Oliver Daumke

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Structural basis of phosphatidylinositol 3-kinase C2α function. Nature Structural and Molecular Biology, 2022, 29, 218-228.	8.2	14
2	SPFH protein cage—Âone ring to rule them all. Cell Research, 2022, 32, 117-118.	12.0	8
3	GIMAP6 regulates autophagy, immune competence, and inflammation in mice and humans. Journal of Experimental Medicine, 2022, 219, .	8.5	4
4	The ARFRP1-dependent Golgi scaffolding protein GOPC is required for insulin secretion from pancreatic β-cells. Molecular Metabolism, 2021, 45, 101151.	6.5	10
5	Quantification and demonstration of the collective constriction-by-ratchet mechanism in the dynamin molecular motor. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, e2101144118.	7.1	5
6	Lysine acetylation regulates the interaction between proteins and membranes. Nature Communications, 2021, 12, 6466.	12.8	27
7	Monogenic variants in dystonia: an exome-wide sequencing study. Lancet Neurology, The, 2020, 19, 908-918.	10.2	139
8	Divergent architecture of the heterotrimeric NatC complex explains N-terminal acetylation of cognate substrates. Nature Communications, 2020, 11, 5506.	12.8	23
9	Age attenuates the Tâ€ŧype Ca _V 3.2â€RyR axis in vascular smooth muscle. Aging Cell, 2020, 19, e13134.	6.7	18
10	EHD2-mediated restriction of caveolar dynamics regulates cellular fatty acid uptake. Proceedings of the United States of America, 2020, 117, 7471-7481.	7.1	41
11	hGBP1 Coordinates Chlamydia Restriction and Inflammasome Activation through Sequential GTP Hydrolysis. Cell Reports, 2020, 31, 107667.	6.4	27
12	53BP1 Supports Immunoglobulin Class Switch Recombination Independently of Its DNA Double-Strand Break End Protection Function. Cell Reports, 2019, 28, 1389-1399.e6.	6.4	23
13	Structure and assembly of the mitochondrial membrane remodelling GTPase Mgm1. Nature, 2019, 571, 429-433.	27.8	86
14	eNOS-NO-induced small blood vessel relaxation requires EHD2-dependent caveolae stabilization. PLoS ONE, 2019, 14, e0223620.	2.5	14
15	Polymer-like Model to Study the Dynamics of Dynamin Filaments on Deformable Membrane Tubes. Biophysical Journal, 2019, 117, 1870-1891.	0.5	13
16	Autocrine LTA signaling drives NF-κB and JAK-STAT activity and myeloid gene expression in Hodgkin lymphoma. Blood, 2019, 133, 1489-1494.	1.4	20
17	Pathophysiological Role of Caveolae in Hypertension. Frontiers in Medicine, 2019, 6, 153.	2.6	12
18	FIP200 Claw Domain Binding to p62 Promotes Autophagosome Formation at Ubiquitin Condensates. Molecular Cell, 2019, 74, 330-346.e11.	9.7	223

OLIVER DAUMKE

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19	eNOS-NO-induced small blood vessel relaxation requires EHD2-dependent caveolae stabilization. , 2019, 14, e0223620.		0
20	eNOS-NO-induced small blood vessel relaxation requires EHD2-dependent caveolae stabilization. , 2019, 14, e0223620.		0
21	eNOS-NO-induced small blood vessel relaxation requires EHD2-dependent caveolae stabilization. , 2019, 14, e0223620.		Ο
22	eNOS-NO-induced small blood vessel relaxation requires EHD2-dependent caveolae stabilization. , 2019, 14, e0223620.		0
23	Effects of allelic variations in the human myxovirus resistance protein A on its antiviral activity. Journal of Biological Chemistry, 2018, 293, 3056-3072.	3.4	18
24	Structural insights into the activation mechanism of dynamin-like EHD ATPases. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, 5629-5634.	7.1	34
25	Mitochondrial Homeostasis: How Do Dimers of Mitofusins Mediate Mitochondrial Fusion?. Current Biology, 2017, 27, R353-R356.	3.9	33
26	Quantitative GTPase Affinity Purification Identifies Rho Family Protein Interaction Partners. Molecular and Cellular Proteomics, 2017, 16, 73-85.	3.8	20
27	Regulated membrane remodeling by Mic60 controls formation of mitochondrial crista junctions. Nature Communications, 2017, 8, 15258.	12.8	84
28	Structural Basis for Aryl Hydrocarbon Receptor-Mediated Gene Activation. Structure, 2017, 25, 1025-1033.e3.	3.3	95
29	Characterization of the CD177 interaction with the ANCA antigen proteinase 3. Scientific Reports, 2017, 7, 43328.	3.3	31
30	Membrane fission by dynamin: what we know and what we need to know. EMBO Journal, 2016, 35, 2270-2284.	7.8	388
31	Protein-mediated membrane remodeling. Journal of Structural Biology, 2016, 196, 1-2.	2.8	1
32	Invited review: Mechanisms of GTP hydrolysis and conformational transitions in the dynamin superfamily. Biopolymers, 2016, 105, 580-593.	2.4	85
33	Quantitative interaction mapping reveals an extended UBX domain in ASPL that disrupts functional p97 hexamers. Nature Communications, 2016, 7, 13047.	12.8	35
34	Dynamics of the Ligand Binding Domain Layer during AMPA Receptor Activation. Biophysical Journal, 2016, 110, 896-911.	0.5	19
35	The immunity-related GTPase Irga6 dimerizes in a parallel head-to-head fashion. BMC Biology, 2016, 14, 14.	3.8	19
36	Structure of the Hantavirus Nucleoprotein Provides Insights into the Mechanism of RNA Encapsidation. Cell Reports, 2016, 14, 2092-2099.	6.4	28

OLIVER DAUMKE

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37	Role of Nucleotide Binding and GTPase Domain Dimerization in Dynamin-like Myxovirus Resistance Protein A for GTPase Activation and Antiviral Activity. Journal of Biological Chemistry, 2015, 290, 12779-12792.	3.4	48
38	New role for the (pro)renin receptor in T-cell development. Blood, 2015, 126, 504-507.	1.4	20
39	Protein kinase C (PKC)-mediated phosphorylation of PACSIN2 triggers the removal of caveolae from the plasma membrane. Journal of Cell Science, 2015, 128, 2766-80.	2.0	39
40	Crystal structure of the dynamin tetramer. Nature, 2015, 525, 404-408.	27.8	115
41	Structural insights into RNA encapsidation and helical assembly of the Toscana virus nucleoprotein. Nucleic Acids Research, 2014, 42, 6025-6037.	14.5	30
42	Structural Insights into Membrane Interaction and Caveolar Targeting of Dynamin-like EHD2. Structure, 2014, 22, 409-420.	3.3	41
43	BAR Domain Scaffolds in Dynamin-Mediated Membrane Fission. Cell, 2014, 156, 882-892.	28.9	199
44	Structural Insights into the Mechanism of GTPase Activation in the GIMAP Family. Structure, 2013, 21, 550-559.	3.3	39
45	Oligomerization of Dynamin Superfamily Proteins in Health and Disease. Progress in Molecular Biology and Translational Science, 2013, 117, 411-443.	1.7	49
46	Structural insights into oligomerization and mitochondrial remodelling of dynamin 1-like protein. EMBO Journal, 2013, 32, 1280-1292.	7.8	243
47	Functional Mapping of Human Dynamin-1-Like GTPase Domain Based on X-ray Structure Analyses. PLoS ONE, 2013, 8, e71835.	2.5	63
48	A stomatin dimer modulates the activity of acid-sensing ion channels. EMBO Journal, 2012, 31, 3635-3646.	7.8	72
49	EHD2 regulates caveolar dynamics via ATP-driven targeting and oligomerization. Molecular Biology of the Cell, 2012, 23, 1316-1329.	2.1	165
50	Structural Insights into Dynamin-Mediated Membrane Fission. Structure, 2012, 20, 1621-1628.	3.3	60
51	Crystal structure of nucleotide-free dynamin. Nature, 2011, 477, 556-560.	27.8	277
52	Structure of Myxovirus Resistance Protein A Reveals Intra- and Intermolecular Domain Interactions Required for the Antiviral Function. Immunity, 2011, 35, 514-525.	14.3	188
53	GTP-dependent scaffold formation in the GTPase of Immunity-Associated Protein family. Small GTPases, 2011, 2, 27-30.	1.6	9
54	Structural insights into membrane fusion at the endoplasmic reticulum. Proceedings of the National Academy of Sciences of the United States of America, 2011, 108, 2175-2176.	7.1	17

OLIVER DAUMKE

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55	Purification, crystallization and preliminary X-ray analysis of human GIMAP2. Acta Crystallographica Section F: Structural Biology Communications, 2010, 66, 725-729.	0.7	5
56	Structural basis of oligomerization in the stalk region of dynamin-like MxA. Nature, 2010, 465, 502-506.	27.8	229
57	Dynamin-like MxA GTPase: Structural Insights into Oligomerization and Implications for Antiviral Activity. Journal of Biological Chemistry, 2010, 285, 28419-28424.	3.4	89
58	Structural basis of oligomerization in septin-like GTPase of immunity-associated protein 2 (GIMAP2). Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20299-20304.	7.1	49
59	Structure of the MxA stalk elucidates the assembly of ring-like units of an antiviral module. Small GTPases, 2010, 1, 62-64.	1.6	20
60	Architectural and mechanistic insights into an EHD ATPase involved in membrane remodelling. Nature, 2007, 449, 923-927.	27.8	282
61	Structure and Analysis of FCHo2 F-BAR Domain: A Dimerizing and Membrane Recruitment Module that	3.3	261