108, 214a.	0.2	0
46	Gating Mechanism and Movements in Acid Sensing Ion Channel 1A. <i>Biophysical Journal</i> , 2015, 108, 288a.	0.2	0
47	Relative Cosolute Size Influences the Kinetics of Protein-Protein Interactions. <i>Biophysical Journal</i> , 2015, 109, 510-520.	0.2	11
48	Post-Translational Modification of P27 Regulates Signal Transmission via a Dynamic Interaction with Cdk2/Cyclin. <i>Biophysical Journal</i> , 2015, 108, 193a.	0.2	1
49	High Precision FRET Reveals Dynamic Structures in the Drosophila Scaffold Protein Complex Stardust-DPATJ-DLin-7 Mediated by L27 Domains. <i>Biophysical Journal</i> , 2014, 106, 256a.	0.2	0
50	Visualizing Structures, Dynamics and Function of Enzymes. <i>Biophysical Journal</i> , 2014, 106, 663a.	0.2	0
51	Deciphering Folding Pathways of Phage T4 Lysozyme: Influence of Multiple Conformations. <i>Biophysical Journal</i> , 2014, 106, 260a.	0.2	0
52	Temporal Dynamics and FRET Restrained Modeling of an "Invisible" Excited State of T4 Lysozyme. <i>Biophysical Journal</i> , 2013, 104, 346a.	0.2	0
53	Analyzing Förster Resonance Energy Transfer with Fluctuation Algorithms. <i>Methods in Enzymology</i> , 2013, 519, 39-85.	0.4	38
54	Unraveling Folding Pathways and Kinetics Transition of T4 Lysozyme with High Temporal Resolution by Single Molecule FRET. <i>Biophysical Journal</i> , 2012, 102, 216a.	0.2	0

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55	Homo-FRET Studies of the Signal Recognition Particle Protein FFH by Multiparameter Fluorescence Detection (MFD) and Filtered Fluorescence Correlation Spectroscopy (FFCs). <i>Biophysical Journal</i> , 2012, 102, 402a.	0.2	0
56	Filtered FCS: Species Auto- and Cross-Correlation Functions Highlight Binding and Dynamics in Biomolecules. <i>ChemPhysChem</i> , 2012, 13, 1036-1053.	1.0	90
57	Quantifying Translational Mobility in Neurons: Comparison between Current Optical Techniques. <i>Journal of Neuroscience</i> , 2010, 30, 16409-16416.	1.7	18
58	Transient Anomalous Subdiffusion: Effects of Specific and Nonspecific Probe Binding with Actin Gels. <i>Journal of Physical Chemistry B</i> , 2010, 114, 959-972.	1.2	13
59	\hat{I}^2 CaMKII Regulates Actin Assembly and Structure. <i>Journal of Biological Chemistry</i> , 2009, 284, 9770-9780.	1.6	62
60	Modulation of Calmodulin Plasticity by the Effect of Macromolecular Crowding. <i>Journal of Molecular Biology</i> , 2009, 391, 933-943.	2.0	52
61	Effects of Oscillatory Electric Fields on Internal Membranes: An Analytical Model. <i>Biophysical Journal</i> , 2008, 94, 2043-2052.	0.2	48
62	Macromolecular Crowding and Size Effects on Probe Microviscosity. <i>Biophysical Journal</i> , 2008, 95, 5362-5373.	0.2	89
63	Spatial Diffusivity and Availability of Intracellular Calmodulin. <i>Biophysical Journal</i> , 2008, 95, 6002-6015.	0.2	43
64	Multiple Diffusion Mechanisms Due to Nanostructuring in Crowded Environments. <i>Biophysical Journal</i> , 2007, 92, 313-322.	0.2	76
65	Impedance Spectroscopy of \hat{I}^{\pm} - \hat{I}^2 Tubulin Heterodimer Suspensions. <i>Biophysical Journal</i> , 2006, 90, 4644-4650.	0.2	19
66	Relaxation processes due to the electrode-electrolyte interface in ionic solutions. <i>Physical Review E</i> , 2006, 74, 051505.	0.8	66
67	Towards Experimental Tests of Quantum Effects in Cytoskeletal Proteins. , 2006, , 95-170.		6
68	Unraveling multi-state molecular dynamics in single-molecule FRET experiments. II. Quantitative analysis of multi-state kinetic networks. <i>Journal of Chemical Physics</i> , 0, , .	1.2	8