

Christian Altenbach

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56
papers

6,826
citations

38
h-index

56
g-index

56
ext. papers

7,260
ext. citations

6.1
avg, IF

5.41
L-index

#	Paper	IF	Citations
56	Identifying conformational changes with site-directed spin labeling. <i>Nature Structural Biology</i> , 2000 , 7, 735-9		670
55	Transmembrane protein structure: spin labeling of bacteriorhodopsin mutants. <i>Science</i> , 1990 , 248, 1088-92	3.2	438
54	Structural Insights into the Dynamic Process of β -Adrenergic Receptor Signaling. <i>Cell</i> , 2015 , 161, 1101-1112	16.2	409
53	Watching proteins move using site-directed spin labeling. <i>Structure</i> , 1996 , 4, 779-83	5.2	395
52	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, 7439-44	11.5	385
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	8.1	377
50	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, 243-90		295
49	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, 12470-8	3.2	284
48	Structural studies on transmembrane proteins. 2. Spin labeling of bacteriorhodopsin mutants at unique cysteines. <i>Biochemistry</i> , 1989 , 28, 7806-12	3.2	254
47	Technological advances in site-directed spin labeling of proteins. <i>Current Opinion in Structural Biology</i> , 2013 , 23, 725-33	8.1	215
46	Estimation of inter-residue distances in spin labeled proteins at physiological temperatures: experimental strategies and practical limitations. <i>Biochemistry</i> , 2001 , 40, 15471-82	3.2	211
45	Interaction of alpha-crystallin with spin-labeled peptides. <i>Biochemistry</i> , 1995 , 34, 509-16	3.2	204
44	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, 21637-42	11.5	196
43	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, 16504-9	11.5	155
42	Spin labeled cysteines as sensors for protein-lipid interaction and conformation in rhodopsin. <i>Photochemistry and Photobiology</i> , 1992 , 56, 1019-33	3.6	129
41	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, 7931-7	3.2	123
40	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, 10324-35	3.2	116

39	Accessibility of nitroxide side chains: absolute Heisenberg exchange rates from power saturation EPR. <i>Biophysical Journal</i> , 2005 , 89, 2103-12	2.9	105
38	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, 15493-500	3.2	104
37	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, 14040-6	3.2	104
36	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, 12566-77	5.4	102
35	Arrangement of subunits and ordering of beta-strands in an amyloid sheet. <i>Nature Structural Biology</i> , 2002 , 9, 734-9		101
34	Structural features of the C-terminal domain of bovine rhodopsin: a site-directed spin-labeling study. <i>Biochemistry</i> , 1999 , 38, 7918-24	3.2	97
33	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, 7945-9	3.2	97
32	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, 12508-13	11.5	96
31	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, 15483-92	3.2	96
30	Structure and function of the visual arrestin oligomer. <i>EMBO Journal</i> , 2007 , 26, 1726-36	13	92
29	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, 230-42	4.2	92
28	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, 7925-30	3.2	80
27	Conformational states and dynamics of rhodopsin in micelles and bilayers. <i>Biochemistry</i> , 2006 , 45, 5538-50	3.2	70
26	Identification of a subunit interface in transthyretin amyloid fibrils: evidence for self-assembly from oligomeric building blocks. <i>Biochemistry</i> , 2001 , 40, 9089-96	3.2	67
25	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, 7938-44	3.2	66
24	Accessibility and dynamics of nitroxide side chains in T4 lysozyme measured by saturation recovery EPR. <i>Biophysical Journal</i> , 2005 , 89, 2059-68	2.9	48
23	Site-directed spin labeling of proteins. Applications to diphtheria toxin. <i>Methods in Molecular Biology</i> , 2000 , 145, 147-69	1.4	47
22	G- and G-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	11.5	45

21	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, 10336-43	3.2	41
20	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	1.7	39
19	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	11.5	38
18	Structural states and dynamics of the D-loop in actin. <i>Biophysical Journal</i> , 2012 , 103, 930-9	2.9	32
17	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	3	30
16	Engineering visual arrestin-1 with special functional characteristics. <i>Journal of Biological Chemistry</i> , 2013 , 288, 3394-405	5.4	29
15	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, 12479-85	3.2	28
14	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, 15970-7	3.2	28
13	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, 12472-8	3.2	27
12	Site directed spin labeling studies of structure and dynamics in bacteriorhodopsin. <i>Biophysical Chemistry</i> , 1995 , 56, 89-94	3.5	27
11	Site-Directed Spin Labeling of Membrane Proteins 1994 , 224-248		25
10	Self-association of arrestin family members. <i>Handbook of Experimental Pharmacology</i> , 2014 , 219, 205-233	3.2	21
9	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	11.5	20
8	Rapid degeneration of rod photoreceptors expressing self-association-deficient arrestin-1 mutant. <i>Cellular Signalling</i> , 2013 , 25, 2613-24	4.9	20
7	Hydrophobic loop dynamics and actin filament stability. <i>Biochemistry</i> , 2006 , 45, 13576-84	3.2	19
6	Site-directed spin labeling of a bacterial chemoreceptor reveals a dynamic, loosely packed transmembrane domain. <i>Protein Science</i> , 2002 , 11, 1472-81	6.3	13
5	Saturation Recovery EPR and Nitroxide Spin Labeling for Exploring Structure and Dynamics in Proteins. <i>Methods in Enzymology</i> , 2015 , 564, 3-27	1.7	9
4	High-Pressure EPR and Site-Directed Spin Labeling for Mapping Molecular Flexibility in Proteins. <i>Methods in Enzymology</i> , 2015 , 564, 29-57	1.7	7

3	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	6.5	5
2	Site-directed spin labeling electron paramagnetic resonance study of the ORF1 protein from a mouse L1 retrotransposon. <i>Protein Science</i> , 2011 , 20, 1231-43	6.3	2
1	Analysis of Saturation Recovery Amplitudes to Characterize Conformational Exchange in Spin-Labeled Proteins. <i>Applied Magnetic Resonance</i> , 2017 , 48, 1315-1340	0.8	1