Christoph Mayer

List of Publications by Year
in descending order

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125	10,299	53939 47	45040 94
papers	citations	h-index	g-index

134	134	134	13256
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	NamZ1 and NamZ2 from the Oral Pathogen Tannerella forsythia Are Peptidoglycan Processing Exo-Î²-N -Acetylmuramidases with Distinct Substrate Specificities. Journal of Bacteriology, 2022, 204, jb0059721.	1.0	1
2	The genetic basis of a novel reproductive strategy in Sulawesi ricefishes: How modularity and a low number of loci shape pelvic brooding. Evolution; International Journal of Organic Evolution, 2022, 76, 1033-1051.	1.1	1
3	Synergetic Antimicrobial Activity and Mechanism of Clotrimazole-Linked CO-Releasing Molecules. ACS Bio & Med Chem Au, 2022, 2, 419-436.	1.7	19
4	Fluorogenic RNA-Based Biosensor to Sense the Glycolytic Flux in Mammalian Cells. ACS Chemical Biology, 2022, 17, 1164-1173.	1.6	7
5	Delimiting continuity: Comparison of target enrichment and double digest restrictionâ€site associated DNA sequencing for delineating admixing parapatric Melitaea butterflies. Systematic Entomology, 2022, 47, 637-654.	1.7	2
6	Phylogeny, taxonomics, and ovipositor length variation of thePteromalus albipennisspecies group (Hymenoptera: Chalcidoidea: Pteromalidae: Pteromalinae). Journal of Zoological Systematics and Evolutionary Research, 2021, 59, 349-358.	0.6	2
7	Chitin, Chitin Oligosaccharide, and Chitin Disaccharide Metabolism of <i>Escherichia coli</i> Revisited: Reassignment of the Roles of ChiA, ChbR, ChbF, and ChbG. Microbial Physiology, 2021, 31, 178-194.	1.1	8
8	Analysis of RNA-Seq, DNA Target Enrichment, and Sanger Nucleotide Sequence Data Resolves Deep Splits in the Phylogeny of Cuckoo Wasps (Hymenoptera: Chrysididae). Insect Systematics and Diversity, 2021, 5, .	0.7	8
9	Peptidoglycan Salvage Enables the Periodontal Pathogen <i>Tannerella forsythia</i> to Survive within the Oral Microbial Community. Microbial Physiology, 2021, 31, 123-134.	1.1	9
10	Beyond Drosophila: resolving the rapid radiation of schizophoran flies with phylotranscriptomics. BMC Biology, 2021, 19, 23.	1.7	22
11	Adding leaves to the Lepidoptera tree: capturing hundreds of nuclear genes from old museum specimens. Systematic Entomology, 2021, 46, 649-671.	1.7	40
12	Museomics: Phylogenomics of the Moth Family Epicopeiidae (Lepidoptera) Using Target Enrichment. Insect Systematics and Diversity, 2021, 5, .	0.7	14
13	Phylogenomic analyses clarify the pattern of evolution of Adephaga (Coleoptera) and highlight phylogenetic artefacts due to model misspecification and excessive data trimming. Systematic Entomology, 2021, 46, 991-1018.	1.7	12
14	Combining molecular datasets with strongly heterogeneous taxon coverage enlightens the peculiar biogeographic history of stoneflies (Insecta: Plecoptera). Systematic Entomology, 2021, 46, 952-967.	1.7	13
15	Development and evaluation of a custom bait design based on 469 single-copy protein-coding genes for exon capture of isopods (Philosciidae: Haloniscus). PLoS ONE, 2021, 16, e0256861.	1.1	2
16	Evolutionary history and divergence times of Odonata (dragonflies and damselflies) revealed through transcriptomics. IScience, 2021, 24, 103324.	1.9	25
17	Identification of Drug Resistance Determinants in a Clinical Isolate of Pseudomonas aeruginosa by High-Density Transposon Mutagenesis. Antimicrobial Agents and Chemotherapy, 2020, 64, .	1.4	18
18	Genome-Wide Novel Genic Microsatellite Marker Resource Development and Validation for Genetic Diversity and Population Structure Analysis of Banana. Genes, 2020, 11, 1479.	1.0	13

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19	Comparing diversity levels in environmental samples: DNA sequence capture and metabarcoding approaches using 18S and COI genes. Molecular Ecology Resources, 2020, 20, 1333-1345.	2.2	40
20	An integrative phylogenomic approach to elucidate the evolutionary history and divergence times of Neuropterida (Insecta: Holometabola). BMC Evolutionary Biology, 2020, 20, 64.	3.2	48
21	Phosphoglycerol-type wall and lipoteichoic acids are enantiomeric polymers differentiated by the stereospecific glycerophosphodiesterase GlpQ. Journal of Biological Chemistry, 2020, 295, 4024-4034.	1.6	16
22	Analyzing drivers of speciation in the Southern Ocean using the sea spider species complex Colossendeis megalonyx as a test case. Polar Biology, 2020, 43, 319-342.	0.5	5
23	A Plea for Standardized Nuclear Markers in Metazoan DNA Taxonomy. Trends in Ecology and Evolution, 2020, 35, 336-345.	4.2	53
24	Sawfly Genomes Reveal Evolutionary Acquisitions That Fostered the Mega-Radiation of Parasitoid and Eusocial Hymenoptera. Genome Biology and Evolution, 2020, 12, 1099-1188.	1.1	17
25	Inducible expression of (pp)pGpp synthetases in Staphylococcus aureus is associated with activation of stress response genes. PLoS Genetics, 2020, 16, e1009282.	1.5	23
26	Bacteria's different ways to recycle their own cell wall. International Journal of Medical Microbiology, 2019, 309, 151326.	1.5	44
27	Peptidoglycan Recycling, a Promising Target for Antibiotic Adjuvants in Antipseudomonal Therapy. Journal of Infectious Diseases, 2019, 220, 1713-1715.	1.9	13
28	Phylogenomics reveals the evolutionary timing and pattern of butterflies and moths. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 22657-22663.	3.3	291
29	Patterns and Constraints in the Evolution of Sperm Individualization Genes in Insects, with an Emphasis on Beetles. Genes, 2019, 10, 776.	1.0	1
30	Combining morphological and genomic evidence to resolve species diversity and study speciation processes of the Pallenopsis patagonica (Pycnogonida) species complex. Frontiers in Zoology, 2019, 16, 36.	0.9	12
31	Peptidoglycan-type analysis of the N-acetylmuramic acid auxotrophic oral pathogen Tannerella forsythia and reclassification of the peptidoglycan-type of Porphyromonas gingivalis. BMC Microbiology, 2019, 19, 200.	1.3	8
32	Editorial: Bacterial Cell Wall Structure and Dynamics. Frontiers in Microbiology, 2019, 10, 2051.	1.5	68
33	Phylogenomics of the longitarsal Colossendeidae: The evolutionary history of an Antarctic sea spider radiation. Molecular Phylogenetics and Evolution, 2019, 136, 206-214.	1.2	23
34	Phylogenomics of the superfamily Dytiscoidea (Coleoptera: Adephaga) with an evaluation of phylogenetic conflict and systematic error. Molecular Phylogenetics and Evolution, 2019, 135, 270-285.	1.2	36
35	The evolution and genomic basis of beetle diversity. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 24729-24737.	3.3	372
36	Evolutionary history of Polyneoptera and its implications for our understanding of early winged insects. Proceedings of the National Academy of Sciences of the United States of America, 2019, 116, 3024-3029.	3.3	150

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37	Cost effective microsatellite isolation and genotyping by high throughput sequencing. Journal of Arachnology, 2019, 47, 190.	0.3	4
38	New data, same story: phylogenomics does not support Syrphoidea (Diptera: Syrphidae, Pipunculidae). Systematic Entomology, 2018, 43, 447-459.	1.7	53
39	Transcriptome sequence-based phylogeny of chalcidoid wasps (Hymenoptera: Chalcidoidea) reveals a history of rapid radiations, convergence, and evolutionary success. Molecular Phylogenetics and Evolution, 2018, 120, 286-296.	1.2	83
40	Recovery of the Peptidoglycan Turnover Product Released by the Autolysin Atl in Staphylococcus aureus Involves the Phosphotransferase System Transporter MurP and the Novel 6-phospho-N-acetylmuramidase MupG. Frontiers in Microbiology, 2018, 9, 2725.	1.5	22
41	Phylogenomics and the evolution of hemipteroid insects. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 12775-12780.	3.3	275
42	N-Acetylmuramic Acid (MurNAc) Auxotrophy of the Oral Pathogen Tannerella forsythia: Characterization of a MurNAc Kinase and Analysis of Its Role in Cell Wall Metabolism. Frontiers in Microbiology, 2018, 9, 19.	1.5	11
43	Regulation of the opposing (p)ppGpp synthetase and hydrolase activities in a bifunctional RelA/SpoT homologue from Staphylococcus aureus. PLoS Genetics, 2018, 14, e1007514.	1.5	67
44	Anchored phylogenomics unravels the evolution of spider flies (Diptera, Acroceridae) and reveals discordance between nucleotides and amino acids. Molecular Phylogenetics and Evolution, 2018, 128, 233-245.	1.2	35
45	Phylogenomic analysis of Apoidea sheds new light on the sister group of bees. BMC Evolutionary Biology, 2018, 18, 71.	3.2	131
46	Staphylococcus aureus counters phosphate limitation by scavenging wall teichoic acids from other staphylococci via the teichoicase GlpQ. Journal of Biological Chemistry, 2018, 293, 14916-14924.	1.6	26
47	Evolutionary genomics of the cold-adapted diatom Fragilariopsis cylindrus. Nature, 2017, 541, 536-540.	13.7	332
48	Pentapeptideâ€rich peptidoglycan at the Bacillus subtilis cellâ€division site. Molecular Microbiology, 2017, 104, 319-333.	1.2	25
49	Absence of ppGpp Leads to Increased Mobilization of Intermediately Accumulated Poly(3-Hydroxybutyrate) in Ralstonia eutropha H16. Applied and Environmental Microbiology, 2017, 83, .	1.4	33
50	Evolutionary History of the Hymenoptera. Current Biology, 2017, 27, 1013-1018.	1.8	611
51	Enzymatic synthesis and semi-preparative isolation of N-acetylmuramic acid 6-phosphate. Carbohydrate Research, 2017, 445, 98-103.	1.1	7
52	The N -Acetylmuramic Acid 6-Phosphate Phosphatase MupP Completes the Pseudomonas Peptidoglycan Recycling Pathway Leading to Intrinsic Fosfomycin Resistance. MBio, 2017, 8, .	1.8	27
53	Activation of the glmS Ribozyme Confers Bacterial Growth Inhibition. ChemBioChem, 2017, 18, 435-440.	1.3	24
54	Transcriptome and target DNA enrichment sequence data provide new insights into the phylogeny of vespid wasps (Hymenoptera: Aculeata: Vespidae). Molecular Phylogenetics and Evolution, 2017, 116, 213-226.	1.2	87

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55	Utilization of glycerophosphodiesters by <scp>S</scp>taphylococcus aureus. Molecular Microbiology, 2017, 103, 229-241.	1.2	21
56	An efficient synthesis of 1,6-anhydro-N-acetylmuramic acid from N-acetylglucosamine. Beilstein Journal of Organic Chemistry, 2017, 13, 2631-2636.	1.3	8
57	Repeats in the transcribed regions: comprehensive characterization and comparison of Citrus spp.. Frontiers of Agricultural Science and Engineering, 2017, 4, 421.	0.9	0
58	Identification of a Novel N -Acetylmuramic Acid Transporter in Tannerella forsythia. Journal of Bacteriology, 2016, 198, 3119-3125.	1.0	24
59	Peptidoglycan Recycling in Gram-Positive Bacteria Is Crucial for Survival in Stationary Phase. MBio, 2016, 7, .	1.8	89
60	Differentiation of Trypanosoma cruzi I (TcI) and T. cruzi II (TcII) genotypes using genes encoding serine carboxypeptidases. Parasitology Research, 2016, 115, 4211-4219.	0.6	2
61	Transcriptomic data from panarthropods shed new light on the evolution of insulator binding proteins in insects. BMC Genomics, 2016, 17, 861.	1.2	23
62	BaitFisher: A Software Package for Multispecies Target DNA Enrichment Probe Design. Molecular Biology and Evolution, 2016, 33, 1875-1886.	3.5	71
63	Phylogenetic Origin and Diversification of RNAi Pathway Genes in Insects. Genome Biology and Evolution, 2016, 8, evw281.	1.1	92
64	The Absence of a Mature Cell Wall Sacculus in Stable Listeria monocytogenes L-Form Cells Is Independent of Peptidoglycan Synthesis. PLoS ONE, 2016, 11, e0154925.	1.1	12
65	<scp>rRNA</scp> regulation during growth and under stringent conditions in <scp>S</scp>taphylococcus aureus. Environmental Microbiology, 2015, 17, 4394-4405.	1.8	30
66	Regional differentiation and extensive hybridization between mitochondrial clades of the Southern Ocean giant sea spider Colossendeis megalonyx. Royal Society Open Science, 2015, 2, 140424.	1.1	30
67	Peptidoglycan perceptionâ€"Sensing bacteria by their common envelope structure. International Journal of Medical Microbiology, 2015, 305, 217-223.	1.5	33
68	Planctomycetes do possess a peptidoglycan cell wall. Nature Communications, 2015, 6, 7116.	5.8	149
69	Automatic selection of partitioning schemes for phylogenetic analyses using iterative k-means clustering of site rates. BMC Evolutionary Biology, 2015, 15, 13.	3.2	95
70	Crystal Structure of the N-Acetylmuramic Acid Î±-1-Phosphate (MurNAc-Î±1-P) Uridylyltransferase MurU, a Minimal Sugar Nucleotidyltransferase and Potential Drug Target Enzyme in Gram-negative Pathogens. Journal of Biological Chemistry, 2015, 290, 10804-10813.	1.6	14
71	Response to Comment on â€œPhylogenomics resolves the timing and pattern of insect evolutionâ€. Science, 2015, 349, 487-487.	6.0	17
72	Genome-Wide Computational Analysis of Musa Microsatellites: Classification, Cross-Taxon Transferability, Functional Annotation, Association with Transposons & miRNAs, and Genetic Marker Potential. PLoS ONE, 2015, 10, e0131312.	1.1	15

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73	Phylogenomics resolves the timing and pattern of insect evolution. Science, 2014, 346, 763-767.	6.0	2,096
74	Blocking Peptidoglycan Recycling in Pseudomonas aeruginosa Attenuates Intrinsic Resistance to Fosfomycin. Microbial Drug Resistance, 2014, 20, 231-237.	0.9	68
75	The evolutionary history of holometabolous insects inferred from transcriptome-based phylogeny and comprehensive morphological data. BMC Evolutionary Biology, 2014, 14, 52.	3.2	147
76	Selecting optimal partitioning schemes for phylogenomic datasets. BMC Evolutionary Biology, 2014, 14, 82.	3.2	575
77	Sulphoglycolysis in Escherichia coli K-12 closes a gap in the biogeochemical sulphur cycle. Nature, 2014, 507, 114-117.	13.7	105
78	Genome Wide Characterization of Short Tandem Repeat Markers in Sweet Orange (Citrus sinensis). PLoS ONE, 2014, 9, e104182.	1.1	50
79	Isolation and characterization of nine polymorphic microsatellite markers for the deep-sea shrimp Nematocarcinus lanceopes (Crustacea: Decapoda: Caridea). BMC Research Notes, 2013, 6, 75.	0.6	7
80	Morphological and genetic analyses of xeniid soft coral diversity (Octocorallia; Alcyonacea). Organisms Diversity and Evolution, 2013, 13, 135-150.	0.7	16
81	A cell wall recycling shortcut that bypasses peptidoglycan de novo biosynthesis. Nature Chemical Biology, 2013, 9, 491-493.	3.9	104
82	Pan genome of the phytoplankton Emiliania underpins its global distribution. Nature, 2013, 499, 209-213.	13.7	448
83	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. Current Biology, 2013, 23, 1388.	1.8	1
84	Increased Cell Wall Teichoic Acid Production and D-alanylation Are Common Phenotypes among Daptomycin-Resistant Methicillin-Resistant Staphylococcus aureus (MRSA) Clinical Isolates. PLoS ONE, 2013, 8, e67398.	1.1	86
85	Genomic and Morphological Evidence Converge to Resolve the Enigma of Strepsiptera. Current Biology, 2012, 22, 1309-1313.	1.8	140
86	Exploring Pandora's Box: Potential and Pitfalls of Low Coverage Genome Surveys for Evolutionary Biology. PLoS ONE, 2012, 7, e49202.	1.1	31
87	Exploiting BAC-end sequences for the mining, characterization and utility of new short sequences repeat (SSR) markers in Citrus. Molecular Biology Reports, 2012, 39, 5373-5386.	1.0	41
88	Are shoals of minnow Phoxinus phoxinus formed by close kin?. Journal of Fish Biology, 2012, 80, 713-721.	0.7	6
89	Long Branch Effects Distort Maximum Likelihood Phylogenies in Simulations Despite Selection of the Correct Model. PLoS ONE, 2012, 7, e36593.	1.1	70
90	Characterization of a Glucosamine/Glucosaminide N -Acetyltransferase of Clostridium acetobutylicum. Journal of Bacteriology, 2011, 193, 5393-5399.	1.0	26

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91	Peptidoglycan turnover and recycling in Gram-positive bacteria. Applied Microbiology and Biotechnology, 2011, 92, 1-11.	1.7	168
92	Molecular evolution of a chordate specific family of G protein-coupled receptors. BMC Evolutionary Biology, 2011, 11, 234.	3.2	16
93	The mitochondrial genome of Colossendeis megalonyx supports a basal position of Colossendeidae within the Pycnogonida. Molecular Phylogenetics and Evolution, 2011, 58, 553-558.	1.2	20
94	Characterization of anN-Acetylmuramic Acid/N-Acetylglucosamine Kinase of Clostridium acetobutylicum. Journal of Bacteriology, 2011, 193, 5386-5392.	1.0	33
95	Cryptic mitochondrial lineages in the widespread pycnogonid Colossendeis megalonyx Hoek, 1881 from Antarctic and Subantarctic waters. Polar Biology, 2010, 33, 281-292.	0.5	95
96	Genome-wide analysis of tandem repeats in Daphnia pulex - a comparative approach. BMC Genomics, 2010, 11, 277.	1.2	87
97	Predator-induced defences in Daphnia pulex: Selection and evaluation of internal reference genes for gene expression studies with real-time PCR. BMC Molecular Biology, 2010, 11, 50.	3.0	52
98	Muropeptide Rescue in Bacillus subtilis Involves Sequential Hydrolysis by Î²- N -Acetylglucosaminidase and N -Acetylmuramyl- <scp>l</scp> -Alanine Amidase. Journal of Bacteriology, 2010, 192, 3132-3143.	1.0	68
99	Structural and Kinetic Analysis of Bacillus subtilis N-Acetylglucosaminidase Reveals a Unique Asp-His Dyad Mechanism. Journal of Biological Chemistry, 2010, 285, 35675-35684.	1.6	117
100	The Murein Sacculus. , 2010, , 3-52.		16
101	Multiple origins of deep-sea Asellota (Crustacea: Isopoda) from shallow waters revealed by molecular data. Proceedings of the Royal Society B: Biological Sciences, 2009, 276, 799-808.	1.2	104
102	STAMP: Extensions to the STADEN sequence analysis package for high throughput interactive microsatellite marker design. BMC Bioinformatics, 2009, 10, 41.	1.2	40
103	Phylogenetic support values are not necessarily informative: the case of the Serialia hypothesis (a) Tj ETQq1 1 0.784314 rgBT /Overlock	0.9	49
104	Cytokine induction by Gram-positive bacteria. Immunobiology, 2008, 213, 285-296.	0.8	68
105	Mechanistic Studies on N-Acetylmuramic Acid 6-Phosphate Hydrolase (MurQ): An Etherase Involved in Peptidoglycan Recycling. Biochemistry, 2008, 47, 11547-11558.	1.2	22
106	The Transcriptional Factors MurR and Catabolite Activator Protein Regulate N -Acetylmuramic Acid Catabolism in Escherichia coli. Journal of Bacteriology, 2008, 190, 6598-6608.	1.0	40
107	Isolation of microsatellites from unknown genomes using known genomes as enrichment templates. Limnology and Oceanography: Methods, 2008, 6, 412-426.	1.0	31
108	The Trimeric Periplasmic Chaperone Skp of Escherichia coli Forms 1:1 Complexes with Outer Membrane Proteins via Hydrophobic and Electrostatic Interactions. Journal of Molecular Biology, 2007, 374, 91-105.	2.0	101

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109	Visualizing differences in phylogenetic information content of alignments and distinction of three classes of long-branch effects. BMC Evolutionary Biology, 2007, 7, 147.	3.2	104
110	Sequence characterization and expression patterns of defensin and lysozyme encoding genes from the gut of the reduviid bug Triatoma brasiliensis. Insect Biochemistry and Molecular Biology, 2006, 36, 547-560.	1.2	92
111	Characterization of a beta-N-acetylhexosaminidase and a beta-N-acetylglucosaminidase/beta-glucosidase from Cellulomonas fimi. FEBS Journal, 2006, 273, 2929-2941.	2.2	60
112	MurQ Etherase Is Required by Escherichia coli in Order To Metabolize Anhydro- N -Acetylmuramic Acid Obtained either from the Environment or from Its Own Cell Wall. Journal of Bacteriology, 2006, 188, 1660-1662.	1.0	60
113	Hexose/Pentose and Hexitol/Pentitol Metabolism. EcoSal Plus, 2005, 1, .	2.1	22
114	Serine proteinases of the human body louse (Pediculus humanus): sequence characterization and expression patterns. Parasitology Research, 2005, 97, 486-500.	0.6	14
115	Scission of the Lactyl Ether Bond of N-Acetylmuramic Acid by Escherichia coli â€œEtheraseâ€• Journal of Biological Chemistry, 2005, 280, 30100-30106.	1.6	48
116	Identification of a Phosphotransferase System of Escherichia coli Required for Growth on N -Acetylmuramic Acid. Journal of Bacteriology, 2004, 186, 2385-2392.	1.0	55
117	Cell wall-associated enzymes in fungi. Phytochemistry, 2003, 64, 339-366.	1.4	94
118	Towards a third-order topological invariant for magnetic fields. Journal of Physics A, 2002, 35, 3945-3959.	1.6	21
119	Solid-Phase Oligosaccharide and Glycopeptide Synthesis Using Glycosynthases. Journal of Organic Chemistry, 2002, 67, 4143-4149.	1.7	79
120	Enzymatic Synthesis of Carbonâ^'Fluorine Bonds. Journal of the American Chemical Society, 2001, 123, 4350-4351.	6.6	64
121	Directed evolution of new glycosynthases from Agrobacterium Î²-glucosidase: a general screen to detect enzymes for oligosaccharide synthesis. Chemistry and Biology, 2001, 8, 437-443.	6.2	87
122	The E358S mutant of Agrobacterium sp. Î²-glucosidase is a greatly improved glycosynthase. FEBS Letters, 2000, 466, 40-44.	1.3	113
123	Mechanism of Action and Identification of Asp242 as the Catalytic Nucleophile of Vibrio furnisii N-Acetyl-Î²-d-glucosaminidase Using 2-Acetamido-2-deoxy-5-fluoro-Î±-l-idopyranosyl Fluoride. Biochemistry, 2000, 39, 117-126.	1.2	106
124	Î²-N-Acetylhexosaminidase: A target for the design of antifungal agents. , 1997, 76, 187-218.		86
125	Stereochemical Requirements of Chitin Synthase for Ligand Binding at the Allosteric Site for N-Acetylglucosamine. FEBS Journal, 1996, 237, 476-482.	0.2	18