

Mark Paetzel

List of Publications by Year in descending order

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49
papers

3,135
citations

186265

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223800

46
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all docs

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docs citations

50
times ranked

2933
citing authors

#	ARTICLE	IF	CITATIONS
1	Crystallographic structure of wild-type SARS-CoV-2 main protease acyl-enzyme intermediate with physiological C-terminal autoprocessing site. <i>Nature Communications</i> , 2020, 11, 5877.	12.8	141
2	Bacterial Signal Peptidases. <i>Sub-Cellular Biochemistry</i> , 2019, 92, 187-219.	2.4	20
3	Expression and Purification of the Individual Bam Components BamB&E. <i>Methods in Molecular Biology</i> , 2015, 1329, 179-188.	0.9	0
4	Structure and mechanism of Escherichia coli type I signal peptidase. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2014, 1843, 1497-1508.	4.1	65
5	¹ H, ¹³ C and ¹⁵ N resonance assignments and peptide binding site chemical shift perturbation mapping for the Escherichia coli redox enzyme chaperone DmsD. <i>Biomolecular NMR Assignments</i> , 2013, 7, 193-197.	0.8	5
6	Structure of Signal Peptide Peptidase A with C-Termini Bound in the Active Sites: Insights into Specificity, Self-Processing, and Regulation. <i>Biochemistry</i> , 2013, 52, 8811-8822.	2.5	5
7	The structure of cardiac troponin C regulatory domain with bound Cd ²⁺ reveals a closed conformation and unique ion coordination. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2013, 69, 722-734.	2.5	9
8	Crystal Structures of Yellowtail Ascites Virus VP4 Protease. <i>Journal of Biological Chemistry</i> , 2013, 288, 13068-13081.	3.4	4
9	Tellina virus 1 VP4 peptidase. , 2013, , 3523-3527.		1
10	UmuD and UmuD ² Proteins. , 2013, , 3487-3492.		1
11	Purification of a Tat leader peptide by co-expression with its chaperone. <i>Protein Expression and Purification</i> , 2012, 84, 167-172.	1.3	6
12	Crystal Structure of Bacillus subtilis Signal Peptide Peptidase A. <i>Journal of Molecular Biology</i> , 2012, 419, 347-358.	4.2	15
13	The bacterial outer membrane β -barrel assembly machinery. <i>Protein Science</i> , 2012, 21, 751-768.	7.6	98
14	Structural Characterization of Escherichia coli BamE, a Lipoprotein Component of the β -Barrel Assembly Machinery Complex. <i>Biochemistry</i> , 2011, 50, 1081-1090.	2.5	45
15	Synthesis and Characterization of the Arylomycin Lipoglycopeptide Antibiotics and the Crystallographic Analysis of Their Complex with Signal Peptidase. <i>Journal of the American Chemical Society</i> , 2011, 133, 17869-17877.	13.7	49
16	Crystal Structure of Escherichia coli BamB, a Lipoprotein Component of the β -Barrel Assembly Machinery Complex. <i>Journal of Molecular Biology</i> , 2011, 406, 667-678.	4.2	72
17	Crystal Structure of Cardiac Troponin C Regulatory Domain in Complex with Cadmium and Deoxycholic Acid Reveals Novel Conformation. <i>Journal of Molecular Biology</i> , 2011, 413, 699-711.	4.2	4
18	Expression, purification and crystallization of VP4 protease from Tellina virus 1. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 157-160.	0.7	2

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19	Crystallographic analysis of the C-terminal domain of the <i>Escherichia coli</i> lipoprotein BamC. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2011, 67, 1350-1358.	0.7	20
20	Crystal Structure of a Viral Protease Intramolecular Acyl-enzyme Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 12475-12482.	3.4	15
21	Crystal Structure of \hat{I}^2 -Barrel Assembly Machinery BamCD Protein Complex. <i>Journal of Biological Chemistry</i> , 2011, 286, 39116-39121.	3.4	71
22	Profiling the Substrate Specificity of Viral Protease VP4 by a FRET-Based Peptide Library Approach. <i>Biochemistry</i> , 2009, 48, 5753-5759.	2.5	12
23	Crystallographic Analysis of Bacterial Signal Peptidase in Ternary Complex with Arylomycin A ₂ and a \hat{I}^2 -Sultam Inhibitor. <i>Biochemistry</i> , 2009, 48, 8976-8984.	2.5	61
24	Structural Analysis of a Monomeric Form of the Twin-Arginine Leader Peptide Binding Chaperone <i>Escherichia coli</i> DmsD. <i>Journal of Molecular Biology</i> , 2009, 389, 124-133.	4.2	31
25	Unconventional serine proteases: Variations on the catalytic Ser/His/Asp triad configuration. <i>Protein Science</i> , 2008, 17, 2023-2037.	7.6	254
26	Crystal Structure of a Bacterial Signal Peptide Peptidase. <i>Journal of Molecular Biology</i> , 2008, 376, 352-366.	4.2	44
27	<i>Escherichia coli</i> Signal Peptide Peptidase A Is a Serine-Lysine Protease with a Lysine Recruited to the Nonconserved Amino-Terminal Domain in the S49 Protease Family. <i>Biochemistry</i> , 2008, 47, 6361-6369.	2.5	20
28	Identification of Residues in DmsD for Twin-Arginine Leader Peptide Binding, Defined through Random and Bioinformatics-Directed Mutagenesis. <i>Biochemistry</i> , 2008, 47, 2749-2759.	2.5	35
29	Altered -3 Substrate Specificity of <i>Escherichia coli</i> Signal Peptidase 1 Mutants as Revealed by Screening a Combinatorial Peptide Library. <i>Journal of Biological Chemistry</i> , 2007, 282, 417-425.	3.4	18
30	Crystal Structure of the VP4 Protease from Infectious Pancreatic Necrosis Virus Reveals the Acyl-Enzyme Complex for an Intermolecular Self-cleavage Reaction. <i>Journal of Biological Chemistry</i> , 2007, 282, 24928-24937.	3.4	25
31	Crystal Structure of a Novel Viral Protease with a Serine/Lysine Catalytic Dyad Mechanism. <i>Journal of Molecular Biology</i> , 2006, 358, 1378-1389.	4.2	62
32	Purification, crystallization and preliminary X-ray analysis of truncated and mutant forms of VP4 protease from infectious pancreatic necrosis virus. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2006, 62, 1235-1238.	0.7	2
33	The Identification of Residues That Control Signal Peptidase Cleavage Fidelity and Substrate Specificity. <i>Journal of Biological Chemistry</i> , 2005, 280, 6731-6741.	3.4	30
34	Crystallographic and Biophysical Analysis of a Bacterial Signal Peptidase in Complex with a Lipopeptide-based Inhibitor. <i>Journal of Biological Chemistry</i> , 2004, 279, 30781-30790.	3.4	89
35	Crystal Structure of a Bacterial Signal Peptidase Apoenzyme. <i>Journal of Biological Chemistry</i> , 2002, 277, 9512-9519.	3.4	96
36	Signal Peptidases. <i>Chemical Reviews</i> , 2002, 102, 4549-4580.	47.7	440

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37	Crystal Structure of LexA. <i>Cell</i> , 2001, 106, 585-594.	28.9	197
38	Effect of Divalent Metal Cations on the Dimerization of OXA-10 and -14 Class D β -Lactamases from <i>Pseudomonas aeruginosa</i> . <i>Biochemistry</i> , 2001, 40, 9412-9420.	2.5	33
39	The structure and mechanism of bacterial type I signal peptidases. , 2000, 87, 27-49.		147
40	The Role of the Conserved Box E Residues in the Active Site of the <i>Escherichia coli</i> Type I Signal Peptidase. <i>Journal of Biological Chemistry</i> , 2000, 275, 6490-6498.	3.4	33
41	The Role of the Membrane-spanning Domain of Type I Signal Peptidases in Substrate Cleavage Site Selection. <i>Journal of Biological Chemistry</i> , 2000, 275, 38813-38822.	3.4	51
42	Mutational Evidence of Transition State Stabilization by Serine 88 in <i>Escherichia coli</i> Type I Signal Peptidase. <i>Biochemistry</i> , 2000, 39, 7276-7283.	2.5	24
43	Common protein architecture and binding sites in proteases utilizing a Ser/Lys dyad mechanism. <i>Protein Science</i> , 1999, 8, 2533-2536.	7.6	45
44	Crystal structure of a bacterial signal peptidase in complex with a β -lactam inhibitor. <i>Nature</i> , 1998, 396, 186-190.	27.8	291
45	Phosphatidylethanolamine mediates insertion of the catalytic domain of leader peptidase in membranes. <i>FEBS Letters</i> , 1998, 431, 75-79.	2.8	49
46	Use of Site-directed Chemical Modification to Study an Essential Lysine in <i>Escherichia coli</i> Leader Peptidase. <i>Journal of Biological Chemistry</i> , 1997, 272, 9994-10003.	3.4	72
47	Catalytic hydroxyl/amine dyads within serine proteases. <i>Trends in Biochemical Sciences</i> , 1997, 22, 28-31.	7.5	136
48	Crystallization of a soluble, catalytically active form of <i>Escherichia coli</i> leader peptidase. <i>Proteins: Structure, Function and Bioinformatics</i> , 1995, 23, 122-125.	2.6	25
49	Characterization of a soluble, catalytically active form of <i>Escherichia coli</i> leader peptidase: requirement of detergent or phospholipid for optimal activity. <i>Biochemistry</i> , 1995, 34, 3935-3941.	2.5	67