

Wayne L Hubbell

List of Publications by Year in descending order

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72
papers

7,883
citations

61687

45
h-index

100535

70
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74
all docs

74
docs citations

74
times ranked

6677
citing authors

#	ARTICLE	IF	CITATIONS
1	Lipid bilayer induces contraction of the denatured state ensemble of a helical-bundle membrane protein. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, .	3.3	9
2	DEER Analysis of GPCR Conformational Heterogeneity. <i>Biomolecules</i> , 2021, 11, 778.	1.8	24
3	Viewing rare conformations of the β_2 adrenergic receptor with pressure-resolved DEER spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 31824-31831.	3.3	31
4	Resolving dynamics and function of transient states in single enzyme molecules. <i>Nature Communications</i> , 2020, 11, 1231.	5.8	71
5	Angiotensin Analogs with Divergent Bias Stabilize Distinct Receptor Conformations. <i>Cell</i> , 2019, 176, 468-478.e11.	13.5	194
6	Conformational heterogeneity of the allosteric drug and metabolite (ADaM) site in AMP-activated protein kinase (AMPK). <i>Journal of Biological Chemistry</i> , 2018, 293, 16994-17007.	1.6	13
7	DEER Spectroscopy Measurements Reveal Multiple Conformations of HIV-1 SOSIP Envelopes that Show Similarities with Envelopes on Native Virions. <i>Immunity</i> , 2018, 49, 235-246.e4.	6.6	68
8	Conformational equilibria of light-activated rhodopsin in nanodiscs. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3268-E3275.	3.3	84
9	Analysis of Saturation Recovery Amplitudes to Characterize Conformational Exchange in Spin-Labeled Proteins. <i>Applied Magnetic Resonance</i> , 2017, 48, 1315-1340.	0.6	3
10	Identification of Phosphorylation Codes for Arrestin Recruitment by G Protein-Coupled Receptors. <i>Cell</i> , 2017, 170, 457-469.e13.	13.5	344
11	A triarylmethyl spin label for long-range distance measurement at physiological temperatures using T ₁ relaxation enhancement. <i>Journal of Magnetic Resonance</i> , 2016, 269, 50-54.	1.2	50
12	Conformational Mobility in Cytochrome P450 3A4 Explored by Pressure-Perturbation EPR Spectroscopy. <i>Biophysical Journal</i> , 2016, 110, 1485-1498.	0.2	25
13	A PII-Like Protein Regulated by Bicarbonate: Structural and Biochemical Studies of the Carboxysome-Associated CPII Protein. <i>Journal of Molecular Biology</i> , 2016, 428, 4013-4030.	2.0	20
14	Biophysical and Biochemical Characterization of Avian Secretory Component Provides Structural Insights into the Evolution of the Polymeric Ig Receptor. <i>Journal of Immunology</i> , 2016, 197, 1408-1414.	0.4	17
15	Steric trapping reveals a cooperativity network in the intramembrane protease GlpG. <i>Nature Chemical Biology</i> , 2016, 12, 353-360.	3.9	45
16	Saturation Recovery EPR and Nitroxide Spin Labeling for Exploring Structure and Dynamics in Proteins. <i>Methods in Enzymology</i> , 2015, 564, 3-27.	0.4	15
17	High-Pressure EPR and Site-Directed Spin Labeling for Mapping Molecular Flexibility in Proteins. <i>Methods in Enzymology</i> , 2015, 564, 29-57.	0.4	11
18	Exploring Structure, Dynamics, and Topology of Nitroxide Spin-Labeled Proteins Using Continuous-Wave Electron Paramagnetic Resonance Spectroscopy. <i>Methods in Enzymology</i> , 2015, 564, 59-100.	0.4	44

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19	The guanine nucleotide exchange factor Ric-8A induces domain separation and Ras domain plasticity in G1±11. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 1404-1409.	3.3	23
20	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. <i>Nature</i> , 2015, 523, 561-567.	13.7	683
21	Structural basis for nucleotide exchange in heterotrimeric G proteins. <i>Science</i> , 2015, 348, 1361-1365.	6.0	250
22	Structure-relaxation mechanism for the response of T4 lysozyme cavity mutants to hydrostatic pressure. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E2437-46.	3.3	36
23	Structural Insights into the Dynamic Process of β_2 -Adrenergic Receptor Signaling. <i>Cell</i> , 2015, 161, 1101-1111.	13.5	562
24	Mapping protein conformational heterogeneity under pressure with site-directed spin labeling and double electron-electron resonance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E1201-10.	3.3	40
25	Structural and energetic determinants of adhesive binding specificity in type I cadherins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, E4175-84.	3.3	78
26	Technological advances in site-directed spin labeling of proteins. <i>Current Opinion in Structural Biology</i> , 2013, 23, 725-733.	2.6	262
27	Conformational selection and adaptation to ligand binding in T4 lysozyme cavity mutants. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4306-15.	3.3	46
28	Circular dichroism and site-directed spin labeling reveal structural and dynamical features of high-pressure states of myoglobin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, E4714-22.	3.3	44
29	Probing Protein Secondary Structure Using EPR: Investigating a Dynamic Region of Visual Arrestin. <i>Applied Magnetic Resonance</i> , 2012, 43, 405-419.	0.6	5
30	Mapping Molecular Flexibility of Proteins with Site-Directed Spin Labeling: A Case Study of Myoglobin. <i>Biochemistry</i> , 2012, 51, 6568-6583.	1.2	56
31	Structure and dynamics of a conformationally constrained nitroxide side chain and applications in EPR spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 16241-16246.	3.3	152
32	High-pressure EPR reveals conformational equilibria and volumetric properties of spin-labeled proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 1331-1336.	3.3	88
33	Interaction of a G protein with an activated receptor opens the interdomain interface in the alpha subunit. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2011, 108, 9420-9424.	3.3	145
34	Resolving Conformational and Rotameric Exchange in Spin-Labeled Proteins Using Saturation Recovery EPR. <i>Applied Magnetic Resonance</i> , 2010, 37, 363-390.	0.6	60
35	Osmolyte perturbation reveals conformational equilibria in spin-labeled proteins. <i>Protein Science</i> , 2009, 18, 1637-1652.	3.1	99
36	Structural origin of weakly ordered nitroxide motion in spin-labeled proteins. <i>Protein Science</i> , 2009, 18, 893-908.	3.1	103

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37	Structural determinants of nitroxide motion in spin-labeled proteins: Solvent-exposed sites in helix B of T4 lysozyme. <i>Protein Science</i> , 2008, 17, 228-239.	3.1	111
38	High-resolution distance mapping in rhodopsin reveals the pattern of helix movement due to activation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7439-7444.	3.3	436
39	A site-directed spin labeling study of arrestin conformation in solution and bound to activated rhodopsin. <i>FASEB Journal</i> , 2008, 22, 645.6.	0.2	0
40	Structural determinants of nitroxide motion in spin-labeled proteins: Tertiary contact and solvent-inaccessible sites in helix G of T4 lysozyme. <i>Protein Science</i> , 2007, 16, 1069-1086.	3.1	101
41	Conformational States and Dynamics of Rhodopsin in Micelles and Bilayers. <i>Biochemistry</i> , 2006, 45, 5538-5550.	1.2	83
42	Structural basis of receptor-dependent G protein activation. <i>FASEB Journal</i> , 2006, 20, A918.	0.2	0
43	Accessibility and Dynamics of Nitroxide Side Chains in T4 Lysozyme Measured by Saturation Recovery EPR. <i>Biophysical Journal</i> , 2005, 89, 2059-2068.	0.2	65
44	Accessibility of Nitroxide Side Chains: Absolute Heisenberg Exchange Rates from Power Saturation EPR. <i>Biophysical Journal</i> , 2005, 89, 2103-2112.	0.2	125
45	Mapping Backbone Dynamics in Solution with Site-Directed Spin Labeling: GCN4 ^{bZip} Free and Bound to DNA. <i>Biochemistry</i> , 2004, 43, 7273-7287.	1.2	128
46	Rhodopsin structure, dynamics, and activation: A perspective from crystallography, site-directed spin labeling, sulfhydryl reactivity, and disulfide cross-linking. <i>Advances in Protein Chemistry</i> , 2003, 63, 243-290.	4.4	332
47	Structure and Dynamics of a Helical Hairpin and Loop Region in Annexin 12: A Site-Directed Spin Labeling Study. <i>Biochemistry</i> , 2002, 41, 1464-1473.	1.2	118
48	Helix Packing in the Lactose Permease of <i>Escherichia coli</i> : Distances between Site-Directed Nitroxides and a Lanthanide. <i>Biochemistry</i> , 2001, 40, 3184-3188.	1.2	27
49	Molecular Motion of Spin Labeled Side Chains in α -Helices: Analysis by Variation of Side Chain Structure. <i>Biochemistry</i> , 2001, 40, 3828-3846.	1.2	266
50	Structure and Function in Rhodopsin: Mapping Light-Dependent Changes in Distance between Residue 65 in Helix TM1 and Residues in the Sequence 306 ³¹⁹ at the Cytoplasmic End of Helix TM7 and in Helix H8. <i>Biochemistry</i> , 2001, 40, 15483-15492.	1.2	107
51	Probing the Dark State Tertiary Structure in the Cytoplasmic Domain of Rhodopsin: Proximities between Amino Acids Deduced from Spontaneous Disulfide Bond Formation between Cysteine Pairs Engineered in Cytoplasmic Loops 1, 3, and 4. <i>Biochemistry</i> , 2001, 40, 12479-12485.	1.2	29
52	Quantitative Analysis of the Isolated GAAA Tetraloop/Receptor Interaction in Solution: A Site-Directed Spin Labeling Study. <i>Biochemistry</i> , 2001, 40, 6929-6936.	1.2	125
53	Probing the Dark State Tertiary Structure in the Cytoplasmic Domain of Rhodopsin: Proximities between Amino Acids Deduced from Spontaneous Disulfide Bond Formation between Cys316 and Engineered Cysteines in Cytoplasmic Loop 1. <i>Biochemistry</i> , 2001, 40, 12472-12478.	1.2	27
54	Crystal Structures of Spin Labeled T4 Lysozyme Mutants: Implications for the Interpretation of EPR Spectra in Terms of Structure. <i>Biochemistry</i> , 2000, 39, 8396-8405.	1.2	242

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55	Protein global fold determination using site-directed spin and isotope labeling. <i>Protein Science</i> , 2000, 9, 302-309.	3.1	81
56	Structure of the KcsA Potassium Channel from <i>Streptomyces lividans</i> : A Site-Directed Spin Labeling Study of the Second Transmembrane Segment. <i>Biochemistry</i> , 1999, 38, 10324-10335.	1.2	122
57	Structure and Function in Rhodopsin: Effects of Disulfide Cross-Links in the Cytoplasmic Face of Rhodopsin on Transducin Activation and Phosphorylation by Rhodopsin Kinase. <i>Biochemistry</i> , 1999, 38, 12893-12898.	1.2	78
58	Motion of Spin-Labeled Side Chains in T4 Lysozyme: Effect of Side Chain Structure. <i>Biochemistry</i> , 1999, 38, 2947-2955.	1.2	97
59	Structural Features and Light-Dependent Changes in the Sequence 59~75 Connecting Helices I and II in Rhodopsin: A Site-Directed Spin-Labeling Study. <i>Biochemistry</i> , 1999, 38, 7945-7949.	1.2	103
60	Single-Cysteine Substitution Mutants at Amino Acid Positions 306~321 in Rhodopsin, the Sequence between the Cytoplasmic End of Helix VII and the Palmitoylation Sites: Sulfhydryl Reactivity and Transducin Activation Reveal a Tertiary Structure. <i>Biochemistry</i> , 1999, 38, 7925-7930.	1.2	80
61	Proximity between Periplasmic Loops in the Lactose Permease of <i>Escherichia coli</i> As Determined by Site-Directed Spin Labeling. <i>Biochemistry</i> , 1999, 38, 3100-3105.	1.2	31
62	Proximity between Glu126 and Arg144 in the Lactose Permease of <i>Escherichia coli</i> . <i>Biochemistry</i> , 1999, 38, 7407-7412.	1.2	67
63	Structure in the channel forming domain of colicin E1 bound to membranes: The 402~424 sequence. <i>Protein Science</i> , 1999, 8, 562-572.	3.1	24
64	Arginine 302 (Helix IX) in the Lactose Permease of <i>Escherichia coli</i> Is in Close Proximity to Glutamate 269 (Helix VIII) as Well as Glutamate 325 (Helix X). <i>Biochemistry</i> , 1997, 36, 13682-13687.	1.2	24
65	Site-Directed Spin-Labeling of Transmembrane Domain VII and the 4B1 Antibody Epitope in the Lactose Permease of <i>Escherichia coli</i> . <i>Biochemistry</i> , 1997, 36, 15055-15061.	1.2	39
66	Structural Features and Light-Dependent Changes in the Cytoplasmic Interhelical E~F Loop Region of Rhodopsin: A Site-Directed Spin-Labeling Study. <i>Biochemistry</i> , 1996, 35, 12470-12478.	1.2	301
67	Structure and Function in Rhodopsin. Cysteines 65 and 316 Are in Proximity in a Rhodopsin Mutant As Indicated by Disulfide Formation and Interactions between Attached Spin Labels. <i>Biochemistry</i> , 1996, 35, 14040-14046.	1.2	111
68	Site-Directed Spin Labeling Demonstrates That Transmembrane Domain XII in the Lactose Permease of <i>Escherichia coli</i> Is an α -Helix. <i>Biochemistry</i> , 1996, 35, 12915-12918.	1.2	47
69	Tear lipocalins bind a broad array of lipid ligands. <i>Current Eye Research</i> , 1995, 14, 363-372.	0.7	165
70	SPIN LABELED CYSTEINES AS SENSORS FOR PROTEIN~LIPID INTERACTION AND CONFORMATION IN RHODOPSIN. <i>Photochemistry and Photobiology</i> , 1992, 56, 1019-1033.	1.3	140
71	The aggregation state of spin-labeled melittin in solution and bound to phospholipid membranes: Evidence that membrane-bound melittin is monomeric. <i>Proteins: Structure, Function and Bioinformatics</i> , 1988, 3, 230-242.	1.5	101
72	Continuous and stopped flow EPR spectrometer based on a loop gap resonator. <i>Review of Scientific Instruments</i> , 1987, 58, 1879-1886.	0.6	150