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Anisotropy decay of fluorescence as an experimental approach to protein dynamics

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#	Paper	IF	Citations
56	Investigating State Restriction in Fluorescent Protein FRET Using Time-Resolved Fluorescence and Anisotropy.		
55	Local phenomena and distribution of molecular species during the unfolding of heme-free myoglobin in the presence of GdnHCl and urea as seen by time-resolved fluorescence spectroscopy. <i>Biophysical Chemistry</i> , 1989 , 33, 143-51	3.5	2
54	A 10-GHz frequency-domain fluorometer. <i>Review of Scientific Instruments</i> , 1990 , 61, 2331-2337	1.7	189
53	Rotational correlation times of peptides determined by perturbed angular correlations of E-rays. <i>European Biophysics Journal</i> , 1991 , 20, 193	1.9	11
52	Interaction of the p85 subunit of PI 3-kinase and its N-terminal SH2 domain with a PDGF receptor phosphorylation site: structural features and analysis of conformational changes.. <i>EMBO Journal</i> , 1992 , 11, 4261-4272	13	102
51	Fluorescence intensity and anisotropy decays of the intrinsic tryptophan emission of hemoglobin measured with a 10-GHz fluorometer using front-face geometry on a free liquid surface. <i>Journal of Fluorescence</i> , 1992 , 2, 29-36	2.4	11
50	Enhanced biopotency of synthetic C3a analogues by membrane binding. A fluorescence anisotropy decay study. <i>Biophysical Chemistry</i> , 1992 , 44, 151-61	3.5	8
49	Structure of neuropeptide Y dimer in solution. <i>FEBS Journal</i> , 1992 , 205, 1099-106		66
48	A novel photoactivatable cross-linker for the functionally-directed region-specific fluorescent labeling of proteins. <i>FEBS Journal</i> , 1992 , 206, 471-7		15
47	A study of the hinge-bending mechanism of yeast 3-phosphoglycerate kinase. <i>FEBS Journal</i> , 1992 , 208, 115-23		11
46	Tryptophan mutants of human C5a anaphylatoxin: a fluorescence anisotropy decay and energy transfer study. <i>Biophysical Chemistry</i> , 1993 , 46, 237-48	3.5	12
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44	Segmental dynamics of the cytoplasmic domain of erythrocyte band 3 determined by time-resolved fluorescence anisotropy: sensitivity to pH and ligand binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1994 , 91, 1741-5	11.5	40
43	Monitoring the effect of subunit assembly on the structural flexibility of human alpha apohemoglobin by steady-state fluorescence. <i>The Protein Journal</i> , 1994 , 13, 561-7		8
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41	Thermodynamic characterization of the cooperativity of 40S complex formation during the initiation of eukaryotic protein synthesis. <i>Biochemistry</i> , 1994 , 33, 15168-77	3.2	8
40	Application of fluorescence spectroscopy for determining the structure and function of proteins. <i>Pharmaceutical Biotechnology</i> , 1995 , 7, 1-63		12

39	Time-resolved fluorescence spectroscopy. <i>Methods in Enzymology</i> , 1995 , 246, 334-62	1.7	55
38	Structure and rotational dynamics of fluorescently labeled insulin in aqueous solution and at the amphiphile-water interface of reversed micelles. <i>Biochemistry</i> , 1995 , 34, 6130-41	3.2	17
37	Time-resolved fluorescence and anisotropy of covalently coupled 1-pyrenebutyric acid for monitoring the crystallization conditions of lysozyme. <i>Journal of Crystal Growth</i> , 1997 , 171, 226-235	1.6	10
36	The signal transducer gp130--bacterial expression, refolding and properties of the carboxy-terminal domain of the cytokine-binding module. <i>FEBS Journal</i> , 1997 , 247, 425-31		8
35	A comparative study on viscosity of human, bovine and pig IgG immunoglobulins in aqueous solutions. <i>International Journal of Biological Macromolecules</i> , 1999 , 26, 155-9	7.9	35
34	Probing the Structure, Function, Dynamics, and Folding of Snake Venom Cardiotoxins. <i>ACS Symposium Series</i> , 1999 , 222-248	0.4	
33	Nanosecond dynamics of tryptophans in different conformational states of apomyoglobin proteins. <i>Biochemistry</i> , 2000 , 39, 1879-89	3.2	42
32	Hormone-triggered conformational changes within the insulin-receptor ectodomain: requirement for transmembrane anchors. <i>Biochemical Journal</i> , 2001 , 360, 189-98	3.8	17
31	Hormone-triggered conformational changes within the insulin-receptor ectodomain: requirement for transmembrane anchors. <i>Biochemical Journal</i> , 2001 , 360, 189-198	3.8	29
30	DNA bends in TATA-binding protein-TATA complexes in solution are DNA sequence-dependent. <i>Journal of Biological Chemistry</i> , 2001 , 276, 14614-22	5.4	60
29	Time-resolved fluorescence resonance energy transfer studies of DNA bending in double-stranded oligonucleotides and in DNA-protein complexes. <i>Biopolymers</i> , 2001 , 61, 180-200	2.2	47
28	Mass spectrometric approaches using electrospray ionization charge states and hydrogen-deuterium exchange for determining protein structures and their conformational changes. <i>Molecular and Cellular Proteomics</i> , 2004 , 3, 10-23	7.6	79
27	Fluorescence anisotropy as a probe to study tracer proteins in crowded solutions. <i>Journal of Molecular Recognition</i> , 2004 , 17, 408-16	2.6	16
26	Fluorescence techniques for studying protein structure. <i>Methods of Biochemical Analysis</i> , 1991 , 35, 127-205		260
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19	The effect of local dynamics of Atto 390-labeled lysozyme on fluorescence anisotropy modeling. <i>Biopolymers</i> , 2015 , 103, 285-95	2.2	2
18	Sucralose Destabilization of Protein Structure. <i>Journal of Physical Chemistry Letters</i> , 2015 , 6, 1441-6	6.4	13
17	Multiscale modeling for interpreting nuclear magnetic resonance relaxation in flexible molecules. <i>International Journal of Quantum Chemistry</i> , 2016 , 116, 1706-1722	2.1	3
16	Molecular dynamics simulations indicate that deoxyhemoglobin, oxyhemoglobin, carboxyhemoglobin, and glycated hemoglobin under compression and shear exhibit an anisotropic mechanical behavior. <i>Journal of Biomolecular Structure and Dynamics</i> , 2018 , 36, 1417-1429	3.6	7
15	Stochastic modeling of macromolecules in solution. I. Relaxation processes. <i>Journal of Chemical Physics</i> , 2019 , 150, 184107	3.9	4
14	Stochastic modeling of macromolecules in solution. II. Spectral densities. <i>Journal of Chemical Physics</i> , 2019 , 150, 184108	3.9	4
13	Detailed characterization of the solution kinetics and thermodynamics of biotin, biocytin and HABA binding to avidin and streptavidin. <i>PLoS ONE</i> , 2019 , 14, e0204194	3.7	17
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11	On the Interpretation of subtilisin Carlsberg Time-Resolved Fluorescence Anisotropy Decays: Modeling with Classical Simulations. <i>Journal of Chemical Information and Modeling</i> , 2020 , 60, 747-755	6.1	2
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- 2 Improved Characterization of the Solution Kinetics and Thermodynamics of Biotin, Biocytin and HABA Binding to Avidin and Streptavidin.
- 1 Interaction of the p85 subunit of PI 3-kinase and its N-terminal SH2 domain with a PDGF receptor phosphorylation site: structural features and analysis of conformational changes. *EMBO Journal*, **1992**, 11, 4261-72 13 41