

# Mads Gabrielsen

## List of Publications by Year in descending order

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49  
papers

1,493  
citations

304743

22  
h-index

330143

37  
g-index

50  
all docs

50  
docs citations

50  
times ranked

2438  
citing authors

#	ARTICLE	IF	CITATIONS
1	Structure of UBE2Kâ€“Ub/E3/polyUb reveals mechanisms of K48-linked Ub chain extension. <i>Nature Chemical Biology</i> , 2022, 18, 422-431.	8.0	19
2	Crystal structures of Wrba, a spurious target of the salicylidene acylhydrazide inhibitors of type III secretion in Gram-negative pathogens, and verification of improved specificity of next-generation compounds. <i>Microbiology (United Kingdom)</i> , 2022, 168, .	1.8	1
3	E3 ligase-inactivation rewires CBL interactome to elicit oncogenesis by hijacking RTKâ€“CBLâ€“CIN85 axis. <i>Oncogene</i> , 2021, 40, 2149-2164.	5.9	6
4	Structural insights into ADP-ribosylation of ubiquitin by Deltex family E3 ubiquitin ligases. <i>Science Advances</i> , 2020, 6, .	10.3	51
5	DELTEX2 C-terminal domain recognizes and recruits ADP-ribosylated proteins for ubiquitination. <i>Science Advances</i> , 2020, 6, .	10.3	29
6	High-resolution structure of the alcohol dehydrogenase domain of the bifunctional bacterial enzyme AdhE. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2020, 76, 414-421.	0.8	1
7	Identification and Characterization of Mutations in Ubiquitin Required for Non-covalent Dimer Formation. <i>Structure</i> , 2019, 27, 1452-1459.e4.	3.3	5
8	Calicivirus VP2 forms a portal-like assembly following receptor engagement. <i>Nature</i> , 2019, 565, 377-381.	27.8	103
9	Structure and ligand binding of As-p18, an extracellular fatty acid binding protein from the eggs of a parasitic nematode. <i>Bioscience Reports</i> , 2019, 39, .	2.4	3
10	Single-Turnover RING/U-Box E3-Mediated Lysine Discharge Assays. <i>Methods in Molecular Biology</i> , 2018, 1844, 19-31.	0.9	5
11	Structure of the <i>Macrobrachium rosenbergii</i> nodavirus: A new genus within the Nodaviridae?. <i>PLoS Biology</i> , 2018, 16, e3000038.	5.6	36
12	Regulation of atypical MAP kinases ERK3 and ERK4 by the phosphatase DUSP2. <i>Scientific Reports</i> , 2017, 7, 43471.	3.3	28
13	A General Strategy for Discovery of Inhibitors and Activators of RING and U-box E3 Ligases with Ubiquitin Variants. <i>Molecular Cell</i> , 2017, 68, 456-470.e10.	9.7	56
14	A Highly Conserved Bacterial D-Serine Uptake System Links Host Metabolism and Virulence. <i>PLoS Pathogens</i> , 2016, 12, e1005359.	4.7	55
15	Diversity in the structures and ligand-binding sites of nematode fatty acid and retinol-binding proteins revealed by Na-FAR-1 from <i>Necator americanus</i> . <i>Biochemical Journal</i> , 2015, 471, 403-414.	3.7	27
16	Elevated LIM Kinase 1 in Nonmetastatic Prostate Cancer Reflects Its Role in Facilitating Androgen Receptor Nuclear Translocation. <i>Molecular Cancer Therapeutics</i> , 2015, 14, 246-258.	4.1	30
17	Polarized Cell Motility Induces Hydrogen Peroxide to Inhibit Cofilin via Cysteine Oxidation. <i>Current Biology</i> , 2015, 25, 1520-1525.	3.9	64
18	Activation of a Primed RING E3-E2â€“Ubiquitin Complex by Non-Covalent Ubiquitin. <i>Molecular Cell</i> , 2015, 58, 297-310.	9.7	105

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19	LIM kinase inhibitors disrupt mitotic microtubule organization and impair tumor cell proliferation. <i>Oncotarget</i> , 2015, 6, 38469-38486.	1.8	34
20	Structures and binding specificity of galactose- and mannose-binding lectins from champedak: differences from jackfruit lectins. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2014, 70, 709-716.	0.8	10
21	Cucurbitacin covalent bonding to cysteine thiols: the filamentous-actin severing protein Cofilin1 as an exemplary target. <i>Cell Communication and Signaling</i> , 2013, 11, 58.	6.5	23
22	High-Throughput Methods for the Detection of Protein Overexpression Using Fluorescence Markers. <i>Methods in Cell Biology</i> , 2013, 113, 189-208.	1.1	0
23	Analysis of the human cofilin 1 structure reveals conformational changes required for actin binding. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 1780-1788.	2.5	23
24	Useable diffraction data from a multiple microdomain-containing crystal of <i>Ascaris suum</i> p18 fatty-acid-binding protein using a microfocus beamline. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 939-941.	0.7	2
25	High-Throughput Methods for the Identification of Protein Purification Conditions Using a Cleavable Tag System. <i>Methods in Cell Biology</i> , 2012, 112, 93-110.	1.1	2
26	Structural Characterisation of Tpx from <i>Yersinia pseudotuberculosis</i> Reveals Insights into the Binding of Salicylidene Acylhydrazide Compounds. <i>PLoS ONE</i> , 2012, 7, e32217.	2.5	17
27	Express Your LOV: An Engineered Flavoprotein as a Reporter for Protein Expression and Purification. <i>PLoS ONE</i> , 2012, 7, e52962.	2.5	24
28	FolX from <i>Pseudomonas aeruginosa</i> is octameric in both crystal and solution. <i>FEBS Letters</i> , 2012, 586, 1160-1165.	2.8	3
29	The structure of an orthorhombic crystal form of a 'forced reduced' thiol peroxidase reveals lattice formation aided by the presence of the affinity tag. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 522-526.	0.7	2
30	Two crystal forms of a helix-rich fatty acid- and retinol-binding protein, Na-FAR-1, from the parasitic nematode <i>Necator americanus</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2012, 68, 835-838.	0.7	5
31	High-throughput identification of purification conditions leads to preliminary crystallization conditions for three inner membrane proteins. <i>Molecular Membrane Biology</i> , 2011, 28, 445-453.	2.0	8
32	Identification of Bacterial Target Proteins for the Salicylidene Acylhydrazide Class of Virulence-blocking Compounds. <i>Journal of Biological Chemistry</i> , 2011, 286, 29922-29931.	3.4	94
33	Self-interaction chromatography as a tool for optimizing conditions for membrane protein crystallization. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2010, 66, 44-50.	2.5	16
34	A triclinic crystal form of <i>Escherichia coli</i> 4-diphosphocytidyl-2-C-methyl-erythritol kinase and reassessment of the quaternary structure. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 237-241.	0.7	11
35	Crystallization and initial X-ray diffraction analysis of a mannose-binding lectin from champedak. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 592-594.	0.7	4
36	Expression, purification, crystallization and initial X-ray diffraction analysis of thiol peroxidase from <i>Yersinia pseudotuberculosis</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2010, 66, 1606-1609.	0.7	6

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37	Chapter 6 Membrane Protein Crystallization: Approaching the Problem and Understanding the Solutions. <i>Current Topics in Membranes</i> , 2009, , 127-149.	0.9	1
38	Crystallization and preliminary structural studies of champedak galactose-binding lectin. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2009, 65, 895-897.	0.7	6
39	Instantaneous Mapping of Coherently Coupled Electronic Transitions and Energy Transfers in a Photosynthetic Complex Using Angle-Resolved Coherent Optical Wave-Mixing. <i>Physical Review Letters</i> , 2009, 102, 057402.	7.8	77
40	Spectral Diffusion and Electron-Phonon Coupling of the B800 BChl a Molecules in LH2 Complexes from Three Different Species of Purple Bacteria. <i>Biophysical Journal</i> , 2009, 97, 2604-2612.	0.5	24
41	A protocol for high throughput methods for the expression and purification of inner membrane proteins. <i>Molecular Membrane Biology</i> , 2008, 25, 599-608.	2.0	8
42	The crystal structure of a plant 2C-methyl-D-erythritol 4-phosphate cytidyltransferase exhibits a distinct quaternary structure compared to bacterial homologues and a possible role in feedback regulation for cytidine monophosphate. <i>FEBS Journal</i> , 2006, 273, 1065-1073.	4.7	28
43	Structural and biochemical characterization of a mitochondrial peroxiredoxin from <i>Plasmodium falciparum</i> . <i>Molecular Microbiology</i> , 2006, 61, 948-959.	2.5	48
44	Hexameric Assembly of the Bifunctional Methylerythritol 2,4-Cyclodiphosphate Synthase and Protein-Protein Associations in the Deoxy-xylulose-dependent Pathway of Isoprenoid Precursor Biosynthesis. <i>Journal of Biological Chemistry</i> , 2004, 279, 52753-52761.	3.4	43
45	Biosynthesis of isoprenoids. <i>FEBS Journal</i> , 2004, 271, 3028-3035.	0.2	43
46	Tryparedoxins from <i>Crithidia fasciculata</i> and <i>Trypanosoma brucei</i> . <i>Journal of Biological Chemistry</i> , 2003, 278, 25919-25925.	3.4	43
47	Structure and reactivity in the non-mevalonate pathway of isoprenoid biosynthesis. <i>Biochemical Society Transactions</i> , 2003, 31, 537-542.	3.4	15
48	Distinct Binding Determinants for ERK2/p38 $\hat{\pm}$ and JNK MAP Kinases Mediate Catalytic Activation and Substrate Selectivity of MAP Kinase Phosphatase-1. <i>Journal of Biological Chemistry</i> , 2001, 276, 16491-16500.	3.4	242
49	The Structure of Purple Bacterial Antenna Complexes. , 0, , 325-340.		4