

# Christian Altenbach

## List of Publications by Year in descending order

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56  
papers

7,706  
citations

87888

38  
h-index

161849

54  
g-index

56  
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56  
docs citations

56  
times ranked

4710  
citing authors

#	ARTICLE	IF	CITATIONS
1	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
2	G <sup>i</sup> - and G <sup>s</sup> -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
3	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
4	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
5	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
6	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
7	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
8	Structural Insights into the Dynamic Process of $\beta_2$ -Adrenergic Receptor Signaling. <i>Cell</i> , 2015, 161, 1101-1111.	28.9	562
9	Self-Association of Arrestin Family Members. <i>Handbook of Experimental Pharmacology</i> , 2014, 219, 205-223.	1.8	25
10	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
11	Technological advances in site-directed spin labeling of proteins. <i>Current Opinion in Structural Biology</i> , 2013, 23, 725-733.	5.7	262
12	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
13	Rapid degeneration of rod photoreceptors expressing self-association-deficient arrestin-1 mutant. <i>Cellular Signalling</i> , 2013, 25, 2613-2624.	3.6	26
14	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
15	Engineering Visual Arrestin-1 with Special Functional Characteristics. <i>Journal of Biological Chemistry</i> , 2013, 288, 3394-3405.	3.4	32
16	Structural States and Dynamics of the D-Loop in Actin. <i>Biophysical Journal</i> , 2012, 103, 930-939.	0.5	42
17	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
18	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

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19	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
20	Structure and function of the visual arrestin oligomer. <i>EMBO Journal</i> , 2007, 26, 1726-1736.	7.8	104
21	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
22	Hydrophobic Loop Dynamics and Actin Filament Stability. <i>Biochemistry</i> , 2006, 45, 13576-13584.	2.5	21
23	Conformational States and Dynamics of Rhodopsin in Micelles and Bilayers. <i>Biochemistry</i> , 2006, 45, 5538-5550.	2.5	83
24	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
25	Accessibility of Nitroxide Side Chains: Absolute Heisenberg Exchange Rates from Power Saturation EPR. <i>Biophysical Journal</i> , 2005, 89, 2103-2112.	0.5	125
26	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
27	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
28	Arrangement of subunits and ordering of $\beta$ -strands in an amyloid sheet. <i>Nature Structural Biology</i> , 2002, 9, 734-739.	9.7	108
29	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
30	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
31	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
32	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
33	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
34	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
35	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
36	Identifying conformational changes with site-directed spin labeling. <i>Nature Structural Biology</i> , 2000, 7, 735-739.	9.7	737

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37	Site-Directed Spin Labeling of Proteins: Applications to Diphtheria Toxin. , 2000, 145, 147-169.		50
38	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
39	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
40	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
41	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
42	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
43	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
44	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
45	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.	2.5	80
46	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
47	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
48	Watching proteins move using site-directed spin labeling. <i>Structure</i> , 1996, 4, 779-783.	3.3	433
49	Site directed spin labeling studies of structure and dynamics in bacteriorhodopsin. <i>Biophysical Chemistry</i> , 1995, 56, 89-94.	2.8	31
50	Interaction of .alpha.-crystallin with Spin-Labeled Peptides. <i>Biochemistry</i> , 1995, 34, 509-516.	2.5	209
51	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
52	Site-Directed Spin Labeling of Membrane Proteins. , 1994, , 224-248.		29
53	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
54	Transmembrane protein structure: spin labeling of bacteriorhodopsin mutants. <i>Science</i> , 1990, 248, 1088-1092.	12.6	488

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55	Structural studies on transmembrane proteins. 2. Spin labeling of bacteriorhodopsin mutants at unique cysteines. <i>Biochemistry</i> , 1989, 28, 7806-7812.	2.5	291
56	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