

Matthias Wilmanns

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

65
papers

2,215
citations

25
h-index

46
g-index

71
ext. papers

2,686
ext. citations

8.6
avg, IF

4.6
L-index

#	Paper	IF	Citations
65	Synergy of protease binding sites within the ecotin homodimer is crucial for inhibition of MASP enzymes and for blocking lectin pathway activation.. <i>Journal of Biological Chemistry</i> , 2022 , 101985	5.4	0
64	TBX2 controls a proproliferative gene expression program in melanoma. <i>Genes and Development</i> , 2021 , 35, 1657-1677	12.6	0
63	Molecular basis for the allosteric activation mechanism of the heterodimeric imidazole glycerol phosphate synthase complex. <i>Nature Communications</i> , 2021 , 12, 2748	17.4	5
62	Structure of the mycobacterial ESX-5 type VII secretion system pore complex. <i>Science Advances</i> , 2021 , 7,	14.3	7
61	Versatile allosteric properties in Pex5-like tetratricopeptide repeat proteins to induce diverse downstream function. <i>Traffic</i> , 2021 , 22, 140-152	5.7	0
60	The XBI BioLab for life science experiments at the European XFEL. <i>Journal of Applied Crystallography</i> , 2021 , 54, 7-21	3.8	6
59	Conserved and specialized functions of Type VII secretion systems in non-tuberculous mycobacteria. <i>Microbiology (United Kingdom)</i> , 2021 , 167,	2.9	5
58	Across scales: novel insights into kidney health and disease by structural biology. <i>Kidney International</i> , 2021 , 100, 281-288	9.9	
57	Tuning Transcription Factor Availability through Acetylation-Mediated Genomic Redistribution. <i>Molecular Cell</i> , 2020 , 79, 472-487.e10	17.6	20
56	H, C, and N backbone assignments of the C-terminal region of the human retinoic acid-induced protein 2. <i>Biomolecular NMR Assignments</i> , 2020 , 14, 271-275	0.7	0
55	A kinase bioscavenger provides antibiotic resistance by extremely tight substrate binding. <i>Science Advances</i> , 2020 , 6, eaaz9861	14.3	7
54	Structural basis of p62/SQSTM1 helical filaments and their role in cellular cargo uptake. <i>Nature Communications</i> , 2020 , 11, 440	17.4	33
53	Mechanism of conditional partner selectivity in MITF/TFE family transcription factors with a conserved coiled coil stammer motif. <i>Nucleic Acids Research</i> , 2020 , 48, 934-948	20.1	9
52	The ATPases of the mycobacterial type VII secretion system: Structural and mechanistic insights into secretion. <i>Progress in Biophysics and Molecular Biology</i> , 2020 , 152, 25-34	4.7	4
51	The crystal structure of mycobacterial epoxide hydrolase A. <i>Scientific Reports</i> , 2020 , 10, 16539	4.9	0
50	Structure-Based Identification and Functional Characterization of a Lipocalin in the Malaria Parasite Plasmodium falciparum. <i>Cell Reports</i> , 2020 , 31, 107817	10.6	9
49	The pMy vector series: A versatile cloning platform for the recombinant production of mycobacterial proteins in Mycobacterium smegmatis. <i>Protein Science</i> , 2020 , 29, 2528-2537	6.3	4

48	Multiscale computation delivers organophosphorus reactivity and stereoselectivity to immunoglobulin scavengers. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 22841-22848	11.5	3
47	Uncovering targeting priority to yeast peroxisomes using an in-cell competition assay. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020 , 117, 21432-21440	11.5	8
46	MITF has a central role in regulating starvation-induced autophagy in melanoma. <i>Scientific Reports</i> , 2019 , 9, 1055	4.9	34
45	Subcellular localization and stability of MITF are modulated by the bHLH-Zip domain. <i>Pigment Cell and Melanoma Research</i> , 2019 , 32, 41-54	4.5	15
44	An NAD Phosphorylase Toxin Triggers Mycobacterium tuberculosis Cell Death. <i>Molecular Cell</i> , 2019 , 73, 1282-1291.e8	17.6	37
43	Structural diversity in the atomic resolution 3D fingerprint of the titin M-band segment. <i>PLoS ONE</i> , 2019 , 14, e0226693	3.7	1
42	Structural Variability of EspG Chaperones from Mycobacterial ESX-1, ESX-3, and ESX-5 Type VII Secretion Systems. <i>Journal of Molecular Biology</i> , 2019 , 431, 289-307	6.5	13
41	The von Willebrand factor Tyr2561 allele is a gain-of-function variant and a risk factor for early myocardial infarction. <i>Blood</i> , 2019 , 133, 356-365	2.2	15
40	Structure and dynamics of the platelet integrin-binding C4 domain of von Willebrand factor. <i>Blood</i> , 2019 , 133, 366-376	2.2	9
39	The Von Willebrand Factor Tyr2561 Allele Is a Gain-of-Function Variant and a Potential Risk Factor for Early Myocardial Infarction. <i>Blood</i> , 2018 , 132, 2459-2459	2.2	1
38	Structure of the mycobacterial ESX-5 type VII secretion system membrane complex by single-particle analysis. <i>Nature Microbiology</i> , 2017 , 2, 17047	26.6	74
37	Intermolecular base stacking mediates RNA-RNA interaction in a crystal structure of the RNA chaperone Hfq. <i>Scientific Reports</i> , 2017 , 7, 9903	4.9	6
36	Model-based local density sharpening of cryo-EM maps. <i>ELife</i> , 2017 , 6,	8.9	113
35	Structural biology of the import pathways of peroxisomal matrix proteins. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2016 , 1863, 804-13	4.9	26
34	Robotic QM/MM-driven maturation of antibody combining sites. <i>Science Advances</i> , 2016 , 2, e1501695	14.3	10
33	Death-Associated Protein Kinase Activity Is Regulated by Coupled Calcium/Calmodulin Binding to Two Distinct Sites. <i>Structure</i> , 2016 , 24, 851-61	5.2	12
32	Higher-order assemblies of oligomeric cargo receptor complexes form the membrane scaffold of the Cvt vesicle. <i>EMBO Reports</i> , 2016 , 17, 1044-60	6.5	20
31	Towards the molecular mechanism of the integration of peroxisomal membrane proteins. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2016 , 1863, 863-9	4.9	14

30	A standardized production pipeline for high profile targets from <i>Mycobacterium tuberculosis</i> . <i>Proteomics - Clinical Applications</i> , 2016 , 10, 1049-1057	3.1	4
29	Suppression of early hematogenous dissemination of human breast cancer cells to bone marrow by retinoic Acid-induced 2. <i>Cancer Discovery</i> , 2015 , 5, 506-19	24.4	27
28	Characterization of the mycobacterial acyl-CoA carboxylase holo complexes reveals their functional expansion into amino acid catabolism. <i>PLoS Pathogens</i> , 2015 , 11, e1004623	7.6	11
27	Structural insights into cargo recognition by the yeast PTS1 receptor. <i>Journal of Biological Chemistry</i> , 2015 , 290, 26610-26	5.4	18
26	Ligand-induced compaction of the PEX5 receptor-binding cavity impacts protein import efficiency into peroxisomes. <i>Traffic</i> , 2015 , 16, 85-98	5.7	27
25	Induction of insulin-like growth factor 1 splice forms by subfragments of myofibrillar proteins. <i>Molecular and Cellular Endocrinology</i> , 2015 , 399, 69-77	4.4	8
24	Refined requirements for protein regions important for activity of the TALE AvrBs3. <i>PLoS ONE</i> , 2015 , 10, e0120214	3.7	24
23	Role of light-chain constant-domain switch in the structure and functionality of A17 reactibody. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014 , 70, 708-19		15
22	Crystal structure of the VapBC-15 complex from <i>Mycobacterium tuberculosis</i> reveals a two-metal ion dependent PIN-domain ribonuclease and a variable mode of toxin-antitoxin assembly. <i>Journal of Structural Biology</i> , 2014 , 188, 249-58	3.4	37
21	Structure of the <i>Mycobacterium tuberculosis</i> type VII secretion system chaperone EspG5 in complex with PE25-PPE41 dimer. <i>Molecular Microbiology</i> , 2014 , 94, 367-82	4.1	58
20	WXG100 protein superfamily consists of three subfamilies and exhibits an helical C-terminal conserved residue pattern. <i>PLoS ONE</i> , 2014 , 9, e89313	3.7	69
19	Crystal structure of the S187F variant of human liver alanine: glyoxylate [corrected] aminotransferase associated with primary hyperoxaluria type I and its functional implications. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013 , 81, 1457-65	4.2	20
18	MITF mutations associated with pigment deficiency syndromes and melanoma have different effects on protein function. <i>Human Molecular Genetics</i> , 2013 , 22, 4357-67	5.6	37
17	Catalysis uncoupling in a glutamine amidotransferase bienzyme by unblocking the glutaminase active site. <i>Chemistry and Biology</i> , 2012 , 19, 1589-99		33
16	Molecular requirements for peroxisomal targeting of alanine-glyoxylate aminotransferase as an essential determinant in primary hyperoxaluria type 1. <i>PLoS Biology</i> , 2012 , 10, e1001309	9.7	52
15	Restricted leucine zipper dimerization and specificity of DNA recognition of the melanocyte master regulator MITF. <i>Genes and Development</i> , 2012 , 26, 2647-58	12.6	71
14	Improved mycobacterial protein production using a <i>Mycobacterium smegmatis</i> groEL10 expression strain. <i>BMC Biotechnology</i> , 2011 , 11, 27	3.5	44
13	Proteome-wide identification of mycobacterial pupylation targets. <i>Molecular Systems Biology</i> , 2010 , 6, 386	12.2	86

12	Stoichiometric protein complex formation and over-expression using the prokaryotic native operon structure. <i>FEBS Letters</i> , 2010 , 584, 669-74	3.8	24
11	Solution structure of human Pex5.Pex14.PTS1 protein complexes obtained by small angle X-ray scattering. <i>Journal of Biological Chemistry</i> , 2009 , 284, 25334-42	5.4	34
10	Structural basis for competitive interactions of Pex14 with the import receptors Pex5 and Pex19. <i>EMBO Journal</i> , 2009 , 28, 745-54	13	69
9	A previously unobserved conformation for the human Pex5p receptor suggests roles for intrinsic flexibility and rigid domain motions in ligand binding. <i>BMC Structural Biology</i> , 2007 , 7, 24	2.7	21
8	Structure-based approaches to drug discovery against tuberculosis. <i>Current Protein and Peptide Science</i> , 2007 , 8, 365-75	2.8	16
7	Recognition of a functional peroxisome type 1 target by the dynamic import receptor pex5p. <i>Molecular Cell</i> , 2006 , 24, 653-663	17.6	134
6	Structural evidence for ammonia tunneling across the (beta alpha)(8) barrel of the imidazole glycerol phosphate synthase bienzyme complex. <i>Structure</i> , 2002 , 10, 185-93	5.2	99
5	Topography for independent binding of alpha-helical and PPII-helical ligands to a peroxisomal SH3 domain. <i>Molecular Cell</i> , 2002 , 10, 1007-17	17.6	73
4	Efficient expression, purification and crystallisation of two hyperthermostable enzymes of histidine biosynthesis. <i>FEBS Letters</i> , 1999 , 454, 1-6	3.8	35
3	Structural basis for activation of the titin kinase domain during myofibrillogenesis. <i>Nature</i> , 1998 , 395, 863-9	50.4	300
2	High-resolution crystal structures of tyrosine kinase SH3 domains complexed with proline-rich peptides. <i>Nature Structural Biology</i> , 1994 , 1, 546-51		244
1	Structure of the mycobacterial ESX-5 Type VII Secretion System hexameric pore complex		4