## Hugo Sanabria

List of Publications by Year in descending order

Source: https://exaly.com/author-pdf/989939/publications.pdf

Version: 2024-02-01

68 papers 1,484 citations

430754 18 h-index 35 g-index

74 all docs

74 docs citations

times ranked

74

2002 citing authors

#	Article	IF	CITATIONS
1	Precision and accuracy of single-molecule FRET measurements—a multi-laboratory benchmark study. Nature Methods, 2018, 15, 669-676.	9.0	350
2	Filtered FCS: Species Auto―and Crossâ€Correlation Functions Highlight Binding and Dynamics in Biomolecules. ChemPhysChem, 2012, 13, 1036-1053.	1.0	90
3	Macromolecular Crowding and Size Effects on Probe Microviscosity. Biophysical Journal, 2008, 95, 5362-5373.	0.2	89
4	Multiple Diffusion Mechanisms Due to Nanostructuring in Crowded Environments. Biophysical Journal, 2007, 92, 313-322.	0.2	76
5	Dynamic anticipation by Cdk2/Cyclin A-bound p27 mediates signal integration in cell cycle regulation. Nature Communications, 2019, 10, 1676.	5.8	71
6	Resolving dynamics and function of transient states in single enzyme molecules. Nature Communications, 2020, 11, 1231.	5.8	71
7	Relaxation processes due to the electrode-electrolyte interface in ionic solutions. Physical Review E, 2006, 74, 051505.	0.8	66
8	Î <sup>2</sup> CaMKII Regulates Actin Assembly and Structure. Journal of Biological Chemistry, 2009, 284, 9770-9780.	1.6	62
9	Modulation of Calmodulin Plasticity by the Effect of Macromolecular Crowding. Journal of Molecular Biology, 2009, 391, 933-943.	2.0	52
10	Effects of Oscillatory Electric Fields on Internal Membranes: An Analytical Model. Biophysical Journal, 2008, 94, 2043-2052.	0.2	48
11	Spatial Diffusivity and Availability of Intracellular Calmodulin. Biophysical Journal, 2008, 95, 6002-6015.	0.2	43
12	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
13	Spontaneous Switching among Conformational Ensembles in Intrinsically Disordered Proteins. Biomolecules, 2019, 9, 114.	1.8	41
14	Automated and optimally FRET-assisted structural modeling. Nature Communications, 2020, 11, 5394.	5.8	39
15	Analyzing Förster Resonance Energy Transfer with Fluctuation Algorithms. Methods in Enzymology, 2013, 519, 39-85.	0.4	38
16	Conformational Selection and Submillisecond Dynamics of the Ligand-binding Domain of the N-Methyl-d-aspartate Receptor. Journal of Biological Chemistry, 2016, 291, 16175-16185.	1.6	34
17	The correlation between phase transition and photoluminescence properties of CsPbX <sub>3</sub> (X) Tj ETQq2	1 1 0.7843 2.2	314 rgBT / <mark>Ov</mark> 
18	Specific Conformational Dynamics and Expansion Underpin a Multi-Step Mechanism for Specific Binding of p27 with Cdk2/Cyclin A. Journal of Molecular Biology, 2020, 432, 2998-3017.	2.0	26

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19	Unraveling multi-state molecular dynamics in single-molecule FRET experiments. I. Theory of FRET-lines. Journal of Chemical Physics, 2022, 156, 141501.	1.2	23
20	Impedance Spectroscopy of $\hat{l}\pm\hat{l}^2$ Tubulin Heterodimer Suspensions. Biophysical Journal, 2006, 90, 4644-4650.	0.2	19
21	Quantifying Translational Mobility in Neurons: Comparison between Current Optical Techniques. Journal of Neuroscience, 2010, 30, 16409-16416.	1.7	18
22	Unraveling protein's structural dynamics: from configurational dynamics to ensemble switching guides functional mesoscale assemblies. Current Opinion in Structural Biology, 2021, 66, 129-138.	2.6	18
23	High Precision FRET at Single-molecule Level for Biomolecule Structure Determination. Journal of Visualized Experiments, 2017, , .	0.2	15
24	Ensemble switching unveils a kinetic rheostat mechanism of the eukaryotic thiamine pyrophosphate riboswitch. Rna, 2021, 27, 771-790.	1.6	15
25	Transient Anomalous Subdiffusion: Effects of Specific and Nonspecific Probe Binding with Actin Gels. Journal of Physical Chemistry B, 2010, 114, 959-972.	1.2	13
26	Intrinsically Disordered Regions of the DNA-Binding Domain of Human FoxP1 Facilitate Domain Swapping. Journal of Molecular Biology, 2020, 432, 5411-5429.	2.0	12
27	Relative Cosolute Size Influences the Kinetics of Protein-Protein Interactions. Biophysical Journal, 2015, 109, 510-520.	0.2	11
28	Out-of-Equilibrium Biophysical Chemistry: The Case for Multidimensional, Integrated Single-Molecule Approaches. Journal of Physical Chemistry B, 2021, 125, 10404-10418.	1.2	9
29	Integrative structural dynamics probing of the conformational heterogeneity in synaptosomal-associated protein 25. Cell Reports Physical Science, 2021, 2, 100616.	2.8	9
30	<b>Unraveling multi-state molecular dynamics in single-molecule FRET experiments. II. Quantitative analysis of multi-state kinetic networks</b> . Journal of Chemical Physics, 0, , .	1.2	8
31	Cytoskeletal-like Filaments of Ca <sup>2+</sup> -Calmodulin-Dependent Protein Kinase II Are Formed in a Regulated and Zn <sup>2+</sup> -Dependent Manner. Biochemistry, 2017, 56, 2149-2160.	1.2	7
32	Manipulating Charge Transfer from Core to Shell in CdSe/CdS/Au Heterojunction Quantum Dots. ACS Applied Materials & Dots. ACS	4.0	7
33	Structural Dynamics of Glutamate Signaling Systems by smFRET. Biophysical Journal, 2020, 119, 1929-1936.	0.2	6
34	Towards Experimental Tests of Quantum Effects in Cytoskeletal Proteins., 2006,, 95-170.		6
35	Multiparameter fluorescence spectroscopy of single molecules. , 2019, , 269-333.		5
36	smFRET and DEER Distance Measurements as Applied to Disordered and Structured Proteins. Biophysical Journal, 2016, 110, 559a.	0.2	2

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37	Post-Translational Modification of P27 Regulates Signal Transmission via a Dynamic Interaction with Cdk2/Cyclin. Biophysical Journal, 2015, 108, 193a.	0.2	1
38	A Multiscalar Framework describes Fluorescence and FRET of Fluctuating Molecular Species and Resolves Kinetic Networks. Biophysical Journal, 2017, 112, 133a-134a.	0.2	1
39	Automated and Optimally FRET-Assisted Structural Modeling. Biophysical Journal, 2019, 116, 333a.	0.2	1
40	Unraveling Folding Pathways and Kinetics Transition of T4 Lysozyme with High Temporal Resolution by Single Molecule FRET. Biophysical Journal, 2012, 102, 216a.	0.2	O
41	Homo-FRET Studies of the Signal Recognition Particle Protein FFH by Multiparameter Fluorescence Detection (MFD) and Filtered Fluorescence Correlation Spectroscopy (FFCs). Biophysical Journal, 2012, 102, 402a.	0.2	0
42	Temporal Dynamics and FRET Restrained Modeling of an "Invisible―Excited State of T4 Lysozyme. Biophysical Journal, 2013, 104, 346a.	0.2	0
43	High Precision FRET Reveals Dynamic Structures in the Drosophila Scaffold Protein Complex Stardust-DPATJ-DLin-7 Mediated by L27 Domains. Biophysical Journal, 2014, 106, 256a.	0.2	0
44	Visualizing Structures, Dynamics and Function of Enzymes. Biophysical Journal, 2014, 106, 663a.	0.2	0
45	Deciphering Folding Pathways of Phage T4 Lysozyme: Influence of Multiple Conformations. Biophysical Journal, 2014, 106, 260a.	0.2	0
46	Tuning of Structure-Function Relationships by Macromolecular Crowding. Biophysical Journal, 2015, 108, 214a.	0.2	0
47	Gating Mechanism and Movements in Acid Sensing Ion Channel 1A. Biophysical Journal, 2015, 108, 288a.	0.2	0
48	Sub-Millisecond Unfolding Kinetic Spectra Reveals Intermediate Transitions. Biophysical Journal, 2016, 110, 180a-181a.	0.2	0
49	Resolving the Heterogeneity of the Ensemble of Unfolded States by a Combination of Fluorescence Spectroscopic Methods. Biophysical Journal, 2016, 110, 390a.	0.2	0
50	Intra and Interdomain Motions of the NMDA Receptor using Single Molecule FRET. Biophysical Journal, 2016, 110, 288a.	0.2	0
51	Fluorescence Evidences for Non-Homogeneity and Residual Structure of Denatured States. Biophysical Journal, 2017, 112, 57a.	0.2	0
52	Dynamic Equilibrium of the TPP Riboswitch as Observed by MFD Fret. Biophysical Journal, 2017, 112, 368a.	0.2	0
53	Submillisecond Dynamics of the NMDA Receptor. Biophysical Journal, 2017, 112, 37a.	0.2	0
54	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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55	Transient Interactions in Multidomain Proteins Identified by FRET. Biophysical Journal, 2018, 114, 565a.	0.2	O
56	Single Molecule Study of Long-Range Electrostatic Binding Affinity of Cytoplasmic Dynein's Microtubule Binding Domain. Biophysical Journal, 2018, 114, 512a.	0.2	0
57	Connection between Electrostatic Interactions and Binding Affinity of Dynein and Microtubules. Biophysical Journal, 2019, 116, 409a.	0.2	0
58	Probing Structural States in Fast Exchanging Proteins by FRET and Computational Methods. Biophysical Journal, 2019, 116, 469a.	0.2	0
59	Effects of Local and Global Dynamics on the Supertertiary Organization of Postsynaptic Density Protein 95. Biophysical Journal, 2019, 116, 188a-189a.	0.2	0
60	Integrative Dynamic Structural Biology with Fluorescence Spectroscopy. Biophysical Journal, 2019, 116, 469a-470a.	0.2	0
61	Secondary Structure Predictions and Determination of Folding Pathways for TPP Riboswitch. Biophysical Journal, 2019, 116, 354a.	0.2	0
62	Expansion Upon Binding Guides p27 Binding to Cdk2/cyclinA. Biophysical Journal, 2020, 118, 371a.	0.2	0
63	Interdomain Dynamics Underlie Function and Regulation of Postsynaptic Density Protein 95. Biophysical Journal, 2020, 118, 336a.	0.2	0
64	Dynamic Organization in the Supertertiary Structure of PDZ3-SH3-GuK Core Supramodule of PSD-95 Scaffold Protein. Biophysical Journal, 2020, 118, 206a.	0.2	0
65	Quantitative Fluorescence Quenching by Aromatic Amino Acids. Biophysical Journal, 2020, 118, 472a.	0.2	0
66	Sequence and Structure Based Approach for Automated FRET Network Design. Biophysical Journal, 2021, 120, 188a.	0.2	0
67	Ensemble Switching of the DNA-Binding Domain of Human FoxP1. Biophysical Journal, 2021, 120, 18a.	0.2	0
68	Structural Dynamics of the Heterodimerization Between the DNA-Binding Domains from Human FoxP1 and FoP2 Transcription Factors. Biophysical Journal, 2021, 120, 127a.	0.2	0