

Timm Maier

List of Publications by Year in descending order

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76
papers

5,607
citations

94269

37
h-index

82410

72
g-index

85
all docs

85
docs citations

85
times ranked

7221
citing authors

#	ARTICLE	IF	CITATIONS
1	The Crystal Structure of a Mammalian Fatty Acid Synthase. <i>Science</i> , 2008, 321, 1315-1322.	6.0	408
2	Trigger factor in complex with the ribosome forms a molecular cradle for nascent proteins. <i>Nature</i> , 2004, 431, 590-596.	13.7	347
3	Architecture of Mammalian Fatty Acid Synthase at 4.5 Å Resolution. <i>Science</i> , 2006, 311, 1258-1262.	6.0	344
4	The structure of a cytolytic β -helical toxin pore reveals its assembly mechanism. <i>Nature</i> , 2009, 459, 726-730.	13.7	303
5	Architecture of human mTOR complex 1. <i>Science</i> , 2016, 351, 48-52.	6.0	280
6	Structure of the Type VI Secretion System Contractile Sheath. <i>Cell</i> , 2015, 160, 952-962.	13.5	216
7	Catch-bond mechanism of the bacterial adhesin FimH. <i>Nature Communications</i> , 2016, 7, 10738.	5.8	164
8	The multienzyme architecture of eukaryotic fatty acid synthases. <i>Current Opinion in Structural Biology</i> , 2008, 18, 714-725.	2.6	163
9	The architectures of iterative type I PKS and FAS. <i>Natural Product Reports</i> , 2018, 35, 1046-1069.	5.2	143
10	Molecular mechanism and structure of Trigger Factor bound to the translating ribosome. <i>EMBO Journal</i> , 2008, 27, 1622-1632.	3.5	142
11	Architecture of a Fungal Fatty Acid Synthase at 5 Å Resolution. <i>Science</i> , 2006, 311, 1263-1267.	6.0	138
12	Structural basis for regulation of human acetyl-CoA carboxylase. <i>Nature</i> , 2018, 558, 470-474.	13.7	135
13	Structure and function of eukaryotic fatty acid synthases. <i>Quarterly Reviews of Biophysics</i> , 2010, 43, 373-422.	2.4	122
14	mTOR substrate phosphorylation in growth control. <i>Cell</i> , 2022, 185, 1814-1836.	13.5	120
15	The structural basis of autotransporter translocation by TamA. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1318-1320.	3.6	116
16	The antibiotic darobactin mimics a β -strand to inhibit outer membrane insertase. <i>Nature</i> , 2021, 593, 125-129.	13.7	112
17	The X-ray Crystal Structure of Human β -Hexosaminidase B Provides New Insights into Sandhoff Disease. <i>Journal of Molecular Biology</i> , 2003, 328, 669-681.	2.0	109
18	STIL binding to Polo-box 3 of PLK4 regulates centriole duplication. <i>ELife</i> , 2015, 4, .	2.8	109

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19	Cryo-EM structure of the extended type VI secretion system sheathâ€“tube complex. <i>Nature Microbiology</i> , 2017, 2, 1507-1512.	5.9	107
20	A peptide deformylaseâ€“ribosome complex reveals mechanism of nascent chain processing. <i>Nature</i> , 2008, 452, 108-111.	13.7	93
21	A cradle for new proteins: trigger factor at the ribosome. <i>Current Opinion in Structural Biology</i> , 2005, 15, 204-212.	2.6	88
22	FimH Antagonists: Bioisosteres To Improve the in Vitro and in Vivo PK/PD Profile. <i>Journal of Medicinal Chemistry</i> , 2015, 58, 2221-2239.	2.9	84
23	Crystal Structures of Human Saposins C and D: Implications for Lipid Recognition and Membrane Interactions. <i>Structure</i> , 2008, 16, 809-817.	1.6	78
24	Long-lived T follicular helper cells retain plasticity and help sustain humoral immunity. <i>Science Immunology</i> , 2020, 5, .	5.6	78
25	Structure of the unusual seryl-tRNA synthetase reveals a distinct zinc-dependent mode of substrate recognition. <i>EMBO Journal</i> , 2006, 25, 2498-2509.	3.5	77
26	Binding of the Bacterial Adhesin FimH to Its Natural, Multivalent High-Mannose Type Glycan Targets. <i>Journal of the American Chemical Society</i> , 2019, 141, 936-944.	6.6	76
27	Mycocerosic acid synthase exemplifies the architecture of reducing polyketide synthases. <i>Nature</i> , 2016, 531, 533-537.	13.7	70
28	Insect Immune Activation by Apolipoprotein III Is Correlated with the Lipid-Binding Properties of This Proteinâ€“. <i>Biochemistry</i> , 2001, 40, 11502-11508.	1.2	63
29	Crystal Structure of Mistletoe Lectin I from <i>Viscum album</i> . <i>Biochemical and Biophysical Research Communications</i> , 1999, 257, 418-424.	1.0	60
30	Architecture of the human mTORC2 core complex. <i>ELife</i> , 2018, 7, .	2.8	59
31	The 3.2-Å... resolution structure of human mTORC2. <i>Science Advances</i> , 2020, 6, .	4.7	57
32	Crystal Structure of <i>Thermotoga maritima</i> Î±-Glucosidase AglA Defines a New Clan of NAD ⁺ -dependent Glycosidases. <i>Journal of Biological Chemistry</i> , 2003, 278, 19151-19158.	1.6	56
33	Homologs of aminoacyl-tRNA synthetases acylate carrier proteins and provide a link between ribosomal and nonribosomal peptide synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 14585-14590.	3.3	55
34	E-selectin ligand complexes adopt an extended high-affinity conformation. <i>Journal of Molecular Cell Biology</i> , 2016, 8, 62-72.	1.5	50
35	Architecture and activation of phosphatidylinositol 3-kinase related kinases. <i>Current Opinion in Structural Biology</i> , 2018, 49, 177-189.	2.6	50
36	The structural organization of substrate loading in iterative polyketide synthases. <i>Nature Chemical Biology</i> , 2018, 14, 474-479.	3.9	50

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37	The Tyrosine Gate of the Bacterial Lectin FimH: A Conformational Analysis by NMR Spectroscopy and X-ray Crystallography. <i>ChemBioChem</i> , 2015, 16, 1235-1246.	1.3	42
38	Amylose recognition and ring-size determination of amylomaltase. <i>Science Advances</i> , 2017, 3, e1601386.	4.7	42
39	Dimeric Structure of the Bacterial Extracellular Foldase PrsA. <i>Journal of Biological Chemistry</i> , 2015, 290, 3278-3292.	1.6	41
40	The dynamic organization of fungal acetyl-CoA carboxylase. <i>Nature Communications</i> , 2016, 7, 11196.	5.8	39
41	A folding nucleus and minimal ATP binding domain of Hsp70 identified by single-molecule force spectroscopy. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4666-4671.	3.3	38
42	Evolutionary Origins of the Multienzyme Architecture of Giant Fungal Fatty Acid Synthase. <i>Structure</i> , 2014, 22, 1775-1785.	1.6	36
43	Structural basis of the activation of the CC chemokine receptor 5 by a chemokine agonist. <i>Science Advances</i> , 2021, 7, .	4.7	36
44	Characterization of the insertase BamA in three different membrane mimetics by solution NMR spectroscopy. <i>Journal of Biomolecular NMR</i> , 2015, 61, 333-345.	1.6	32
45	The dynamic mechanism of 4E-BP1 recognition and phosphorylation by mTORC1. <i>Molecular Cell</i> , 2021, 81, 2403-2416.e5.	4.5	32
46	Conserved Omp85 lid-lock structure and substrate recognition in FhaC. <i>Nature Communications</i> , 2015, 6, 7452.	5.8	31
47	A Large Hinge Bending Domain Rotation Is Necessary for the Catalytic Function of <i>Escherichia coli</i> 5'-Nucleotidase. <i>Biochemistry</i> , 2005, 44, 2244-2252.	1.2	30
48	Reinforced HNA Backbone Hydration in the Crystal Structure of a Decameric HNA/RNA Hybrid. <i>Journal of the American Chemical Society</i> , 2005, 127, 2937-2943.	6.6	30
49	Functional and Structural Analysis of Programmed C-Methylation in the Biosynthesis of the Fungal Polyketide Citrinin. <i>Cell Chemical Biology</i> , 2017, 24, 316-325.	2.5	30
50	The enzyme-binding region of human GM2-activator protein. <i>FEBS Journal</i> , 2006, 273, 982-991.	2.2	28
51	Improvement of Aglycone π - π Stacking Yields Nanomolar to Subnanomolar FimH Antagonists. <i>ChemMedChem</i> , 2019, 14, 749-757.	1.6	27
52	Structural basis for ion selectivity in TMEM175 K ⁺ channels. <i>ELife</i> , 2020, 9, .	2.8	27
53	Sweet Drugs for Bad Bugs: A Glycomimetic Strategy against the DC-SIGN-Mediated Dissemination of SARS-CoV-2. <i>Journal of the American Chemical Society</i> , 2021, 143, 17465-17478.	6.6	27
54	Enzyme repurposing of a hydrolase as an emergent peroxidase upon metal binding. <i>Chemical Science</i> , 2015, 6, 4060-4065.	3.7	26

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55	The price of flexibility – a case study on septanoses as pyranose mimetics. <i>Chemical Science</i> , 2018, 9, 646-654.	3.7	26
56	Mutasynthetic Production and Antimicrobial Characterization of Darobactin Analogs. <i>Microbiology Spectrum</i> , 2021, 9, e0153521.	1.2	26
57	The Signature of the Five-Stranded vRRM Fold Defined by Functional, Structural and Computational Analysis of the hnRNP L Protein. <i>Journal of Molecular Biology</i> , 2015, 427, 3001-3022.	2.0	25
58	Trapping a 96Å° domain rotation in two distinct conformations by engineered disulfide bridges. <i>Protein Science</i> , 2004, 13, 1811-1822.	3.1	24
59	Conformational switch of the bacterial adhesin FimH in the absence of the regulatory domain: Engineering a minimalistic allosteric system. <i>Journal of Biological Chemistry</i> , 2018, 293, 1835-1849.	1.6	23
60	KinITCâ”One Method Supports both Thermodynamic and Kinetic SARs as Exemplified on FimH Antagonists. <i>Chemistry - A European Journal</i> , 2018, 24, 13049-13057.	1.7	21
61	High-Speed Atomic Force Microscopy Visualization of the Dynamics of the Multienzyme Fatty Acid Synthase. <i>ACS Nano</i> , 2017, 11, 10852-10859.	7.3	20
62	Identification of conformation-selective nanobodies against the membrane protein insertase BamA by an integrated structural biology approach. <i>Journal of Biomolecular NMR</i> , 2019, 73, 375-384.	1.6	20
63	Regulation of human mTOR complexes by DEPTOR. <i>ELife</i> , 2021, 10, .	2.8	15
64	Conserved sequence motifs and the structure of the mTOR kinase domain. <i>Biochemical Society Transactions</i> , 2013, 41, 889-895.	1.6	13
65	Carbohydrateâ”Lectin Interactions: An Unexpected Contribution to Affinity. <i>ChemBioChem</i> , 2017, 18, 539-544.	1.3	11
66	Does targeting Arg98 of FimH lead to high affinity antagonists?. <i>European Journal of Medicinal Chemistry</i> , 2021, 211, 113093.	2.6	11
67	Enhancing the enthalpic contribution of hydrogen bonds by solvent shielding. <i>RSC Chemical Biology</i> , 2020, 1, 281-287.	2.0	10
68	Structural and Functional Characterization of a Novel Family of Cyclophilins, the AquaCyps. <i>PLoS ONE</i> , 2016, 11, e0157070.	1.1	8
69	Re-engineering biofactories. <i>Nature Chemical Biology</i> , 2017, 13, 344-345.	3.9	7
70	DARPinS recognizing mTFP1 as novel reagents for <i>in vitro</i> and <i>in vivo</i> protein manipulations. <i>Biology Open</i> , 2018, 7, .	0.6	7
71	Crystallization and preliminary characterization of three different crystal forms of human saposin C heterologously expressed in <i>Pichia pastoris</i> . <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 117-120.	0.7	5
72	Purification and Bicelle Crystallization for Structure Determination of the <i>E. coli</i> Outer Membrane Protein TamA. <i>Methods in Molecular Biology</i> , 2015, 1329, 259-270.	0.4	4

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73	Hybrid Structure of a Dynamic Single-Chain Carboxylase from <i>Deinococcus radiodurans</i> . <i>Structure</i> , 2016, 24, 1227-1236.	1.6	3
74	A central role for a region in the middle. <i>ELife</i> , 2017, 6, .	2.8	1
75	Biochemie und Molekularbiologie 2003. <i>Nachrichten Aus Der Chemie</i> , 2004, 52, 292-305.	0.0	0
76	Editorial overview: Macromolecular assemblies: Assembly, dynamics and control of activity. <i>Current Opinion in Structural Biology</i> , 2018, 49, vi-vii.	2.6	0