

Timm Maier

List of Publications by Year in descending order

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Version: 2024-02-01

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	mTOR substrate phosphorylation in growth control. <i>Cell</i> , 2022, 185, 1814-1836.	13.5	120
2	Does targeting Arg98 of FimH lead to high affinity antagonists?. <i>European Journal of Medicinal Chemistry</i> , 2021, 211, 113093.	2.6	11
3	The antibiotic darobactin mimics a β -strand to inhibit outer membrane insertase. <i>Nature</i> , 2021, 593, 125-129.	13.7	112
4	Structural basis of the activation of the CC chemokine receptor 5 by a chemokine agonist. <i>Science Advances</i> , 2021, 7, .	4.7	36
5	The dynamic mechanism of 4E-BP1 recognition and phosphorylation by mTORC1. <i>Molecular Cell</i> , 2021, 81, 2403-2416.e5.	4.5	32
6	Regulation of human mTOR complexes by DEPTOR. <i>ELife</i> , 2021, 10, .	2.8	15
7	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
8	Mutasynthetic Production and Antimicrobial Characterization of Darobactin Analogs. <i>Microbiology Spectrum</i> , 2021, 9, e0153521.	1.2	26
9	The 3.2-Å... resolution structure of human mTORC2. <i>Science Advances</i> , 2020, 6, .	4.7	57
10	Enhancing the enthalpic contribution of hydrogen bonds by solvent shielding. <i>RSC Chemical Biology</i> , 2020, 1, 281-287.	2.0	10
11	Long-lived T follicular helper cells retain plasticity and help sustain humoral immunity. <i>Science Immunology</i> , 2020, 5, .	5.6	78
12	Structural basis for ion selectivity in TMEM175 K ⁺ channels. <i>ELife</i> , 2020, 9, .	2.8	27
13	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
14	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
15	Improvement of Aglycone π - π Stacking Yields Nanomolar to Subnanomolar FimH Antagonists. <i>ChemMedChem</i> , 2019, 14, 749-757.	1.6	27
16	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
17	Architecture and activation of phosphatidylinositol 3-kinase related kinases. <i>Current Opinion in Structural Biology</i> , 2018, 49, 177-189.	2.6	50
18	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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19	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
20	The price of flexibility – a case study on septanoses as pyranose mimetics. <i>Chemical Science</i> , 2018, 9, 646-654.	3.7	26
21	DARPin 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
22	KinITC – 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
23	Architecture of the human mTORC2 core complex. <i>ELife</i> , 2018, 7, .	2.8	59
24	Editorial overview: Macromolecular assemblies: Assembly, dynamics and control of activity. <i>Current Opinion in Structural Biology</i> , 2018, 49, vi-vii.	2.6	0
25	The architectures of iterative type I PKS and FAS. <i>Natural Product Reports</i> , 2018, 35, 1046-1069.	5.2	143
26	Structural basis for regulation of human acetyl-CoA carboxylase. <i>Nature</i> , 2018, 558, 470-474.	13.7	135
27	Carbohydrate – Lectin Interactions: An Unexpected Contribution to Affinity. <i>ChemBioChem</i> , 2017, 18, 539-544.	1.3	11
28	Amylose recognition and ring-size determination of amylomaltase. <i>Science Advances</i> , 2017, 3, e1601386.	4.7	42
29	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
30	Re-engineering biofactories. <i>Nature Chemical Biology</i> , 2017, 13, 344-345.	3.9	7
31	Cryo-EM structure of the extended type VI secretion system sheath – tube complex. <i>Nature Microbiology</i> , 2017, 2, 1507-1512.	5.9	107
32	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
33	A central role for a region in the middle. <i>ELife</i> , 2017, 6, .	2.8	1
34	Structural and Functional Characterization of a Novel Family of Cyclophilins, the AquaCyps. <i>PLoS ONE</i> , 2016, 11, e0157070.	1.1	8
35	Hybrid Structure of a Dynamic Single-Chain Carboxylase from <i>Deinococcus radiodurans</i> . <i>Structure</i> , 2016, 24, 1227-1236.	1.6	3
36	The dynamic organization of fungal acetyl-CoA carboxylase. <i>Nature Communications</i> , 2016, 7, 11196.	5.8	39

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37	Catch-bond mechanism of the bacterial adhesin FimH. <i>Nature Communications</i> , 2016, 7, 10738.	5.8	164
38	Architecture of human mTOR complex 1. <i>Science</i> , 2016, 351, 48-52.	6.0	280
39	Mycocerosic acid synthase exemplifies the architecture of reducing polyketide synthases. <i>Nature</i> , 2016, 531, 533-537.	13.7	70
40	E-selectin ligand complexes adopt an extended high-affinity conformation. <i>Journal of Molecular Cell Biology</i> , 2016, 8, 62-72.	1.5	50
41	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
42	Enzyme repurposing of a hydrolase as an emergent peroxidase upon metal binding. <i>Chemical Science</i> , 2015, 6, 4060-4065.	3.7	26
43	Dimeric Structure of the Bacterial Extracellular Foldase PrsA. <i>Journal of Biological Chemistry</i> , 2015, 290, 3278-3292.	1.6	41
44	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
45	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
46	Structure of the Type VI Secretion System Contractile Sheath. <i>Cell</i> , 2015, 160, 952-962.	13.5	216
47	Conserved Omp85 lid-lock structure and substrate recognition in FhaC. <i>Nature Communications</i> , 2015, 6, 7452.	5.8	31
48	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
49	Purification and Bicelle Crystallization for Structure Determination of the E. coli Outer Membrane Protein TamA. <i>Methods in Molecular Biology</i> , 2015, 1329, 259-270.	0.4	4
50	STIL binding to Polo-box 3 of PLK4 regulates centriole duplication. <i>ELife</i> , 2015, 4, .	2.8	109
51	Evolutionary Origins of the Multienzyme Architecture of Giant Fungal Fatty Acid Synthase. <i>Structure</i> , 2014, 22, 1775-1785.	1.6	36
52	The structural basis of autotransporter translocation by TamA. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 1318-1320.	3.6	116
53	Conserved sequence motifs and the structure of the mTOR kinase domain. <i>Biochemical Society Transactions</i> , 2013, 41, 889-895.	1.6	13
54	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

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55	Structure and function of eukaryotic fatty acid synthases. Quarterly Reviews of Biophysics, 2010, 43, 373-422.	2.4	122
56	The structure of a cytolytic Î±-helical toxin pore reveals its assembly mechanism. Nature, 2009, 459, 726-730.	13.7	303
57	Molecular mechanism and structure of Trigger Factor bound to the translating ribosome. EMBO Journal, 2008, 27, 1622-1632.	3.5	142
58	A peptide deformylase-ribosome complex reveals mechanism of nascent chain processing. Nature, 2008, 452, 108-111.	13.7	93
59	The multienzyme architecture of eukaryotic fatty acid synthases. Current Opinion in Structural Biology, 2008, 18, 714-725.	2.6	163
60	Crystal Structures of Human Saposins C and D: Implications for Lipid Recognition and Membrane Interactions. Structure, 2008, 16, 809-817.	1.6	78
61	The Crystal Structure of a Mammalian Fatty Acid Synthase. Science, 2008, 321, 1315-1322.	6.0	408
62	Architecture of Mammalian Fatty Acid Synthase at 4.5 Å Resolution. Science, 2006, 311, 1258-1262.	6.0	344
63	Architecture of a Fungal Fatty Acid Synthase at 5 Å Resolution. Science, 2006, 311, 1263-1267.	6.0	138
64	Crystallization and preliminary characterization of three different crystal forms of human saposin C heterologously expressed in Pichia pastoris. Acta Crystallographica Section F: Structural Biology Communications, 2006, 62, 117-120.	0.7	5
65	The enzyme-binding region of human GM2-activator protein. FEBS Journal, 2006, 273, 982-991.	2.2	28
66	Structure of the unusual seryl-tRNA synthetase reveals a distinct zinc-dependent mode of substrate recognition. EMBO Journal, 2006, 25, 2498-2509.	3.5	77
67	A cradle for new proteins: trigger factor at the ribosome. Current Opinion in Structural Biology, 2005, 15, 204-212.	2.6	88
68	A Large Hinge Bending Domain Rotation Is Necessary for the Catalytic Function of Escherichia coli 5'-Nucleotidase. Biochemistry, 2005, 44, 2244-2252.	1.2	30
69	Reinforced HNA Backbone Hydration in the Crystal Structure of a Decameric HNA/RNA Hybrid. Journal of the American Chemical Society, 2005, 127, 2937-2943.	6.6	30
70	Trigger factor in complex with the ribosome forms a molecular cradle for nascent proteins. Nature, 2004, 431, 590-596.	13.7	347
71	Trapping a 96° domain rotation in two distinct conformations by engineered disulfide bridges. Protein Science, 2004, 13, 1811-1822.	3.1	24
72	Biochemie und Molekularbiologie 2003. Nachrichten Aus Der Chemie, 2004, 52, 292-305.	0.0	0

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73	Crystal Structure of <i>Thermotoga maritima</i> α -Glucosidase AglA Defines a New Clan of NAD ⁺ -dependent Glycosidases. <i>Journal of Biological Chemistry</i> , 2003, 278, 19151-19158.	1.6	56
74	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
75	Insect Immune Activation by Apolipoprotein III Is Correlated with the Lipid-Binding Properties of This Protein. <i>Biochemistry</i> , 2001, 40, 11502-11508.	1.2	63
76	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