

# Wayne L Hubbell

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/7457217/publications.pdf>

Version: 2024-02-01

72  
papers

7,883  
citations

53794

45  
h-index

88630

70  
g-index

74  
all docs

74  
docs citations

74  
times ranked

5921  
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, .	7.1	9
2	DEER Analysis of GPCR Conformational Heterogeneity. <i>Biomolecules</i> , 2021, 11, 778.	4.0	24
3	Viewing rare conformations of the $\beta_2$ 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.	7.1	31
4	Resolving dynamics and function of transient states in single enzyme molecules. <i>Nature Communications</i> , 2020, 11, 1231.	12.8	71
5	Angiotensin Analogs with Divergent Bias Stabilize Distinct Receptor Conformations. <i>Cell</i> , 2019, 176, 468-478.e11.	28.9	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.	3.4	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.	14.3	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.	7.1	84
9	Analysis of Saturation Recovery Amplitudes to Characterize Conformational Exchange in Spin-Labeled Proteins. <i>Applied Magnetic Resonance</i> , 2017, 48, 1315-1340.	1.2	3
10	Identification of Phosphorylation Codes for Arrestin Recruitment by G Protein-Coupled Receptors. <i>Cell</i> , 2017, 170, 457-469.e13.	28.9	344
11	A triarylmethyl spin label for long-range distance measurement at physiological temperatures using T <sub>1</sub> relaxation enhancement. <i>Journal of Magnetic Resonance</i> , 2016, 269, 50-54.	2.1	50
12	Conformational Mobility in Cytochrome P450 3A4 Explored by Pressure-Perturbation EPR Spectroscopy. <i>Biophysical Journal</i> , 2016, 110, 1485-1498.	0.5	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.	4.2	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.	0.8	17
15	Steric trapping reveals a cooperativity network in the intramembrane protease GlpG. <i>Nature Chemical Biology</i> , 2016, 12, 353-360.	8.0	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.	1.0	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.	1.0	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.	1.0	44

#	ARTICLE	IF	CITATIONS
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.	7.1	23
20	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. <i>Nature</i> , 2015, 523, 561-567.	27.8	683
21	Structural basis for nucleotide exchange in heterotrimeric G proteins. <i>Science</i> , 2015, 348, 1361-1365.	12.6	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.	7.1	36
23	Structural Insights into the Dynamic Process of $\beta_2$ -Adrenergic Receptor Signaling. <i>Cell</i> , 2015, 161, 1101-1111.	28.9	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.	7.1	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.	7.1	78
26	Technological advances in site-directed spin labeling of proteins. <i>Current Opinion in Structural Biology</i> , 2013, 23, 725-733.	5.7	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.	7.1	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.	7.1	44
29	Probing Protein Secondary Structure Using EPR: Investigating a Dynamic Region of Visual Arrestin. <i>Applied Magnetic Resonance</i> , 2012, 43, 405-419.	1.2	5
30	Mapping Molecular Flexibility of Proteins with Site-Directed Spin Labeling: A Case Study of Myoglobin. <i>Biochemistry</i> , 2012, 51, 6568-6583.	2.5	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.	7.1	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.	7.1	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.	7.1	145
34	Resolving Conformational and Rotameric Exchange in Spin-Labeled Proteins Using Saturation Recovery EPR. <i>Applied Magnetic Resonance</i> , 2010, 37, 363-390.	1.2	60
35	Osmolyte perturbation reveals conformational equilibria in spin-labeled proteins. <i>Protein Science</i> , 2009, 18, 1637-1652.	7.6	99
36	Structural origin of weakly ordered nitroxide motion in spin-labeled proteins. <i>Protein Science</i> , 2009, 18, 893-908.	7.6	103

#	ARTICLE	IF	CITATIONS
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.	7.6	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.	7.1	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.	0.5	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.	7.6	101
41	Conformational States and Dynamics of Rhodopsin in Micelles and Bilayers. <i>Biochemistry</i> , 2006, 45, 5538-5550.	2.5	83
42	Structural basis of receptor-dependent G protein activation. <i>FASEB Journal</i> , 2006, 20, A918.	0.5	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.	0.5	65
44	Accessibility of Nitroxide Side Chains: Absolute Heisenberg Exchange Rates from Power Saturation EPR. <i>Biophysical Journal</i> , 2005, 89, 2103-2112.	0.5	125
45	Mapping Backbone Dynamics in Solution with Site-Directed Spin Labeling: GCN4 <sup>bZip</sup> Free and Bound to DNA. <i>Biochemistry</i> , 2004, 43, 7273-7287.	2.5	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.	2.5	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.	2.5	27
49	Molecular Motion of Spin Labeled Side Chains in $\alpha$ -Helices: Analysis by Variation of Side Chain Structure. <i>Biochemistry</i> , 2001, 40, 3828-3846.	2.5	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 <sup>319</sup> at the Cytoplasmic End of Helix TM7 and in Helix H8. <i>Biochemistry</i> , 2001, 40, 15483-15492.	2.5	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.	2.5	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.	2.5	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.	2.5	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.	2.5	242

#	ARTICLE	IF	CITATIONS
55	Protein global fold determination using site-directed spin and isotope labeling. <i>Protein Science</i> , 2000, 9, 302-309.	7.6	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.	2.5	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.	2.5	78
58	Motion of Spin-Labeled Side Chains in T4 Lysozyme: Effect of Side Chain Structure. <i>Biochemistry</i> , 1999, 38, 2947-2955.	2.5	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.	2.5	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: A Sulfhydryl Reactivity and Transducin Activation Reveal a Tertiary Structure. <i>Biochemistry</i> , 1999, 38, 7925-7930.	2.5	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.	2.5	31
62	Proximity between Glu126 and Arg144 in the Lactose Permease of <i>Escherichia coli</i> . <i>Biochemistry</i> , 1999, 38, 7407-7412.	2.5	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.	7.6	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.	2.5	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.	2.5	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.	2.5	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.	2.5	111
68	Site-Directed Spin Labeling Demonstrates That Transmembrane Domain XII in the Lactose Permease of <i>Escherichia coli</i> Is a Helix. <i>Biochemistry</i> , 1996, 35, 12915-12918.	2.5	47
69	Tear lipocalins bind a broad array of lipid ligands. <i>Current Eye Research</i> , 1995, 14, 363-372.	1.5	165
70	SPIN LABELED CYSTEINES AS SENSORS FOR PROTEIN-LIPID INTERACTION AND CONFORMATION IN RHODOPSIN. <i>Photochemistry and Photobiology</i> , 1992, 56, 1019-1033.	2.5	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.	2.6	101
72	Continuous and stopped flow EPR spectrometer based on a loop gap resonator. <i>Review of Scientific Instruments</i> , 1987, 58, 1879-1886.	1.3	150