Michael Groll

List of Publications by Year
in descending order

96 papers	8,836 citations	71102 41 h-index	42399 92 g-index
102 all docs	102 docs citations	102 times ranked	7283 citing authors

#	Article	IF	Citations
1	Global analysis of biosynthetic gene clusters reveals conserved and unique natural products in entomopathogenic nematode-symbiotic bacteria. Nature Chemistry, 2022, 14, 701-712.	13.6	42
2	Structural insights into cooperative DNA recognition by the CCAAT-binding complex and its bZIP transcription factor HapX. Structure, 2022, 30, 934-946.e4.	3.3	3
3	Design of buried charged networks in artificial proteins. Nature Communications, 2021, 12, 1895.	12.8	7
4	Activation, Structure, Biosynthesis and Bioactivity of Glidobactinâ€like Proteasome Inhibitors from Photorhabdus laumondii. ChemBioChem, 2021, 22, 1582-1588.	2.6	8
5	Structural and Mechanistic Insights into Câ^'S Bond Formation in Gliotoxin. Angewandte Chemie - International Edition, 2021, 60, 14188-14194.	13.8	6
6	Strukturelle und mechanistische Einblicke in die Bildung der Câ€Sâ€Bindungen in Gliotoxin. Angewandte Chemie, 2021, 133, 14307-14314.	2.0	1
7	A Nut for Every Bolt: Subunit-Selective Inhibitors of the Immunoproteasome and Their Therapeutic Potential. Cells, 2021, 10, 1929.	4.1	14
8	Structures in Tetrahydrofolate Methylation in Desulfitobacterial Glycine Betaine Metabolism at Atomic Resolution. ChemBioChem, 2020, 21, 776-779.	2.6	1
9	A monodomain class II terpene cyclase assembles complex isoprenoid scaffolds. Nature Chemistry, 2020, 12, 968-972.	13.6	24
10	Crystal Structure and Active Site Engineering of a Halophilic Î³-Carbonic Anhydrase. Frontiers in Microbiology, 2020, 11, 742.	3.5	16
11	Functional Characterisation of ClpP Mutations Conferring Resistance to Acyldepsipeptide Antibiotics in Firmicutes. ChemBioChem, 2020, 21, 1997-2012.	2.6	13
12	Structural snapshots of the minimal PKS system responsible for octaketide biosynthesis. Nature Chemistry, 2020, 12, 755-763.	13.6	35
13	PINK1-dependent phosphorylation of Serine111 within the SF3 motif of Rab GTPases impairs effector interactions and LRRK2-mediated phosphorylation at Threonine72. Biochemical Journal, 2020, 477, 1651-1668.	3.7	26
14	Legionella effector AnkX displaces the switch II region for Rab1b phosphocholination. Science Advances, 2020, 6, eaaz8041.	10.3	12
15	Structural basis of HapE^{P88L}-linked antifungal triazole resistance in Aspergillus fumigatus. Life Science Alliance, 2020, 3, e202000729.	2.8	19
16	Robust and Versatile Host Protein for the Design and Evaluation of Artificial Metal Centers. ACS Catalysis, 2019, 9, 11371-11380.	11.2	12
17	Engineering a Polyspecific Pyrrolysyl-tRNA Synthetase by a High Throughput FACS Screen. Scientific Reports, 2019, 9, 11971.	3.3	24
18	Molecular mechanism of polyketide shortening in anthraquinone biosynthesis of Photorhabdus luminescens. Chemical Science, 2019, 10, 6341-6349.	7.4	18

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19	Genetically Encoded Biotin Analogues: Incorporation and Application in Bacterial and Mammalian Cells. ChemBioChem, 2019, 20, 1795-1798.	2.6	1
20	An Uncommon Type II PKS Catalyzes Biosynthesis of Aryl Polyene Pigments. Journal of the American Chemical Society, 2019, 141, 16615-16623.	13.7	56
21	Structure-Based Design of Inhibitors Selective for Human Proteasome Î²2c or Î²2i Subunits. Journal of Medicinal Chemistry, 2019, 62, 1626-1642.	6.4	23
22	Defective immuno- and thymoproteasome assembly causes severe immunodeficiency. Scientific Reports, 2018, 8, 5975.	3.3	13
23	A Predictive Approach for the Optical Control of Carbonic Anhydrase II Activity. ACS Chemical Biology, 2018, 13, 793-800.	3.4	19
24	The protease GtgE from Salmonella exclusively targets inactive Rab GTPases. Nature Communications, 2018, 9, 44.	12.8	33
25	Catalytic mechanism and molecular engineering of quinolone biosynthesis in dioxygenase AsqJ. Nature Communications, 2018, 9, 1168.	12.8	30
26	Identification and Experimental Characterization of an Extremophilic Brine Pool Alcohol Dehydrogenase from Single Amplified Genomes. ACS Chemical Biology, 2018, 13, 161-170.	3.4	19
27	Eisenaufnahme in Pilzen der Gattung Aspergillus: strukturelle und biochemische Einblicke in Siderophoresterasen. Angewandte Chemie, 2018, 130, 14834-14839.	2.0	0
28	Discovery of the First-in-Class Dual Histone Deacetylaseâ€“Proteasome Inhibitor. Journal of Medicinal Chemistry, 2018, 61, 10299-10309.	6.4	62
29	Structural and Mechanistic Features of ClyA-Like Î±-Pore-Forming Toxins. Toxins, 2018, 10, 343.	3.4	11
30	Iron Scavenging in Aspergillus Species: Structural and Biochemical Insights into Fungal Siderophore Esterases. Angewandte Chemie - International Edition, 2018, 57, 14624-14629.	13.8	13
31	Structure and mechanism of the two-component Î±-helical pore-forming toxin YaxAB. Nature Communications, 2018, 9, 1806.	12.8	46
32	(â^')-Homosalinosporamide A and Its Mode of Proteasome Inhibition: An X-ray Crystallographic Study. Marine Drugs, 2018, 16, 240.	4.6	7
33	Structural Elucidation of a Nonpeptidic Inhibitor Specific for the Human Immunoproteasome. ChemBioChem, 2017, 18, 523-526.	2.6	18
34	Gliotoxin Biosynthesis: Structure, Mechanism, and Metal Promiscuity of Carboxypeptidase GliJ. ACS Chemical Biology, 2017, 12, 1874-1882.	3.4	24
35	The Methylerythritol Phosphate Pathway to Isoprenoids. Chemical Reviews, 2017, 117, 5675-5703.	47.7	129
36	The CCAAT-binding complex (CBC) in Aspergillus species. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2017, 1860, 560-570.	1.9	43

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37	Mechanism of Allosteric Inhibition of the Enzyme IspD by Three Different Classes of Ligands. ACS Chemical Biology, 2017, 12, 2132-2138.	3.4	12
38	A unified mechanism for proteolysis and autocatalytic activation in the 20S proteasome. Nature Communications, 2016, 7, 10900.	12.8	88
39	A humanized yeast proteasome identifies unique binding modes of inhibitors for the immunosubunit Î²5i. EMBO Journal, 2016, 35, 2602-2613.	7.8	29
40	Structure of the Dioxygenase AsqJ: Mechanistic Insights into a Oneâ€Pot Multistep Quinolone Antibiotic Biosynthesis. Angewandte Chemie - International Edition, 2016, 55, 422-426.	13.8	65
41	Tunable Probes with Direct Fluorescence Signals for the Constitutive and Immunoproteasome. Angewandte Chemie - International Edition, 2016, 55, 13330-13334.	13.8	11
42	Structure-Based Design of Î²5c Selective Inhibitors of Human Constitutive Proteasomes. Journal of Medicinal Chemistry, 2016, 59, 7177-7187.	6.4	19
43	Sequential Inactivation of Gliotoxin by the S-Methyltransferase TmtA. ACS Chemical Biology, 2016, 11, 1082-1089.	3.4	22
44	Selective activators of protein phosphatase 5 target the auto-inhibitory mechanism. Bioscience Reports, 2015, 35, .	2.4	18
45	Reversible Inhibitors Arrest ClpP in a Defined Conformational State that Can Be Revoked by ClpX Association. Angewandte Chemie - International Edition, 2015, 54, 15892-15896.	13.8	42
46	Targeted Delivery of Proteasome Inhibitors to Somatostatinâ€Receptorâ€Expressing Cancer Cells by Octreotide Conjugation. ChemMedChem, 2015, 10, 1969-1973.	3.2	3
47	A Minimal Î²â€Lactone Fragment for Selective Î²5c or Î²5i Proteasome Inhibitors. Angewandte Chemie - International Edition, 2015, 54, 7810-7814.	13.8	14
48	Identification of a Î²1/Î²2â€Specific Sulfonamide Proteasome Ligand by Crystallographic Screening. Angewandte Chemie - International Edition, 2015, 54, 11275-11278.	13.8	12
49	Selective Inhibition of the Immunoproteasome by Structureâ€Based Targeting of a Nonâ€catalytic Cysteine. Angewandte Chemie - International Edition, 2015, 54, 15888-15891.	13.8	25
50	Azobenzene-based inhibitors of human carbonic anhydrase II. Beilstein Journal of Organic Chemistry, 2015, 11, 1129-1135.	2.2	24
51	Systematic Analyses of Substrate Preferences of 20S Proteasomes Using Peptidic Epoxyketone Inhibitors. Journal of the American Chemical Society, 2015, 137, 7835-7842.	13.7	37
52	Bortezomib-Resistant Mutant Proteasomes: Structural and Biochemical Evaluation with Carfilzomib and ONX 0914. Structure, 2015, 23, 407-417.	3.3	55
53	A Mass Spectrometry Platform for a Streamlined Investigation of Proteasome Integrity, Posttranslational Modifications, and Inhibitor Binding. Chemistry and Biology, 2015, 22, 404-411.	6.0	14
54	Atomic-Resolution Structures of Discrete Stages on the Reaction Coordinate of the [Fe 4 S 4] Enzyme IspG (GcpE). Journal of Molecular Biology, 2015, 427, 2220-2228.	4.2	14

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55	Pseudilins: Halogenated, Allosteric Inhibitors of the Nonâ€Mevalonate Pathway Enzyme IspD. Angewandte Chemie - International Edition, 2014, 53, 2235-2239.	13.8	53
56	Systematic Comparison of Peptidic Proteasome Inhibitors Highlights the Î±â€Ketoamide Electrophile as an Auspicious Reversible Lead Motif. Angewandte Chemie - International Edition, 2014, 53, 1679-1683.	13.8	74
57	Flavoenzymeâ€Catalyzed Formation of Disulfide Bonds in Natural Products. Angewandte Chemie - International Edition, 2014, 53, 2221-2224.	13.8	50
58	Inducedâ€Fit Mechanism in Classâ€...I Terpene Cyclases. Angewandte Chemie - International Edition, 2014, 53, 7652-7656.	13.8	174
59	Structure-Based Design of Î²1i or Î²5i Specific Inhibitors of Human Immunoproteasomes. Journal of Medicinal Chemistry, 2014, 57, 6197-6209.	6.4	89
60	Structures of Fluoro, Amino, and Thiol Inhibitors Bound to the [Fe₄S₄] Protein IspH. Angewandte Chemie - International Edition, 2013, 52, 2118-2121.	13.8	25
61	Dimerized Linear Mimics of a Natural Cyclopeptide (TMC-95A) Are Potent Noncovalent Inhibitors of the Eukaryotic 20S Proteasome. Journal of Medicinal Chemistry, 2013, 56, 3367-3378.	6.4	34
62	Incorporation of Non-natural Amino Acids Improves Cell Permeability and Potency of Specific Inhibitors of Proteasome Trypsin-like Sites. Journal of Medicinal Chemistry, 2013, 56, 1262-1275.	6.4	79
63	One-shot NMR analysis of microbial secretions identifies highly potent proteasome inhibitor. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 18367-18371.	7.1	58
64	Covalent and non-covalent reversible proteasome inhibition. Biological Chemistry, 2012, 393, 1101-1120.	2.5	76
65	Exploiting nature's rich source of proteasome inhibitors as starting points in drug development. Chemical Communications, 2012, 48, 1364-1378.	4.1	57
66	Crystal Structures of Mutant IspH Proteins Reveal a Rotation of the Substrate's Hydroxymethyl Group during Catalysis. Journal of Molecular Biology, 2012, 416, 1-9.	4.2	40
67	Immuno- and Constitutive Proteasome Crystal Structures Reveal Differences in Substrate and Inhibitor Specificity. Cell, 2012, 148, 727-738.	28.9	410
68	DNA Minor Groove Sensing and Widening by the CCAAT-Binding Complex. Structure, 2012, 20, 1757-1768.	3.3	53
69	Discovery of acetylene hydratase activity of the ironâ€“sulphur protein IspH. Nature Communications, 2012, 3, 1042.	12.8	34
70	Are Free Radicals Involved in IspH Catalysis? An EPR and Crystallographic Investigation. Journal of the American Chemical Society, 2012, 134, 11225-11234.	13.7	45
71	Analysing Properties of Proteasome Inhibitors Using Kinetic and X-Ray Crystallographic Studies. Methods in Molecular Biology, 2012, 832, 373-390.	0.9	18
72	Inhibitors for the Immunoâ€•and Constitutive Proteasome: Current and Future Trends in Drug Development. Angewandte Chemie - International Edition, 2012, 51, 8708-8720.	13.8	160

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73	Hydroxyureas as Noncovalent Proteasome Inhibitors. Angewandte Chemie - International Edition, 2012, 51, 247-249.	13.8	52
74	Proteasome Structure, Function, and Lessons Learned from Beta-Lactone Inhibitors. Current Topics in Medicinal Chemistry, 2011, 11, 2850-2878.	2.1	46
75	Thiazolopyrimidine Inhibitors of 2â€Methylerythritol 2,4â€Cyclodiphosphate Synthase (IspF) from Mycobacterium tuberculosis and Plasmodium falciparum. ChemMedChem, 2010, 5, 1092-1101.	3.2	66
76	20S Proteasome Inhibition: Designing Noncovalent Linear Peptide Mimics of the Natural Product TMCâ€95A. ChemMedChem, 2010, 5, 1701-1705.	3.2	44
77	Probing the reaction mechanism of IspH protein by x-ray structure analysis. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 1077-1081.	7.1	103
78	Biosynthesis of Isoprenoids: Crystal Structure of the [4Feâ€“4S] Cluster Protein IspG. Journal of Molecular Biology, 2010, 404, 600-610.	4.2	65
79	Structure of Active IspH Enzyme from Escherichia coli Provides Mechanistic Insights into Substrate Reduction. Angewandte Chemie - International Edition, 2009, 48, 5756-5759.	13.8	74
80	Snapshots of the Fluorosalinosporamide/20S Complex Offer Mechanistic Insights for Fine Tuning Proteasome Inhibition. Journal of Medicinal Chemistry, 2009, 52, 5420-5428.	6.4	36
81	A plant pathogen virulence factor inhibits the eukaryotic proteasome by a novel mechanism. Nature, 2008, 452, 755-758.	27.8	281
82	Structural Analysis of Spiro Î²-Lactone Proteasome Inhibitors. Journal of the American Chemical Society, 2008, 130, 14981-14983.	13.7	40
83	Leaving Groups Prolong the Duration of 20S Proteasome Inhibition and Enhance the Potency of Salinosporamides. Journal of Medicinal Chemistry, 2008, 51, 6711-6724.	6.4	57
84	20S Proteasome and Its Inhibitors:â€‰Crystallographic Knowledge for Drug Development. Chemical Reviews, 2007, 107, 687-717.	47.7	394
85	Crystal Structures of Salinosporamide A (NPI-0052) and B (NPI-0047) in Complex with the 20S Proteasome Reveal Important Consequences of Î²-Lactone Ring Opening and a Mechanism for Irreversible Binding. Journal of the American Chemical Society, 2006, 128, 5136-5141.	13.7	294
86	TMC-95-Based Inhibitor Design Provides Evidence for the Catalytic Versatility of the Proteasome. Chemistry and Biology, 2006, 13, 607-614.	6.0	75
87	Crystal Structure of the Boronic Acid-Based Proteasome Inhibitor Bortezomib in Complex with the Yeast 20S Proteasome. Structure, 2006, 14, 451-456.	3.3	431
88	Inhibitor-binding mode of homobelactosin C to proteasomes: New insights into class I MHC ligand generation. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 4576-4579.	7.1	74
89	Molecular Machines for Protein Degradation. ChemBioChem, 2005, 6, 222-256.	2.6	176
90	Purification, Crystallization, and Xâ€Ray Analysis of the Yeast 20S Proteasome. Methods in Enzymology, 2005, 398, 329-336.	1.0	53

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91	Binding Mode of TMC-95A Analogues to Eukaryotic 20S Proteasome. ChemBioChem, 2004, 5, 1256-1266.	2.6	47
92	Crystal structure of the 20 S proteasome:TMC-95A complex: a non-covalent proteasome inhibitor 1 1Edited by I. A. Wilson. Journal of Molecular Biology, 2001, 311, 543-548.	4.2	185
93	A gated channel into the proteasome core particle. Nature Structural Biology, 2000, 7, 1062-1067.	9.7	722
94	Crystal Structure of Epoxomicin:20S Proteasome Reveals a Molecular Basis for Selectivity of Î±â€˜,Î²â€˜-Epoxyketone Proteasome Inhibitors. Journal of the American Chemical Society, 2000, 122, 1237-1238.	13.7	304
95	Bifunctional inhibitors of the trypsin-like activity of eukaryotic proteasomes. Chemistry and Biology, 1999, 6, 197-204.	6.0	66
96	Structure of 20S proteasome from yeast at 2.4Ã... resolution. Nature, 1997, 386, 463-471.	27.8	2,214