## **Timm Maier**

List of Publications by Year in descending order

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TIMM MAIED

#	Article	IF	CITATIONS
1	The Crystal Structure of a Mammalian Fatty Acid Synthase. Science, 2008, 321, 1315-1322.	12.6	408
2	Trigger factor in complex with the ribosome forms a molecular cradle for nascent proteins. Nature, 2004, 431, 590-596.	27.8	347
3	Architecture of Mammalian Fatty Acid Synthase at 4.5 A Resolution. Science, 2006, 311, 1258-1262.	12.6	344
4	The structure of a cytolytic α-helical toxin pore reveals its assembly mechanism. Nature, 2009, 459, 726-730.	27.8	303
5	Architecture of human mTOR complex 1. Science, 2016, 351, 48-52.	12.6	280
6	Structure of the Type VI Secretion System Contractile Sheath. Cell, 2015, 160, 952-962.	28.9	216
7	Catch-bond mechanism of the bacterial adhesin FimH. Nature Communications, 2016, 7, 10738.	12.8	164
8	The multienzyme architecture of eukaryotic fatty acid synthases. Current Opinion in Structural Biology, 2008, 18, 714-725.	5.7	163
9	The architectures of iterative type I PKS and FAS. Natural Product Reports, 2018, 35, 1046-1069.	10.3	143
10	Molecular mechanism and structure of Trigger Factor bound to the translating ribosome. EMBO Journal, 2008, 27, 1622-1632.	7.8	142
11	Architecture of a Fungal Fatty Acid Synthase at 5 A Resolution. Science, 2006, 311, 1263-1267.	12.6	138
12	Structural basis for regulation of human acetyl-CoA carboxylase. Nature, 2018, 558, 470-474.	27.8	135
13	Structure and function of eukaryotic fatty acid synthases. Quarterly Reviews of Biophysics, 2010, 43, 373-422.	5.7	122
14	mTOR substrate phosphorylation in growth control. Cell, 2022, 185, 1814-1836.	28.9	120
15	The structural basis of autotransporter translocation by TamA. Nature Structural and Molecular Biology, 2013, 20, 1318-1320.	8.2	116
16	The antibiotic darobactin mimics a β-strand to inhibit outer membrane insertase. Nature, 2021, 593, 125-129.	27.8	112
17	The X-ray Crystal Structure of Human β-Hexosaminidase B Provides New Insights into Sandhoff Disease. Journal of Molecular Biology, 2003, 328, 669-681.	4.2	109
18	STIL binding to Polo-box 3 of PLK4 regulates centriole duplication. ELife, 2015, 4, .	6.0	109

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19	Cryo-EM structure of the extended type VI secretion system sheath–tube complex. Nature Microbiology, 2017, 2, 1507-1512.	13.3	107
20	A peptide deformylase–ribosome complex reveals mechanism of nascent chain processing. Nature, 2008, 452, 108-111.	27.8	93
21	A cradle for new proteins: trigger factor at the ribosome. Current Opinion in Structural Biology, 2005, 15, 204-212.	5.7	88
22	FimH Antagonists: Bioisosteres To Improve the in Vitro and in Vivo PK/PD Profile. Journal of Medicinal Chemistry, 2015, 58, 2221-2239.	6.4	84
23	Crystal Structures of Human Saposins C and D: Implications for Lipid Recognition and Membrane Interactions. Structure, 2008, 16, 809-817.	3.3	78
24	Long-lived T follicular helper cells retain plasticity and help sustain humoral immunity. Science Immunology, 2020, 5, .	11.9	78
25	Structure of the unusual seryl-tRNA synthetase reveals a distinct zinc-dependent mode of substrate recognition. EMBO Journal, 2006, 25, 2498-2509.	7.8	77
26	Binding of the Bacterial Adhesin FimH to Its Natural, Multivalent High-Mannose Type Glycan Targets. Journal of the American Chemical Society, 2019, 141, 936-944.	13.7	76
27	Mycocerosic acid synthase exemplifies the architecture of reducing polyketide synthases. Nature, 2016, 531, 533-537.	27.8	70
28	Insect Immune Activation by Apolipophorin III Is Correlated with the Lipid-Binding Properties of This Proteinâ€. Biochemistry, 2001, 40, 11502-11508.	2.5	63
29	Crystal Structure of Mistletoe Lectin I fromViscum album. Biochemical and Biophysical Research Communications, 1999, 257, 418-424.	2.1	60
30	Architecture of the human mTORC2 core complex. ELife, 2018, 7, .	6.0	59
31	The 3.2-Ã resolution structure of human mTORC2. Science Advances, 2020, 6, .	10.3	57
32	Crystal Structure of Thermotoga maritima α-Glucosidase AglA Defines a New Clan of NAD+-dependent Glycosidases. Journal of Biological Chemistry, 2003, 278, 19151-19158.	3.4	56
33	Homologs of aminoacyl-tRNA synthetases acylate carrier proteins and provide a link between ribosomal and nonribosomal peptide synthesis. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 14585-14590.	7.1	55
34	E-selectin ligand complexes adopt an extended high-affinity conformation. Journal of Molecular Cell Biology, 2016, 8, 62-72.	3.3	50
35	Architecture and activation of phosphatidylinositol 3-kinase related kinases. Current Opinion in Structural Biology, 2018, 49, 177-189.	5.7	50
36	The structural organization of substrate loading in iterative polyketide synthases. Nature Chemical Biology, 2018, 14, 474-479.	8.0	50

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37	The Tyrosine Gate of the Bacterial Lectin FimH: A Conformational Analysis by NMR Spectroscopy and Xâ€ray Crystallography. ChemBioChem, 2015, 16, 1235-1246.	2.6	42
38	Amylose recognition and ring-size determination of amylomaltase. Science Advances, 2017, 3, e1601386.	10.3	42
39	Dimeric Structure of the Bacterial Extracellular Foldase PrsA. Journal of Biological Chemistry, 2015, 290, 3278-3292.	3.4	41
40	The dynamic organization of fungal acetyl-CoA carboxylase. Nature Communications, 2016, 7, 11196.	12.8	39
41	A folding nucleus and minimal ATP binding domain of Hsp70 identified by single-molecule force spectroscopy. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 4666-4671.	7.1	38
42	Evolutionary Origins of the Multienzyme Architecture of Giant Fungal Fatty Acid Synthase. Structure, 2014, 22, 1775-1785.	3.3	36
43	Structural basis of the activation of the CC chemokine receptor 5 by a chemokine agonist. Science Advances, 2021, 7, .	10.3	36
44	Characterization of the insertase BamA in three different membrane mimetics by solution NMR spectroscopy. Journal of Biomolecular NMR, 2015, 61, 333-345.	2.8	32
45	The dynamic mechanism of 4E-BP1 recognition and phosphorylation by mTORC1. Molecular Cell, 2021, 81, 2403-2416.e5.	9.7	32
46	Conserved Omp85 lid-lock structure and substrate recognition in FhaC. Nature Communications, 2015, 6, 7452.	12.8	31
47	A Large Hinge Bending Domain Rotation Is Necessary for the Catalytic Function ofEscherichia coli5â€ <sup>-</sup> -Nucleotidaseâ€. Biochemistry, 2005, 44, 2244-2252.	2.5	30
48	Reinforced HNA Backbone Hydration in the Crystal Structure of a Decameric HNA/RNA Hybrid. Journal of the American Chemical Society, 2005, 127, 2937-2943.	13.7	30
49	Functional and Structural Analysis of Programmed C-Methylation in the Biosynthesis of the Fungal Polyketide Citrinin. Cell Chemical Biology, 2017, 24, 316-325.	5.2	30
50	The enzyme-binding region of human GM2-activator protein. FEBS Journal, 2006, 273, 982-991.	4.7	28
51	Improvement of Aglycone Ï€â€Stacking Yields Nanomolar to Subâ€nanomolar FimH Antagonists. ChemMedChem, 2019, 14, 749-757.	3.2	27
52	Structural basis for ion selectivity in TMEM175 K+ channels. ELife, 2020, 9, .	6.0	27
53	Sweet Drugs for Bad Bugs: A Glycomimetic Strategy against the DC-SIGN-Mediated Dissemination of SARS-CoV-2. Journal of the American Chemical Society, 2021, 143, 17465-17478.	13.7	27
54	Enzyme repurposing of a hydrolase as an emergent peroxidase upon metal binding. Chemical Science, 2015, 6, 4060-4065.	7.4	26

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55	The price of flexibility – a case study on septanoses as pyranose mimetics. Chemical Science, 2018, 9, 646-654.	7.4	26
56	Mutasynthetic Production and Antimicrobial Characterization of Darobactin Analogs. Microbiology Spectrum, 2021, 9, e0153521.	3.0	26
57	The Signature of the Five-Stranded vRRM Fold Defined by Functional, Structural and Computational Analysis of the hnRNP L Protein. Journal of Molecular Biology, 2015, 427, 3001-3022.	4.2	25
58	Trapping a 96° domain rotation in two distinct conformations by engineered disulfide bridges. Protein Science, 2004, 13, 1811-1822.	7.6	24
59	Conformational switch of the bacterial adhesin FimH in the absence of the regulatory domain: Engineering a minimalistic allosteric system. Journal of Biological Chemistry, 2018, 293, 1835-1849.	3.4	23
60	KinITC—One Method Supports both Thermodynamic and Kinetic SARs as Exemplified on FimH Antagonists. Chemistry - A European Journal, 2018, 24, 13049-13057.	3.3	21
61	High-Speed Atomic Force Microscopy Visualization of the Dynamics of the Multienzyme Fatty Acid Synthase. ACS Nano, 2017, 11, 10852-10859.	14.6	20
62	Identification of conformation-selective nanobodies against the membrane protein insertase BamA by an integrated structural biology approach. Journal of Biomolecular NMR, 2019, 73, 375-384.	2.8	20
63	Regulation of human mTOR complexes by DEPTOR. ELife, 2021, 10, .	6.0	15
64	Conserved sequence motifs and the structure of the mTOR kinase domain. Biochemical Society Transactions, 2013, 41, 889-895.	3.4	13
65	Carbohydrate–Lectin Interactions: An Unexpected Contribution to Affinity. ChemBioChem, 2017, 18, 539-544.	2.6	11
66	Does targeting Arg98 of FimH lead to high affinity antagonists?. European Journal of Medicinal Chemistry, 2021, 211, 113093.	5.5	11
67	Enhancing the enthalpic contribution of hydrogen bonds by solvent shielding. RSC Chemical Biology, 2020, 1, 281-287.	4.1	10
68	Structural and Functional Characterization of a Novel Family of Cyclophilins, the AquaCyps. PLoS ONE, 2016, 11, e0157070.	2.5	8
69	Re-engineering biofactories. Nature Chemical Biology, 2017, 13, 344-345.	8.0	7
70	DARPins recognizing mTFP1 as novel reagents for <i>in vitro</i> and <i>in vivo</i> protein manipulations. Biology Open, 2018, 7, .	1.2	7
71	Crystallization and preliminary characterization of three different crystal forms of human saposin C heterologously expressed inPichia pastoris. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 117-120.	0.7	5
72	Purification and Bicelle Crystallization for Structure Determination of the E. coli Outer Membrane Protein TamA. Methods in Molecular Biology, 2015, 1329, 259-270.	0.9	4

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73	Hybrid Structure of a Dynamic Single-Chain Carboxylase from Deinococcus radiodurans. Structure, 2016, 24, 1227-1236.	3.3	3
74	A central role for a region in the middle. ELife, 2017, 6, .	6.0	1
75	Biochemie und Molekularbiologie 2003. Nachrichten Aus Der Chemie, 2004, 52, 292-305.	0.0	0
76	Editorial overview: Macromolecular assemblies: Assembly, dynamics and control of activity. Current Opinion in Structural Biology, 2018, 49, vi-vii.	5.7	0