

Christian Altenbach

List of Publications by Year in descending order

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56
papers

7,706
citations

87886

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h-index

161844

54
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56
all docs

56
docs citations

56
times ranked

4710
citing authors

#	ARTICLE	IF	CITATIONS
1	Identifying conformational changes with site-directed spin labeling. <i>Nature Structural Biology</i> , 2000, 7, 735-739.	9.7	737
2	Structural Insights into the Dynamic Process of β_2 -Adrenergic Receptor Signaling. <i>Cell</i> , 2015, 161, 1101-1111.	28.9	562
3	Transmembrane protein structure: spin labeling of bacteriorhodopsin mutants. <i>Science</i> , 1990, 248, 1088-1092.	12.6	488
4	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
5	Watching proteins move using site-directed spin labeling. <i>Structure</i> , 1996, 4, 779-783.	3.3	433
6	Investigation of structure and dynamics in membrane proteins using site-directed spin labeling. <i>Current Opinion in Structural Biology</i> , 1994, 4, 566-573.	5.7	409
7	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
8	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
9	Structural studies on transmembrane proteins. 2. Spin labeling of bacteriorhodopsin mutants at unique cysteines. <i>Biochemistry</i> , 1989, 28, 7806-7812.	2.5	291
10	Technological advances in site-directed spin labeling of proteins. <i>Current Opinion in Structural Biology</i> , 2013, 23, 725-733.	5.7	262
11	Estimation of Inter-Residue Distances in Spin Labeled Proteins at Physiological Temperatures: Experimental Strategies and Practical Limitations. <i>Biochemistry</i> , 2001, 40, 15471-15482.	2.5	239
12	Site-directed spin labeling of a genetically encoded unnatural amino acid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2009, 106, 21637-21642.	7.1	230
13	Interaction of α -crystallin with Spin-Labeled Peptides. <i>Biochemistry</i> , 1995, 34, 509-516.	2.5	209
14	Sugar binding induces an outward facing conformation of LacY. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 16504-16509.	7.1	161
15	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
16	Structural Features and Light-Dependent Changes in the Sequence 306 ⁺ 322 Extending from Helix VII to the Palmitoylation Sites in Rhodopsin: A Site-Directed Spin-Labeling Study. <i>Biochemistry</i> , 1999, 38, 7931-7937.	2.5	129
17	Accessibility of Nitroxide Side Chains: Absolute Heisenberg Exchange Rates from Power Saturation EPR. <i>Biophysical Journal</i> , 2005, 89, 2103-2112.	0.5	125
18	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

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19	High Resolution Structure and Double Electron-Electron Resonance of the Zebrafish Voltage-dependent Anion Channel 2 Reveal an Oligomeric Population. <i>Journal of Biological Chemistry</i> , 2014, 289, 12566-12577.	3.4	116
20	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
21	Structure and Function in Rhodopsin: Mapping Light-Dependent Changes in Distance between Residue 316 in Helix 8 and Residues in the Sequence 60 [~] 75, Covering the Cytoplasmic End of Helices TM1 and TM2 and Their Connection Loop CL1. <i>Biochemistry</i> , 2001, 40, 15493-15500.	2.5	110
22	Structural origins of constitutive activation in rhodopsin: Role of the K296/E113 salt bridge. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 12508-12513.	7.1	109
23	Arrangement of subunits and ordering of β^2 -strands in an amyloid sheet. <i>Nature Structural Biology</i> , 2002, 9, 734-739.	9.7	108
24	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.	2.5	107
25	Structure and function of the visual arrestin oligomer. <i>EMBO Journal</i> , 2007, 26, 1726-1736.	7.8	104
26	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
27	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
28	Structural Features of the C-Terminal Domain of Bovine Rhodopsin: A Site-Directed Spin-Labeling Study. <i>Biochemistry</i> , 1999, 38, 7918-7924.	2.5	101
29	Conformational States and Dynamics of Rhodopsin in Micelles and Bilayers. <i>Biochemistry</i> , 2006, 45, 5538-5550.	2.5	83
30	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
31	Single-Cysteine Substitution Mutants at Amino Acid Positions 55 [~] 75, the Sequence Connecting the Cytoplasmic Ends of Helices I and II in Rhodopsin: Reactivity of the Sulfhydryl Groups and Their Derivatives Identifies a Tertiary Structure that Changes upon Light-Activation. <i>Biochemistry</i> , 1999, 38, 7938-7944.	2.5	69
32	Identification of a Subunit Interface in Transthyretin Amyloid Fibrils: Evidence for Self-Assembly from Oligomeric Building Blocks. <i>Biochemistry</i> , 2001, 40, 9089-9096.	2.5	69
33	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
34	G _i - and G _s -coupled GPCRs show different modes of G-protein binding. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 2383-2388.	7.1	64
35	Site-Directed Spin Labeling of Proteins: Applications to Diphtheria Toxin. , 2000, 145, 147-169.		50
36	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

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37	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
38	Structure and dynamics of an imidazoline nitroxide side chain with strongly hindered internal motion in proteins. <i>Journal of Magnetic Resonance</i> , 2013, 232, 53-61.	2.1	43
39	Structural States and Dynamics of the D-Loop in Actin. <i>Biophysical Journal</i> , 2012, 103, 930-939.	0.5	42
40	Conformation of the Diphtheria Toxin T Domain in Membranes: A Site-Directed Spin-Labeling Study of the TH8 Helix and TL5 Loop. <i>Biochemistry</i> , 1999, 38, 10336-10343.	2.5	41
41	Engineering Visual Arrestin-1 with Special Functional Characteristics. <i>Journal of Biological Chemistry</i> , 2013, 288, 3394-3405.	3.4	32
42	Site directed spin labeling studies of structure and dynamics in bacteriorhodopsin. <i>Biophysical Chemistry</i> , 1995, 56, 89-94.	2.8	31
43	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
44	Site-Directed Spin Labeling of Membrane Proteins. , 1994, , 224-248.		29
45	Nitroxide Scanning Electron Paramagnetic Resonance of Helices IV and V and the Intervening Loop in the Lactose Permease of <i>Escherichia coli</i> . <i>Biochemistry</i> , 1999, 38, 15970-15977.	2.5	28
46	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
47	Rapid degeneration of rod photoreceptors expressing self-association-deficient arrestin-1 mutant. <i>Cellular Signalling</i> , 2013, 25, 2613-2624.	3.6	26
48	Protonation state of glutamate 73 regulates the formation of a specific dimeric association of mVDAC1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E172-E179.	7.1	26
49	Self-Association of Arrestin Family Members. <i>Handbook of Experimental Pharmacology</i> , 2014, 219, 205-223.	1.8	25
50	Hydrophobic Loop Dynamics and Actin Filament Stability. <i>Biochemistry</i> , 2006, 45, 13576-13584.	2.5	21
51	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
52	An Eight Amino Acid Segment Controls Oligomerization and Preferred Conformation of the two Non-visual Arrestins. <i>Journal of Molecular Biology</i> , 2021, 433, 166790.	4.2	15
53	Site-directed spin labeling of a bacterial chemoreceptor reveals a dynamic, loosely packed transmembrane domain. <i>Protein Science</i> , 2002, 11, 1472-1481.	7.6	13
54	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

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55	Site-directed spin labeling electron paramagnetic resonance study of the ORF1 protein from a mouse L1 retrotransposon. <i>Protein Science</i> , 2011, 20, 1231-1243.	7.6	3
56	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