Timm Maier

List of Publications by Year in descending order

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TIMM MAIED

#	Article	IF	CITATIONS
1	mTOR substrate phosphorylation in growth control. Cell, 2022, 185, 1814-1836.	28.9	120
2	Does targeting Arg98 of FimH lead to high affinity antagonists?. European Journal of Medicinal Chemistry, 2021, 211, 113093.	5.5	11
3	The antibiotic darobactin mimics a β-strand to inhibit outer membrane insertase. Nature, 2021, 593, 125-129.	27.8	112
4	Structural basis of the activation of the CC chemokine receptor 5 by a chemokine agonist. Science Advances, 2021, 7, .	10.3	36
5	The dynamic mechanism of 4E-BP1 recognition and phosphorylation by mTORC1. Molecular Cell, 2021, 81, 2403-2416.e5.	9.7	32
6	Regulation of human mTOR complexes by DEPTOR. ELife, 2021, 10, .	6.0	15
7	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
8	Mutasynthetic Production and Antimicrobial Characterization of Darobactin Analogs. Microbiology Spectrum, 2021, 9, e0153521.	3.0	26
9	The 3.2-Ã resolution structure of human mTORC2. Science Advances, 2020, 6, .	10.3	57
10	Enhancing the enthalpic contribution of hydrogen bonds by solvent shielding. RSC Chemical Biology, 2020, 1, 281-287.	4.1	10
11	Long-lived T follicular helper cells retain plasticity and help sustain humoral immunity. Science Immunology, 2020, 5, .	11.9	78
12	Structural basis for ion selectivity in TMEM175 K+ channels. ELife, 2020, 9, .	6.0	27
13	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
14	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
15	Improvement of Aglycone Ï€â€Stacking Yields Nanomolar to Subâ€nanomolar FimH Antagonists. ChemMedChem, 2019, 14, 749-757.	3.2	27
16	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
17	Architecture and activation of phosphatidylinositol 3-kinase related kinases. Current Opinion in Structural Biology, 2018, 49, 177-189.	5.7	50
18	The structural organization of substrate loading in iterative polyketide synthases. Nature Chemical Biology, 2018, 14, 474-479.	8.0	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. Journal of Biological Chemistry, 2018, 293, 1835-1849.	3.4	23
20	The price of flexibility – a case study on septanoses as pyranose mimetics. Chemical Science, 2018, 9, 646-654.	7.4	26
21	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
22	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
23	Architecture of the human mTORC2 core complex. ELife, 2018, 7, .	6.0	59
24	Editorial overview: Macromolecular assemblies: Assembly, dynamics and control of activity. Current Opinion in Structural Biology, 2018, 49, vi-vii.	5.7	0
25	The architectures of iterative type I PKS and FAS. Natural Product Reports, 2018, 35, 1046-1069.	10.3	143
26	Structural basis for regulation of human acetyl-CoA carboxylase. Nature, 2018, 558, 470-474.	27.8	135
27	Carbohydrate–Lectin Interactions: An Unexpected Contribution to Affinity. ChemBioChem, 2017, 18, 539-544.	2.6	11
28	Amylose recognition and ring-size determination of amylomaltase. Science Advances, 2017, 3, e1601386.	10.3	42
29	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
30	Re-engineering biofactories. Nature Chemical Biology, 2017, 13, 344-345.	8.0	7
31	Cryo-EM structure of the extended type VI secretion system sheath–tube complex. Nature Microbiology, 2017, 2, 1507-1512.	13.3	107
32	High-Speed Atomic Force Microscopy Visualization of the Dynamics of the Multienzyme Fatty Acid Synthase. ACS Nano, 2017, 11, 10852-10859.	14.6	20
33	A central role for a region in the middle. ELife, 2017, 6, .	6.0	1
34	Structural and Functional Characterization of a Novel Family of Cyclophilins, the AquaCyps. PLoS ONE, 2016, 11, e0157070.	2.5	8
35	Hybrid Structure of a Dynamic Single-Chain Carboxylase from Deinococcus radiodurans. Structure, 2016, 24, 1227-1236.	3.3	3
36	The dynamic organization of fungal acetyl-CoA carboxylase. Nature Communications, 2016, 7, 11196.	12.8	39

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37	Catch-bond mechanism of the bacterial adhesin FimH. Nature Communications, 2016, 7, 10738.	12.8	164
38	Architecture of human mTOR complex 1. Science, 2016, 351, 48-52.	12.6	280
39	Mycocerosic acid synthase exemplifies the architecture of reducing polyketide synthases. Nature, 2016, 531, 533-537.	27.8	70
40	E-selectin ligand complexes adopt an extended high-affinity conformation. Journal of Molecular Cell Biology, 2016, 8, 62-72.	3.3	50
41	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
42	Enzyme repurposing of a hydrolase as an emergent peroxidase upon metal binding. Chemical Science, 2015, 6, 4060-4065.	7.4	26
43	Dimeric Structure of the Bacterial Extracellular Foldase PrsA. Journal of Biological Chemistry, 2015, 290, 3278-3292.	3.4	41
44	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
45	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
46	Structure of the Type VI Secretion System Contractile Sheath. Cell, 2015, 160, 952-962.	28.9	216
47	Conserved Omp85 lid-lock structure and substrate recognition in FhaC. Nature Communications, 2015, 6, 7452.	12.8	31
48	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
49	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
50	STIL binding to Polo-box 3 of PLK4 regulates centriole duplication. ELife, 2015, 4, .	6.0	109
51	Evolutionary Origins of the Multienzyme Architecture of Giant Fungal Fatty Acid Synthase. Structure, 2014, 22, 1775-1785.	3.3	36
52	The structural basis of autotransporter translocation by TamA. Nature Structural and Molecular Biology, 2013, 20, 1318-1320.	8.2	116
53	Conserved sequence motifs and the structure of the mTOR kinase domain. Biochemical Society Transactions, 2013, 41, 889-895.	3.4	13
54	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

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55	Structure and function of eukaryotic fatty acid synthases. Quarterly Reviews of Biophysics, 2010, 43, 373-422.	5.7	122
56	The structure of a cytolytic α-helical toxin pore reveals its assembly mechanism. Nature, 2009, 459, 726-730.	27.8	303
57	Molecular mechanism and structure of Trigger Factor bound to the translating ribosome. EMBO Journal, 2008, 27, 1622-1632.	7.8	142
58	A peptide deformylase–ribosome complex reveals mechanism of nascent chain processing. Nature, 2008, 452, 108-111.	27.8	93
59	The multienzyme architecture of eukaryotic fatty acid synthases. Current Opinion in Structural Biology, 2008, 18, 714-725.	5.7	163
60	Crystal Structures of Human Saposins C and D: Implications for Lipid Recognition and Membrane Interactions. Structure, 2008, 16, 809-817.	3.3	78
61	The Crystal Structure of a Mammalian Fatty Acid Synthase. Science, 2008, 321, 1315-1322.	12.6	408
62	Architecture of Mammalian Fatty Acid Synthase at 4.5 A Resolution. Science, 2006, 311, 1258-1262.	12.6	344
63	Architecture of a Fungal Fatty Acid Synthase at 5 A Resolution. Science, 2006, 311, 1263-1267.	12.6	138
64	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
65	The enzyme-binding region of human GM2-activator protein. FEBS Journal, 2006, 273, 982-991.	4.7	28
66	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
67	A cradle for new proteins: trigger factor at the ribosome. Current Opinion in Structural Biology, 2005, 15, 204-212.	5.7	88
68	A Large Hinge Bending Domain Rotation Is Necessary for the Catalytic Function ofEscherichia coli5â€ ⁻ -Nucleotidaseâ€. Biochemistry, 2005, 44, 2244-2252.	2,5	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.	13.7	30
70	Trigger factor in complex with the ribosome forms a molecular cradle for nascent proteins. Nature, 2004, 431, 590-596.	27.8	347
71	Trapping a 96° domain rotation in two distinct conformations by engineered disulfide bridges. Protein Science, 2004, 13, 1811-1822.	7.6	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 Thermotoga maritima α-Glucosidase AglA Defines a New Clan of NAD+-dependent Glycosidases. Journal of Biological Chemistry, 2003, 278, 19151-19158.	3.4	56
74	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
75	Insect Immune Activation by Apolipophorin III Is Correlated with the Lipid-Binding Properties of This Proteinâ€. Biochemistry, 2001, 40, 11502-11508.	2.5	63
76	Crystal Structure of Mistletoe Lectin I fromViscum album. Biochemical and Biophysical Research Communications, 1999, 257, 418-424.	2.1	60