

Gerlind Sulzenbacher

List of Publications by Year in descending order

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43
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3,981
citations

159573

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254170

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docs citations

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times ranked

5283
citing authors

#	ARTICLE	IF	CITATIONS
1	Carnitine is a pharmacological allosteric chaperone of the human lysosomal β -glucosidase. <i>Journal of Enzyme Inhibition and Medicinal Chemistry</i> , 2021, 36, 2068-2079.	5.2	3
2	Snapshots of ADP-ribose bound to Getah virus macro domain reveal an intriguing choreography. <i>Scientific Reports</i> , 2020, 10, 14422.	3.3	7
3	Lytic xylan oxidases from wood-decay fungi unlock biomass degradation. <i>Nature Chemical Biology</i> , 2018, 14, 306-310.	8.0	269
4	Glycosylate and move! The glycosyltransferase Maf is involved in bacterial flagella formation. <i>Environmental Microbiology</i> , 2018, 20, 228-240.	3.8	20
5	Structure of human lysosomal acid β -glucosidase—a guide for the treatment of Pompe disease. <i>Nature Communications</i> , 2017, 8, 1111.	12.8	169
6	The Quaternary Structure of a Glycoside Hydrolase Dictates Specificity toward β -Glucans. <i>Journal of Biological Chemistry</i> , 2016, 291, 7183-7194.	3.4	13
7	Marine Macrocyclic Imines, Pinnatoxins A and G: Structural Determinants and Functional Properties to Distinguish Neuronal β 7 from Muscle β 12 β 3 β 1 nAChRs. <i>Structure</i> , 2015, 23, 1106-1115.	3.3	42
8	Structural basis for carbohydrate binding properties of a plant chitinase-like agglutinin with conserved catalytic machinery. <i>Journal of Structural Biology</i> , 2015, 190, 115-121.	2.8	10
9	Functional characterization of a vacuolar invertase from <i>Solanum lycopersicum</i> : Post-translational regulation by N-glycosylation and a proteinaceous inhibitor. <i>Biochimie</i> , 2014, 101, 39-49.	2.6	32
10	Exploitation of β -glycosyl azides for the preparation of β -glycosynthases. <i>Biocatalysis and Biotransformation</i> , 2012, 30, 288-295.	2.0	3
11	β -Galactosidase/Sucrose Kinase (AgaSK), a Novel Bifunctional Enzyme from the Human Microbiome Coupling Galactosidase and Kinase Activities. <i>Journal of Biological Chemistry</i> , 2011, 286, 40814-40823.	3.4	32
12	A novel β -N-acetylgalactosaminidase family with an NAD ⁺ -dependent catalytic mechanism suitable for enzymatic removal of blood group A antigens. <i>Biocatalysis and Biotransformation</i> , 2010, 28, 22-32.	2.0	3
13	Crystal Structure of the GalNAc/Gal-Specific Agglutinin from the Phytopathogenic Ascomycete <i>Sclerotinia sclerotiorum</i> Reveals Novel Adaptation of a β -Trefoil Domain. <i>Journal of Molecular Biology</i> , 2010, 400, 715-723.	4.2	33
14	Structural determinants for interaction of partial agonists with acetylcholine binding protein and neuronal β 7 nicotinic acetylcholine receptor. <i>EMBO Journal</i> , 2009, 28, 3040-3051.	7.8	153
15	β -Glycosyl Azides as Substrates for β -Glycosynthases: Preparation of Efficient β -L-Fucosynthases. <i>Chemistry and Biology</i> , 2009, 16, 1097-1108.	6.0	65
16	Glycosyltransferases, glycoside hydrolases: surprise, surprise!. <i>Current Opinion in Structural Biology</i> , 2008, 18, 527-533.	5.7	59
17	Identification of a GH110 Subfamily of β 1,3-Galactosidases. <i>Journal of Biological Chemistry</i> , 2008, 283, 8545-8554.	3.4	52
18	Crystal Structure of the RNA Polymerase Domain of the West Nile Virus Non-structural Protein 5. <i>Journal of Biological Chemistry</i> , 2007, 282, 10678-10689.	3.4	222

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19	Structural Analysis of the Synaptic Protein Neuroligin and Its β -Neurexin Complex: Determinants for Folding and Cell Adhesion. <i>Neuron</i> , 2007, 56, 979-991.	8.1	142
20	Bacterial glycosidases for the production of universal red blood cells. <i>Nature Biotechnology</i> , 2007, 25, 454-464.	17.5	259
21	Substrate and Product Trafficking through the Active Center Gorge of Acetylcholinesterase Analyzed by Crystallography and Equilibrium Binding. <i>Journal of Biological Chemistry</i> , 2006, 281, 29256-29267.	3.4	117
22	Respective importance of protein folding and glycosylation in the thermal stability of recombinant feruloyl esterase A. <i>FEBS Letters</i> , 2006, 580, 5815-5821.	2.8	54
23	LppX is a lipoprotein required for the translocation of phthiocerol dimycocerosates to the surface of <i>Mycobacterium tuberculosis</i> . <i>EMBO Journal</i> , 2006, 25, 1436-1444.	7.8	126
24	Structural Comparison of Three Crystalline Complexes of a Peptidic Toxin With a Synaptic Acetylcholine Recognition Protein. <i>Journal of Molecular Neuroscience</i> , 2006, 30, 103-104.	2.3	3
25	Structures of <i>Aplysia</i> AChBP complexes with nicotinic agonists and antagonists reveal distinctive binding interfaces and conformations. <i>EMBO Journal</i> , 2005, 24, 3635-3646.	7.8	602
26	Crystal structure of the conserved hypothetical protein Rv1155 from <i>Mycobacterium tuberculosis</i> . <i>FEBS Letters</i> , 2005, 579, 215-221.	2.8	25
27	The Three-dimensional Structure of Invertase (β -Fructosidase) from <i>Thermotoga maritima</i> Reveals a Bimodular Arrangement and an Evolutionary Relationship between Retaining and Inverting Glycosidases. <i>Journal of Biological Chemistry</i> , 2004, 279, 18903-18910.	3.4	189
28	Crystal structure of <i>E. coli</i> yddE protein reveals a striking homology with diaminopimelate epimerase. <i>Proteins: Structure, Function and Bioinformatics</i> , 2004, 55, 764-767.	2.6	7
29	Structure of <i>Escherichia coli</i> YhdH, a putative quinone oxidoreductase. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2004, 60, 1855-1862.	2.5	15
30	Crystal Structure of <i>Thermotoga maritima</i> β -L-Fucosidase. <i>Journal of Biological Chemistry</i> , 2004, 279, 13119-13128.	3.4	141
31	Crystal Structure of <i>E. coli</i> Alcohol Dehydrogenase YqhD: Evidence of a Covalently Modified NADP Coenzyme. <i>Journal of Molecular Biology</i> , 2004, 342, 489-502.	4.2	92
32	Medium-Scale Structural Genomics: Strategies for Protein Expression and Crystallization. <i>ChemInform</i> , 2003, 34, no.	0.0	1
33	Medium-Scale Structural Genomics: Strategies for Protein Expression and Crystallization. <i>Accounts of Chemical Research</i> , 2003, 36, 165-172.	15.6	116
34	Identification of the Catalytic Nucleophile of the Family 29 β -L-Fucosidase from <i>Thermotoga maritima</i> through Trapping of a Covalent Glycosyl-Enzyme Intermediate and Mutagenesis. <i>Journal of Biological Chemistry</i> , 2003, 278, 47394-47399.	3.4	70
35	A medium-throughput crystallization approach. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2002, 58, 2109-2115.	2.5	73
36	Crystal Structure of <i>Streptococcus pneumoniae</i> N-Acetylglucosamine-1-phosphate Uridyltransferase Bound to Acetyl-coenzyme A Reveals a Novel Active Site Architecture. <i>Journal of Biological Chemistry</i> , 2001, 276, 11844-11851.	3.4	92

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37	Catalysis and specificity in enzymatic glycoside hydrolysis: a 2,5B conformation for the glycosyl-enzyme intermediate revealed by the structure of the <i>Bacillus agaradhaerens</i> family 11 xylanase. <i>Chemistry and Biology</i> , 1999, 6, 483-492.	6.0	114
38	The Crystal Structure of a 2-Fluorocellotriosyl Complex of the <i>Streptomyces lividans</i> Endoglucanase CelB2 at 1.2 Å... Resolution. <i>Biochemistry</i> , 1999, 38, 4826-4833.	2.5	56
39	Crystal structure of the family 7 endoglucanase I (Cel7B) from <i>Humicola insolens</i> at 2.2 Å... resolution and identification of the catalytic nucleophile by trapping of the covalent glycosyl-enzyme intermediate. <i>Biochemical Journal</i> , 1998, 335, 409-416.	3.7	77
40	The <i>Streptomyces lividans</i> Family 12 Endoglucanase: Construction of the Catalytic Core, Expression, and X-ray Structure at 1.75 Å... Resolution. <i>Biochemistry</i> , 1997, 36, 16032-16039.	2.5	60
41	Structure of the Endoglucanase I from <i>Fusarium oxysporum</i> : Native, Cellobiose, and 3,4-Epoxybutyl β -D-Cellobioside-Inhibited Forms, at 2.3 Å... Resolution. <i>Biochemistry</i> , 1997, 36, 5902-5911.	2.5	90
42	Structure of the <i>Fusarium oxysporum</i> Endoglucanase I with a Nonhydrolyzable Substrate Analogue: Substrate Distortion Gives Rise to the Preferred Axial Orientation for the Leaving Group. <i>Biochemistry</i> , 1996, 35, 15280-15287.	2.5	248
43	Structural versatility of peptides from α -disubstituted glycines: Crystal-state conformational analysis of homopeptides from α -methyl, α -benzylglycine [$(\alpha$ -Me)Phe] $_n$. <i>Biopolymers</i> , 1993, 33, 1617-1625.	2.4	25