Joseph J Falke

List of Publications by Citations

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106 papers	7,990 citations	50 h-index	88 g-index
111 ext. papers	8,682 ext. citations	4.3 avg, IF	6.08 L-index

#	Paper	IF	Citations
106	The C2 domain calcium-binding motif: structural and functional diversity. *Protein Science*, **1996**, 5, 2375-90	6.3	702
105	Bacterial chemoreceptors: high-performance signaling in networked arrays. *Trends in Biochemical Sciences*, **2008**, 33, 9-19	10.3	509
104	The two-component signaling pathway of bacterial chemotaxis: a molecular view of signal transduction by receptors, kinases, and adaptation enzymes. *Annual Review of Cell and Developmental Biology*, **1997**, 13, 457-512	12.6	430
103	Evidence that opioids may have toll-like receptor 4 and MD-2 effects. *Brain, Behavior, and Immunity*, **2010**, 24, 83-95	16.6	374
102	Transmembrane signaling in bacterial chemoreceptors. *Trends in Biochemical Sciences*, **2001**, 26, 257-65	10.3	363
101	Molecular tuning of ion binding to calcium signaling proteins. *Quarterly Reviews of Biophysics*, **1994**, 27, 219-90	7	328
100	Purification of proteins using polyhistidine affinity tags. *Methods in Enzymology*, **2000**, 326, 245-54	1.7	309
99	Signaling and sensory adaptation in Escherichia coli chemoreceptors: 2015 update. *Trends in Microbiology*, **2015**, 23, 257-66	12.4	223
98	Thermal motions of surface alpha-helices in the D-galactose chemosensory receptor. Detection by disulfide trapping. *Journal of Molecular Biology*, **1992**, 226, 1219-35	6.5	214
97	Single molecule diffusion of membrane-bound proteins: window into lipid contacts and bilayer dynamics. *Biophysical Journal*, **2010**, 99, 2879-87	2.9	131
96	Intermolecular tuning of calmodulin by target peptides and proteins: differential effects on Ca2+ binding and implications for kinase activation. *Protein Science*, **1997**, 6, 794-807	6.3	127
95	Ca2+-signaling cycle of a membrane-docking C2 domain. *Biochemistry*, **1997**, 36, 12011-8	3.2	119
94	Lock on/off disulfides identify the transmembrane signaling helix of the aspartate receptor. *Journal of Biological Chemistry*, **1995**, 270, 24043-53	5.4	117
93	Ca2+ influx is an essential component of the positive-feedback loop that maintains leading-edge structure and activity in macrophages. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 16176-81	11.5	116
92	C2 domains from different Ca2+ signaling pathways display functional and mechanistic diversity. *Biochemistry*, **2001**, 40, 3089-100	3.2	106
91	Cysteine and disulfide scanning reveals two amphiphilic helices in the linker region of the aspartate chemoreceptor. *Biochemistry*, **1998**, 37, 10746-56	3.2	104
90	Membrane orientation and position of the C2 domain from cPLA2 by site-directed spin labeling. *Biochemistry*, **2002**, 41, 6282-92	3.2	102

89	Independent folding and ligand specificity of the C2 calcium-dependent lipid binding domain of cytosolic phospholipase A2. *Journal of Biological Chemistry*, **1998**, 273, 1365-72	5.4	101
88	Transmembrane signaling by the aspartate receptor: engineered disulfides reveal static regions of the subunit interface. *Biochemistry*, **1995**, 34, 9722-33	3.2	99
87	C2 domains of protein kinase C isoforms alpha, beta, and gamma: activation parameters and calcium stoichiometries of the membrane-bound state. *Biochemistry*, **2002**, 41, 11411-24	3.2	94
86	Specific translocation of protein kinase Calpha to the plasma membrane requires both Ca2+ and PIP2 recognition by its C2 domain. *Molecular Biology of the Cell*, **2006**, 17, 56-66	3.5	90
85	19F NMR studies of the D-galactose chemosensory receptor. 1. Sugar binding yields a global structural change. *Biochemistry*, **1991**, 30, 4248-56	3.2	90
84	Single-molecule fluorescence studies of a PH domain: new insights into the membrane docking reaction. *Biophysical Journal*, **2009**, 96, 566-82	2.9	88
83	Location of the membrane-docking face on the Ca2+-activated C2 domain of cytosolic phospholipase A2. *Biochemistry*, **1998**, 37, 17642-50	3.2	84
82	Mechanism of specific membrane targeting by C2 domains: localized pools of target lipids enhance Ca2+ affinity. *Biochemistry*, **2007**, 46, 4322-36	3.2	83
81	Structure of the conserved HAMP domain in an intact, membrane-bound chemoreceptor: a disulfide mapping study. *Biochemistry*, **2007**, 46, 13684-95	3.2	81
80	Cysteine and disulfide scanning reveals a regulatory alpha-helix in the cytoplasmic domain of the aspartate receptor. *Journal of Biological Chemistry*, **1997**, 272, 32878-88	5.4	80
79	C2 domain of protein kinase C alpha: elucidation of the membrane docking surface by site-directed fluorescence and spin labeling. *Biochemistry*, **2003**, 42, 1254-65	3.2	80
78	Engineered socket study of signaling through a four-helix bundle: evidence for a yin-yang mechanism in the kinase control module of the aspartate receptor. *Biochemistry*, **2009**, 48, 9266-77	3.2	79
77	Attractant regulation of the aspartate receptor-kinase complex: limited cooperative interactions between receptors and effects of the receptor modification state. *Biochemistry*, **2000**, 39, 9486-93	3.2	76
76	Molecular mechanism of an oncogenic mutation that alters membrane targeting: Glu17Lys modifies the PIP lipid specificity of the AKT1 PH domain. *Biochemistry*, **2008**, 47, 12260-9	3.2	75
75	Use of site-directed cysteine and disulfide chemistry to probe protein structure and dynamics: applications to soluble and transmembrane receptors of bacterial chemotaxis. *Methods in Enzymology*, **2007**, 423, 25-51	1.7	75
74	Side chains at the membrane-water interface modulate the signaling state of a transmembrane receptor. *Biochemistry*, **2004**, 43, 1763-70	3.2	75
73	Large amplitude twisting motions of an interdomain hinge: a disulfide trapping study of the galactose-glucose binding protein. *Biochemistry*, **1995**, 34, 3048-55	3.2	67
72	GRP1 pleckstrin homology domain: activation parameters and novel search mechanism for rare target lipid. *Biochemistry*, **2004**, 43, 16161-73	3.2	66

71	Effects of protein stabilizing agents on thermal backbone motions: a disulfide trapping study. *Biochemistry*, **1996**, 35, 10595-600	3.2	65
70	New insights into bacterial chemoreceptor array structure and assembly from electron cryotomography. *Biochemistry*, **2014**, 53, 1575-85	3.2	62
69	The core signaling proteins of bacterial chemotaxis assemble to form an ultrastable complex. *Biochemistry*, **2009**, 48, 6975-87	3.2	62
68	Attractant- and disulfide-induced conformational changes in the ligand binding domain of the chemotaxis aspartate receptor: a 19F NMR study. *Biochemistry*, **1994**, 33, 6100-9	3.2	62
67	Membrane-docking loops of the cPLA2 C2 domain: detailed structural analysis of the protein-membrane interface via site-directed spin-labeling. *Biochemistry*, **2003**, 42, 13227-40	3.2	60
66	The aspartate receptor cytoplasmic domain: in situ chemical analysis of structure, mechanism and dynamics. *Structure*, **1999**, 7, 829-40	5.2	60
65	Open conformation of a substrate-binding cleft: 19F NMR studies of cleft angle in the D-galactose chemosensory receptor. *Biochemistry*, **1991**, 30, 6484-90	3.2	59
64	Conserved glycine residues in the cytoplasmic domain of the aspartate receptor play essential roles in kinase coupling and on-off switching. *Biochemistry*, **2005**, 44, 7687-95	3.2	57
63	Use of EPR power saturation to analyze the membrane-docking geometries of peripheral proteins: applications to C2 domains. *Annual Review of Biophysics and Biomolecular Structure*, **2005**, 34, 71-90		55
62	Lateral diffusion of peripheral membrane proteins on supported lipid bilayers is controlled by the additive frictional drags of (1) bound lipids and (2) protein domains penetrating into the bilayer hydrocarbon core. *Chemistry and Physics of Lipids*, **2013**, 172-173, 67-77	3.7	54
61	The 3.2 □resolution structure of a receptor: CheA:CheW signaling complex defines overlapping binding sites and key residue interactions within bacterial chemosensory arrays. *Biochemistry*, **2013**, 52, 3852-65	3.2	54
60	Evidence that both ligand binding and covalent adaptation drive a two-state equilibrium in the aspartate receptor signaling complex. *Journal of General Physiology*, **2001**, 118, 693-710	3.4	54
59	Tuning the equilibrium ion affinity and selectivity of the EF-hand calcium binding motif: substitutions at the gateway position. *Biochemistry*, **1996**, 35, 6697-705	3.2	54
58	Adaptation mechanism of the aspartate receptor: electrostatics of the adaptation subdomain play a key role in modulating kinase activity. *Biochemistry*, **2005**, 44, 1550-60	3.2	53
57	Enzymology. A moving story. *Science*, **2002**, 295, 1480-1	33.3	51
56	Self-induced docking site of a deeply embedded peripheral membrane protein. *Biophysical Journal*, **2007**, 92, 517-24	2.9	49
55	CheA Kinase of bacterial chemotaxis: chemical mapping of four essential docking sites. *Biochemistry*, **2006**, 45, 8699-711	3.2	48
54	Structure of a conserved receptor domain that regulates kinase activity: the cytoplasmic domain of bacterial taxis receptors. *Current Opinion in Structural Biology*, **2000**, 10, 462-9	8.1	47

53	Molecular mechanism of membrane binding of the GRP1 PH domain. *Journal of Molecular Biology*, **2013**, 425, 3073-90	6.5	46
52	Kinetic tuning of the EF-hand calcium binding motif: the gateway residue independently adjusts (i) barrier height and (ii) equilibrium. *Biochemistry*, **1996**, 35, 1753-60	3.2	45
51	Membrane docking geometry and target lipid stoichiometry of membrane-bound PKCC2 domain: a combined molecular dynamics and experimental study. *Journal of Molecular Biology*, **2010**, 402, 301-10	6.5	43
50	Signaling domain of the aspartate receptor is a helical hairpin with a localized kinase docking surface: cysteine and disulfide scanning studies. *Biochemistry*, **1999**, 38, 9317-27	3.2	43
49	19F NMR studies of the D-galactose chemosensory receptor. 2. Ca(II) binding yields a local structural change. *Biochemistry*, **1991**, 30, 4257-61	3.2	41
48	Regulation of PI3K by PKC and MARCKS: Single-Molecule Analysis of a Reconstituted Signaling Pathway. *Biophysical Journal*, **2016**, 110, 1811-1825	2.9	41
47	Quantitative analysis of aspartate receptor signaling complex reveals that the homogeneous two-state model is inadequate: development of a heterogeneous two-state model. *Journal of Molecular Biology*, **2003**, 326, 1597-614	6.5	38
46	The piston rises again. *Structure*, **2009**, 17, 1149-51	5.2	37
45	Effect of PIP2 binding on the membrane docking geometry of PKC alpha C2 domain: an EPR site-directed spin-labeling and relaxation study. *Biochemistry*, **2008**, 47, 8301-16	3.2	37
44	Detection of a conserved alpha-helix in the kinase-docking region of the aspartate receptor by cysteine and disulfide scanning. *Journal of Biological Chemistry*, **1998**, 273, 25006-14	5.4	36
43	The kinetic cycle of cardiac troponin C: calcium binding and dissociation at site II trigger slow conformational rearrangements. *Protein Science*, **1998**, 7, 2451-9	6.3	35
42	Architecture and signal transduction mechanism of the bacterial chemosensory array: progress, controversies, and challenges. *Current Opinion in Structural Biology*, **2014**, 29, 85-94	8.1	34
41	Single-Molecule Study Reveals How Receptor and Ras Synergistically Activate PI3K and PIP Signaling. *Biophysical Journal*, **2017**, 113, 2396-2405	2.9	33
40	Defining a key receptor-CheA kinase contact and elucidating its function in the membrane-bound bacterial chemosensory array: a disulfide mapping and TAM-IDS Study. *Biochemistry*, **2013**, 52, 3866-80	3.2	33
39	Single-molecule studies reveal a hidden key step in the activation mechanism of membrane-bound protein kinase C-*Biochemistry*, **2014**, 53, 1697-713	3.2	32
38	Evidence that the adaptation region of the aspartate receptor is a dynamic four-helix bundle: cysteine and disulfide scanning studies. *Biochemistry*, **2005**, 44, 12655-66	3.2	32
37	Molecular tuning of an EF-hand-like calcium binding loop. Contributions of the coordinating side chain at loop position 3. *Journal of General Physiology*, **1997**, 110, 173-84	3.4	30
36	Optimizing the metal binding parameters of an EF-hand-like calcium chelation loop: coordinating side chains play a more important tuning role than chelation loop flexibility. *Biochemistry*, **1997**, 36, 9917-26	3.2	30

35	Assembly of membrane-bound protein complexes: detection and analysis by single molecule diffusion. *Biochemistry*, **2012**, 51, 1638-47	3.2	29
34	Interactions of protein kinase C-□C1A and C1B domains with membranes: a combined computational and experimental study. *Journal of the American Chemical Society*, **2014**, 136, 11757-66	16.4	26
33	Mapping out regions on the surface of the aspartate receptor that are essential for kinase activation. *Biochemistry*, **2003**, 42, 2952-9	3.2	25
32	Chemotaxis receptors and signaling. *Advances in Protein Chemistry*, **2004**, 68, 393-444		24
31	Structure, function, and on-off switching of a core unit contact between CheA kinase and CheW adaptor protein in the bacterial chemosensory array: A disulfide mapping and mutagenesis study. *Biochemistry*, **2013**, 52, 7753-65	3.2	23
30	Hydrophobic contributions to the membrane docking of synaptotagmin 7 C2A domain: mechanistic contrast between isoforms 1 and 7. *Biochemistry*, **2012**, 51, 7654-64	3.2	23
29	The GRP1 PH domain, like the AKT1 PH domain, possesses a sentry glutamate residue essential for specific targeting to plasma membrane PI(3,4,5)P(3). *Biochemistry*, **2011**, 50, 9845-56	3.2	22
28	Cooperativity between bacterial chemotaxis receptors. *Proceedings of the National Academy of Sciences of the United States of America*, **2002**, 99, 6530-2	11.5	21
27	Identification of a site critical for kinase regulation on the central processing unit (CPU) helix of the aspartate receptor. *Biochemistry*, **1999**, 38, 329-36	3.2	20
26	The PH domain of phosphoinositide-dependent kinase-1 exhibits a novel, phospho-regulated monomer-dimer equilibrium with important implications for kinase domain activation: single-molecule and ensemble studies. *Biochemistry*, **2013**, 52, 4820-9	3.2	19
25	Membrane docking geometry of GRP1 PH domain bound to a target lipid bilayer: an EPR site-directed spin-labeling and relaxation study. *PLoS ONE*, **2012**, 7, e33640	3.7	18
24	Ca2+ activation of the cPLA2 C2 domain: ordered binding of two Ca2+ ions with positive cooperativity. *Biochemistry*, **2004**, 43, 16320-8	3.2	18
23	Thermal domain motions of CheA kinase in solution: Disulfide trapping reveals the motional constraints leading to trans-autophosphorylation. *Biochemistry*, **2009**, 48, 3631-44	3.2	17
22	A PKC-MARCKS-PI3K regulatory module links Ca2+ and PIP3 signals at the leading edge of polarized macrophages. *PLoS ONE*, **2018**, 13, e0196678	3.7	16
21	Interplay between phosphoinositide lipids and calcium signals at the leading edge of chemotaxing ameboid cells. *Chemistry and Physics of Lipids*, **2014**, 182, 73-9	3.7	16
20	Chemotaxis receptor complexes: from signaling to assembly. *PLoS Computational Biology*, **2007**, 3, e150	5	16
19	Ion Channels within Ion Transport Proteins: Evidence in the Band 3 System. *Biophysical Journal*, **1984**, 45, 91-2	2.9	16
18	Use of fluorescence resonance energy transfer to monitor Ca(2+)-triggered membrane docking of C2 domains. *Methods in Molecular Biology*, **2002**, 172, 295-303	1.4	15

17	Piston versus scissors: chemotaxis receptors versus sensor His-kinase receptors in two-component signaling pathways. *Structure*, **2014**, 22, 1219-1220	5.2	13
16	Increasing and decreasing the ultrastability of bacterial chemotaxis core signaling complexes by modifying protein-protein contacts. *Biochemistry*, **2014**, 53, 5592-600	3.2	12
15	Isolated bacterial chemosensory array possesses quasi- and ultrastable components: functional links between array stability, cooperativity, and order. *Biochemistry*, **2012**, 51, 10218-28	3.2	11
14	The PICM chemical scanning method for identifying domain-domain and protein-protein interfaces: applications to the core signaling complex of E. coli chemotaxis. *Methods in Enzymology*, **2007**, 423, 3-24	1.7	11
13	Regulation of a Coupled MARCKS-PI3K Lipid Kinase Circuit by Calmodulin: Single-Molecule Analysis of a Membrane-Bound Signaling Module. *Biochemistry*, **2016**, 55, 6395-6405	3.2	10
12	OS-FRET: a new one-sample method for improved FRET measurements. *Biochemistry*, **2011**, 50, 451-7	3.2	8
11	Membrane Recruitment as a Cancer Mechanism: A Case Study of Akt PH Domain. *Cellscience*, **2007**, 4, 25-30		7
10	Cation charge and size selectivity of the C2 domain of cytosolic phospholipase A(2). *Biochemistry*, **2002**, 41, 1109-22	3.2	5
9	The G-Protein Rab5A Activates VPS34 Complex II, a Class III PI3K, by a Dual Regulatory Mechanism. *Biophysical Journal*, **2020**, 119, 2205-2218	2.9	5
8	Lipid targeting domain with dual-membrane specificity that expands the diversity of intracellular targeting reactions. *Proceedings of the National Academy of Sciences of the United States of America*, **2012**, 109, 1816-7	11.5	3
7	Staining of viable and nonviable myotubes and of myofibrils by the fluorescent dye merocyanine 540. *Differentiation*, **1980**, 17, 199-204	3.5	1
6	Single-molecule studies reveal regulatory interactions between master kinases PDK1, AKT1, and PKC. *Biophysical Journal*, **2021**,	2.9	1
5	Ras-guanine nucleotide complexes: A UV spectral deconvolution method to analyze protein concentration, nucleotide stoichiometry, and purity. *Analytical Biochemistry*, **2021**, 618, 114066	3.1	1
4	HPLC method to resolve, identify and quantify guanine nucleotides bound to recombinant ras GTPase. *Analytical Biochemistry*, **2021**, 631, 114338	3.1	1
3	Rapid exposure of macrophages to drugs resolves four classes of effects on the leading edge sensory pseudopod: Non-perturbing, adaptive, disruptive, and activating. *PLoS ONE*, **2020**, 15, e0233012	3.7	
2	Calmodulin Binds to and Inhibits H-Ras Activation of PI3K: A Single Molecule Study. *FASEB Journal*, **2018**, 32, lb127	0.9	
1	Ras and RTK: PI3K Activation, PIP3 Formation, Signal Transduction, Cancer Creation. *FASEB Journal*, **2019**, 33, lb350	0.9	