

Matthias Wilmanns

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/4618642/publications.pdf>

Version: 2024-02-01

65
papers

3,037
citations

201385

27
h-index

174990

52
g-index

71
all docs

71
docs citations

71
times ranked

4371
citing authors

#	ARTICLE	IF	CITATIONS
1	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, 298, 101985.	1.6	4
2	Versatile allosteric properties in Pex5-like tetratricopeptide repeat proteins to induce diverse downstream function. <i>Traffic</i> , 2021, 22, 140-152.	1.3	4
3	The XBI BioLab for life science experiments at the European XFEL. <i>Journal of Applied Crystallography</i> , 2021, 54, 7-21.	1.9	23
4	Molecular basis for the allosteric activation mechanism of the heterodimeric imidazole glycerol phosphate synthase complex. <i>Nature Communications</i> , 2021, 12, 2748.	5.8	22
5	Structure of the mycobacterial ESX-5 type VII secretion system pore complex. <i>Science Advances</i> , 2021, 7, .	4.7	45
6	Conserved and specialized functions of Type VII secretion systems in non-tuberculous mycobacteria. <i>Microbiology (United Kingdom)</i> , 2021, 167, .	0.7	14
7	Across scales: novel insights into kidney health and disease by structural biology. <i>Kidney International</i> , 2021, 100, 281-288.	2.6	0
8	TBX2 controls a proliferative gene expression program in melanoma. <i>Genes and Development</i> , 2021, 35, 1657-1677.	2.7	7
9	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.	6.5	17
10	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.	1.4	11
11	The crystal structure of mycobacterial epoxide hydrolase A. <i>Scientific Reports</i> , 2020, 10, 16539.	1.6	4
12	Structure-Based Identification and Functional Characterization of a Lipocalin in the Malaria Parasite <i>Plasmodium falciparum</i> . <i>Cell Reports</i> , 2020, 31, 107817.	2.9	23
13	The <sc>pMy</sc> vector series: A versatile cloning platform for the recombinant production of mycobacterial proteins in <i>Mycobacterium smegmatis</i>. <i>Protein Science</i> , 2020, 29, 2528-2537.	3.1	9
14	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.	3.3	13
15	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.	3.3	17
16	Tuning Transcription Factor Availability through Acetylation-Mediated Genomic Redistribution. <i>Molecular Cell</i> , 2020, 79, 472-487.e10.	4.5	38
17	¹ H, ¹³ C, and ¹⁵ 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.	0.4	1
18	A kinase bioscavenger provides antibiotic resistance by extremely tight substrate binding. <i>Science Advances</i> , 2020, 6, eaaz9861.	4.7	17

#	ARTICLE	IF	CITATIONS
19	Structural basis of p62/SQSTM1 helical filaments and their role in cellular cargo uptake. <i>Nature Communications</i> , 2020, 11, 440.	5.8	71
20	Gain-of-Function Variant p.Pro2555Arg of von Willebrand Factor Increases Aggregate Size through Altering Stem Dynamics. <i>Thrombosis and Haemostasis</i> , 2020, , .	1.8	3
21	Subcellular localization and stability of <scp>MITF</scp> are modulated by the <scp>bHLH</scp>â€Žip domain. <i>Pigment Cell and Melanoma Research</i> , 2019, 32, 41-54.	1.5	23
22	MITF has a central role in regulating starvation-induced autophagy in melanoma. <i>Scientific Reports</i> , 2019, 9, 1055.	1.6	66
23	An NAD ⁺ Phosphorylase Toxin Triggers Mycobacterium tuberculosis Cell Death. <i>Molecular Cell</i> , 2019, 73, 1282-1291.e8.	4.5	58
24	Structural diversity in the atomic resolution 3D fingerprint of the titin M-band segment. <i>PLoS ONE</i> , 2019, 14, e0226693.	1.1	1
25	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.	2.0	21
26	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.	0.6	24
27	Structure and dynamics of the platelet integrin-binding C4 domain of von Willebrand factor. <i>Blood</i> , 2019, 133, 366-376.	0.6	22
28	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.	0.6	1
29	Structure of the mycobacterial ESX-5 type VII secretion system membrane complex by single-particle analysis. <i>Nature Microbiology</i> , 2017, 2, 17047.	5.9	102
30	Intermolecular base stacking mediates RNA-RNA interaction in a crystal structure of the RNA chaperone Hfq. <i>Scientific Reports</i> , 2017, 7, 9903.	1.6	14
31	Model-based local density sharpening of cryo-EM maps. <i>ELife</i> , 2017, 6, .	2.8	200
32	Higherâ€Žorder assemblies of oligomeric cargo receptor complexes form the membrane scaffold of the Cvt vesicle. <i>EMBO Reports</i> , 2016, 17, 1044-1060.	2.0	26
33	Towards the molecular mechanism of the integration of peroxisomal membrane proteins. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2016, 1863, 863-869.	1.9	18
34	A standardized production pipeline for high profile targets from Mycobacterium tuberculosis. <i>Proteomics - Clinical Applications</i> , 2016, 10, 1049-1057.	0.8	5
35	Robotic QM/MM-driven maturation of antibody combining sites. <i>Science Advances</i> , 2016, 2, e1501695.	4.7	15
36	Death-Associated Protein Kinase Activity Is Regulated by Coupled Calcium/Calmodulin Binding to Two Distinct Sites. <i>Structure</i> , 2016, 24, 851-861.	1.6	21

#	ARTICLE	IF	CITATIONS
37	Structural biology of the import pathways of peroxisomal matrix proteins. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2016, 1863, 804-813.	1.9	45
38	Suppression of Early Hematogenous Dissemination of Human Breast Cancer Cells to Bone Marrow by Retinoic Acid-Induced 2. <i>Cancer Discovery</i> , 2015, 5, 506-519.	7.7	45
39	Characterization of the Mycobacterial Acyl-CoA Carboxylase Holo Complexes Reveals Their Functional Expansion into Amino Acid Catabolism. <i>PLoS Pathogens</i> , 2015, 11, e1004623.	2.1	19
40	Structural Insights into Cargo Recognition by the Yeast PTS1 Receptor. <i>Journal of Biological Chemistry</i> , 2015, 290, 26610-26626.	1.6	27
41	Ligand-Induced Compaction of the PEX5 Receptor Binding Cavity Impacts Protein Import Efficiency into Peroxisomes. <i>Traffic</i> , 2015, 16, 85-98.	1.3	37
42	Induction of insulin-like growth factor 1 splice forms by subfragments of myofibrillar proteins. <i>Molecular and Cellular Endocrinology</i> , 2015, 399, 69-77.	1.6	9
43	Refined Requirements for Protein Regions Important for Activity of the TALE AvrBs3. <i>PLoS ONE</i> , 2015, 10, e0120214.	1.1	29
44	Role of the light-chain constant-domain switch in the structure and functionality of A17 reactibody. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2014, 70, 708-719.	2.5	22
45	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, 249-258.	1.3	47
46	Structure of the <i>Mycobacterium tuberculosis</i> type VII secretion system chaperone EspG ₅ in complex with PE ₂₅ -PPE ₄₁ dimer. <i>Molecular Microbiology</i> , 2014, 94, 367-382.	1.2	83
47	WXG100 Protein Superfamily Consists of Three Subfamilies and Exhibits an α -Helical C-Terminal Conserved Residue Pattern. <i>PLoS ONE</i> , 2014, 9, e89313.	1.1	92
48	Crystal structure of the S187F variant of human liver alanine: Aminotransferase associated with primary hyperoxaluria type I and its functional implications. <i>Proteins: Structure, Function and Bioinformatics</i> , 2013, 81, 1457-1465.	1.5	24
49	MITF mutations associated with pigment deficiency syndromes and melanoma have different effects on protein function. <i>Human Molecular Genetics</i> , 2013, 22, 4357-4367.	1.4	50
50	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.	2.6	64
51	Restricted leucine zipper dimerization and specificity of DNA recognition of the melanocyte master regulator MITF. <i>Genes and Development</i> , 2012, 26, 2647-2658.	2.7	103
52	Catalysis Uncoupling in a Glutamine Amidotransferase Bienzyme by Unblocking the Glutaminase Active Site. <i>Chemistry and Biology</i> , 2012, 19, 1589-1599.	6.2	40
53	Improved mycobacterial protein production using a <i>Mycobacterium smegmatis</i> groEL ⁺ expression strain. <i>BMC Biotechnology</i> , 2011, 11, 27.	1.7	51
54	Proteome-wide identification of mycobacterial pupylation targets. <i>Molecular Systems Biology</i> , 2010, 6, 386.	3.2	94

#	ARTICLE	IF	CITATIONS
55	Stoichiometric protein complex formation and overexpression using the prokaryotic native operon structure. <i>FEBS Letters</i> , 2010, 584, 669-674.	1.3	26
56	Solution Structure of Human Pex5-Pex14-PTS1 Protein Complexes Obtained by Small Angle X-ray Scattering. <i>Journal of Biological Chemistry</i> , 2009, 284, 25334-25342.	1.6	41
57	Structural basis for competitive interactions of Pex14 with the import receptors Pex5 and Pex19. <i>EMBO Journal</i> , 2009, 28, 745-754.	3.5	82
58	Structure-Based Approaches to Drug Discovery Against Tuberculosis. <i>Current Protein and Peptide Science</i> , 2007, 8, 365-375.	0.7	17
59	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.	2.3	23
60	Recognition of a Functional Peroxisome Type 1 Target by the Dynamic Import Receptor Pex5p. <i>Molecular Cell</i> , 2006, 24, 653-663.	4.5	156
61	Topography for Independent Binding of α -Helical and PPII-Helical Ligands to a Peroxisomal SH3 Domain. <i>Molecular Cell</i> , 2002, 10, 1007-1017.	4.5	81
62	Structural Evidence for Ammonia Tunneling across the (12 \pm)8 Barrel of the Imidazole Glycerol Phosphate Synthase Bifunctional Complex. <i>Structure</i> , 2002, 10, 185-193.	1.6	109
63	Efficient expression, purification and crystallisation of two hyperthermostable enzymes of histidine biosynthesis. <i>FEBS Letters</i> , 1999, 454, 1-6.	1.3	35
64	Structural basis for activation of the titin kinase domain during myofibrillogenesis. <i>Nature</i> , 1998, 395, 863-869.	13.7	333
65	High-resolution crystal structures of tyrosine kinase SH3 domains complexed with proline-rich peptides. <i>Nature Structural Biology</i> , 1994, 1, 546-551.	9.7	284