Ned Van Eps

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22 34 g-index

34 2,814 13.6 4.38 ext. papers ext. citations avg, IF L-index

#	Paper	IF	Citations
33	Crystal structure of rhodopsin bound to arrestin by femtosecond X-ray laser. <i>Nature</i> , 2015 , 523, 561-7	50.4	572
32	Identification of Phosphorylation Codes for Arrestin Recruitment by G Protein-Coupled Receptors. <i>Cell</i> , 2017 , 170, 457-469.e13	56.2	225
31	Activation of the A2A adenosine G-protein-coupled receptor by conformational selection. <i>Nature</i> , 2016 , 533, 265-8	50.4	202
30	Cryo-EM structure of human rhodopsin bound to an inhibitory G protein. <i>Nature</i> , 2018 , 558, 553-558	50.4	153
29	Mechanism of the receptor-catalyzed activation of heterotrimeric G proteins. <i>Nature Structural and Molecular Biology</i> , 2006 , 13, 772-7	17.6	146
28	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, 942	20 ⁻ 4·5	118
27	Site-directed spin labeling measurements of nanometer distances in nucleic acids using a sequence-independent nitroxide probe. <i>Nucleic Acids Research</i> , 2006 , 34, 4722-30	20.1	108
26	Conformation of receptor-bound visual arrestin. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012 , 109, 18407-12	11.5	94
25	Structure and function of the visual arrestin oligomer. <i>EMBO Journal</i> , 2007 , 26, 1726-36	13	92
24	Structure of the glucagon receptor in complex with a glucagon analogue. <i>Nature</i> , 2018 , 553, 106-110	50.4	76
23	A model for the solution structure of the rod arrestin tetramer. <i>Structure</i> , 2008 , 16, 924-34	5.2	66
22	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	11.5	64
21	Structural and dynamical changes in an alpha-subunit of a heterotrimeric G protein along the activation pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006 , 103, 16194-9	11.5	63
20	Mapping allosteric connections from the receptor to the nucleotide-binding pocket of heterotrimeric G proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007 , 104, 7927-32	11.5	56
19	The role of arrestin alpha-helix I in receptor binding. <i>Journal of Molecular Biology</i> , 2010 , 395, 42-54	6.5	55
18	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
17	Cryo-EM structure of the native rhodopsin dimer in nanodiscs. <i>Journal of Biological Chemistry</i> , 2019 , 294, 14215-14230	5.4	34

LIST OF PUBLICATIONS

16	The myristoylated amino terminus of Galpha(i)(1) plays a critical role in the structure and function of Galpha(i)(1) subunits in solution. <i>Biochemistry</i> , 2003 , 42, 7931-41	3.2	31
15	X-ray Crystallographic Structure and Oligomerization of Gloeobacter Rhodopsin. <i>Scientific Reports</i> , 2019 , 9, 11283	4.9	26
14	Electron paramagnetic resonance studies of functionally active, nitroxide spin-labeled peptide analogues of the C-terminus of a G-protein alpha subunit. <i>Biochemistry</i> , 2010 , 49, 6877-86	3.2	26
13	pH dependence of the reduction of dioxygen to water by cytochrome c oxidase. 1. The P(R) state is a pH-dependent mixture of three intermediates, A, P, and F. <i>Biochemistry</i> , 2003 , 42, 5065-73	3.2	26
12	pH dependence of the reduction of dioxygen to water by cytochrome c oxidase. 2. Branched electron transfer pathways linked by proton transfer. <i>Biochemistry</i> , 2003 , 42, 5074-90	3.2	23
11	The structure of the lipid-embedded potassium channel voltage sensor determined by double-electron-electron resonance spectroscopy. <i>Protein Science</i> , 2008 , 17, 506-17	6.3	22
10	The guanine nucleotide exchange factor Ric-8A induces domain separation and Ras domain plasticity in Gil. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015 , 112, 1404-9	11.5	19
9	Different dark conformations function in color-sensitive photosignaling by the sensory rhodopsin I-HtrI complex. <i>Biophysical Journal</i> , 2007 , 92, 4045-53	2.9	14
8	A new approach for studying fast biological reactions involving dioxygen: the reaction of fully reduced cytochrome c oxidase with O2. <i>Biochemistry</i> , 2000 , 39, 14576-82	3.2	13
7	Characterizing rhodopsin signaling by EPR spectroscopy: from structure to dynamics. <i>Photochemical and Photobiological Sciences</i> , 2015 , 14, 1586-97	4.2	11
6	Genetically Encoded Quinone Methides Enabling Rapid, Site-Specific, and Photocontrolled Protein Modification with Amine Reagents. <i>Journal of the American Chemical Society</i> , 2020 , 142, 17057-17068	16.4	10
5	Rapid and facile recombinant expression of bovine rhodopsin in HEK293S GnTI(-) cells using a PiggyBac inducible system. <i>Methods in Enzymology</i> , 2015 , 556, 307-30	1.7	8
4	A Novel Polar Core and Weakly Fixed C-Tail in Squid Arrestin Provide New Insight into Interaction with Rhodopsin. <i>Journal of Molecular Biology</i> , 2018 , 430, 4102-4118	6.5	4
3	Utilizing tagged paramagnetic shift reagents to monitor protein dynamics by NMR. <i>Biochimica Et Biophysica Acta - Proteins and Proteomics</i> , 2017 , 1865, 1555-1563	4	3
2	Structural basis of receptor-dependent G protein activation. FASEB Journal, 2006, 20, A918	0.9	
1	A site-directed spin labeling study of arrestin conformation in solution and bound to activated rhodopsin. <i>FASEB Journal</i> , 2008 , 22, 645.6	0.9	