Eilika Weber-Ban

List of Publications by Year
in descending order

65 papers	4,393 citations	117625 34 h-index	110387 64 g-index
67 all docs	67 docs citations	67 times ranked	3371 citing authors

#	Article	IF	Citations
1	Thermotolerance Requires Refolding of Aggregated Proteins by Substrate Translocation through the Central Pore of ClpB. Cell, 2004, 119, 653-665.	28.9	433
2	Global unfolding of a substrate protein by the Hsp100 chaperone ClpA. Nature, 1999, 401, 90-93.	27.8	408
3	Structural basis of enzyme encapsulation into a bacterial nanocompartment. Nature Structural and Molecular Biology, 2008, 15, 939-947.	8.2	347
4	Protein post-translational modifications in bacteria. Nature Reviews Microbiology, 2019, 17, 651-664.	28.6	223
5	Chaperone rings in protein folding and degradation. Proceedings of the National Academy of Sciences of the United States of America, 1999, 96, 11033-11040.	7.1	182
6	Bacterial ubiquitin-like modifier Pup is deamidated and conjugated to substrates by distinct but homologous enzymes. Nature Structural and Molecular Biology, 2009, 16, 647-651.	8.2	173
7	ClpA mediates directional translocation of substrate proteins into the ClpP protease. Proceedings of the National Academy of Sciences of the United States of America, 2001, 98, 3768-3772.	7.1	140
8	Controlled destruction: AAA+ ATPases in protein degradation from bacteria to eukaryotes. Current Opinion in Structural Biology, 2009, 19, 209-217.	5.7	119
9	Protein architecture, dynamics and allostery in tryptophan synthase channeling. Trends in Biochemical Sciences, 1997, 22, 22-27.	7.5	115
10	The mycobacterial Mpaâ€“proteasome unfolds and degrades pupylated substrates by engaging Pup's N-terminus. EMBO Journal, 2010, 29, 1262-1271.	7.8	108
11	Targeted Delivery of an ssrA-Tagged Substrate by the Adaptor Protein SspB to Its Cognate AAA+ Protein ClpX. Molecular Cell, 2003, 12, 373-380.	9.7	104
12	Clp chaperoneâ€“proteases: structure and function. Research in Microbiology, 2009, 160, 618-628.	2.1	104
13	Pilus chaperones represent a new type of protein-folding catalyst. Nature, 2004, 431, 329-333.	27.8	102
14	Dop functions as a depupylase in the prokaryotic ubiquitinâ€like modification pathway. EMBO Reports, 2010, 11, 791-797.	4.5	90
15	A distinct structural region of the prokaryotic ubiquitinâ€like protein (Pup) is recognized by the Nâ€terminal domain of the proteasomal ATPase Mpa. FEBS Letters, 2009, 583, 3151-3157.	2.8	80
16	Monovalent Metal Ions Play an Essential Role in Catalysis and Intersubunit Communication in the Tryptophan Synthase Bienzyme Complex. Biochemistry, 1995, 34, 9466-9476.	2.5	79
17	Mycobacterial Ubiquitin-like Protein Ligase PafA Follows a Two-step Reaction Pathway with a Phosphorylated Pup Intermediate. Journal of Biological Chemistry, 2011, 286, 4412-4419.	3.4	78
18	Pupylation as a signal for proteasomal degradation in bacteria. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 103-113.	4.1	67

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19	Deletion of dop in Mycobacterium smegmatis abolishes pupylation of protein substrates in vivo. Molecular Microbiology, 2010, 75, 744-754.	2.5	65
20	Formation of the Î±-Aminoacrylate Intermediate Limits the Overall Reaction Catalyzed byO-Acetylserine Sulfhydrylaseâ€. Biochemistry, 1996, 35, 4776-4783.	2.5	63
21	Prokaryotic Ubiquitin-like Protein (Pup) Is Coupled to Substrates via the Side Chain of Its C-Terminal Glutamate. Journal of the American Chemical Society, 2010, 132, 5610-5612.	13.7	62
22	The Mycobacterium tuberculosis ClpP1P2 Protease Interacts Asymmetrically with Its ATPase Partners ClpX and ClpC1. PLoS ONE, 2015, 10, e0125345.	2.5	61
23	Allosteric linkages between .beta.-site covalent transformations and .alpha.-site activation and deactivation in the tryptophan synthase bienzyme complex. Biochemistry, 1995, 34, 6552-6561.	2.5	58
24	Structures of Pup ligase PafA and depupylase Dop from the prokaryotic ubiquitin-like modification pathway. Nature Communications, 2012, 3, 1014.	12.8	58
25	The Mycobacterial LexA/RecA-Independent DNA Damage Response Is Controlled by PafBC and the Pup-Proteasome System. Cell Reports, 2018, 23, 3551-3564.	6.4	58
26	Mechanisms of Monovalent Cation Action in Enzyme Catalysis:â€‰ The Tryptophan Synthase Î±-, Î²-, and Î±Î²-Reactions. Biochemistry, 1999, 38, 7131-7141.	2.5	56
27	Investigation of Allosteric Linkages in the Regulation of Tryptophan Synthase:Â The Roles of Salt Bridges and Monovalent Cations Probed by Site-Directed Mutation, Optical Spectroscopy, and Kineticsâ€. Biochemistry, 2001, 40, 3497-3511.	2.5	55
28	The pupylation pathway and its role in mycobacteria. BMC Biology, 2012, 10, 95.	3.8	54
29	The roles of Na+ and K+ in pyridoxal phosphate enzyme catalysis. Coordination Chemistry Reviews, 1995, 144, 147-197.	18.8	48
30	An Intrinsic Degradation Tag on the ClpA C-Terminus Regulates the Balance of ClpAP Complexes with Different Substrate Specificity. Journal of Molecular Biology, 2008, 384, 503-511.	4.2	47
31	Both ATPase Domains of ClpA Are Critical for Processing of Stable Protein Structures. Journal of Biological Chemistry, 2009, 284, 31441-31452.	3.4	47
32	Mechanisms of Monovalent Cation Action in Enzyme Catalysis:â€‰ The First Stage of the Tryptophan Synthase Î²-Reaction. Biochemistry, 1999, 38, 7118-7130.	2.5	39
33	Activity of the Mycobacterial Proteasomal ATPase Mpa Is Reversibly Regulated by Pupylation. Journal of Biological Chemistry, 2012, 287, 7907-7914.	3.4	38
34	Assembly Pathway of an AAA+ Protein:â€‰ Tracking ClpA and ClpAP Complex Formation in Real Time. Biochemistry, 2007, 46, 6183-6193.	2.5	37
35	Toxic Activation of an AAA+ Protease by the Antibacterial Drug Cyclomarin A. Cell Chemical Biology, 2019, 26, 1169-1179.e4.	5.2	36
36	Kinetic Isotope Effects as a Probe of the Î²-Elimination Reaction Catalyzed byO-Acetylserine Sulfhydrylaseâ€. Biochemistry, 1996, 35, 6358-6365.	2.5	35

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37	Mycobacterium smegmatis PafBC is involved in regulation of DNA damage response. Scientific Reports, 2017, 7, 13987.	3.3	34
38	The Bacterial Proteasome at the Core of Diverse Degradation Pathways. Frontiers in Molecular Biosciences, 2019, 6, 23.	3.5	33
39	Optimal Efficiency of ClpAP and ClpXP Chaperone-Proteases Is Achieved by Architectural Symmetry. Structure, 2009, 17, 508-516.	3.3	32
40	Solution Structure and Activation Mechanism of Ubiquitin-Like Small Archaeal Modifier Proteins. Journal of Molecular Biology, 2011, 405, 1040-1055.	4.2	29
41	Bacterial Proteasome Activator Bpa (Rv3780) Is a Novel Ring-Shaped Interactor of the Mycobacterial Proteasome. PLoS ONE, 2014, 9, e114348.	2.5	29
42	Substitution of Pyridoxal 5â€²-Phosphate in the O-Acetylserine Sulfhydrylase from Salmonella typhimurium by Cofactor Analogs Provides a Test of the Mechanism Proposed for Formation of the Î±-Aminoacrylate Intermediate. Journal of Biological Chemistry, 1996, 271, 25842-25849.	3.4	28
43	Crystal Structure of the Complex between Prokaryotic Ubiquitin-like Protein and Its Ligase PafA. Journal of the American Chemical Society, 2013, 135, 6794-6797.	13.7	28
44	The Flexible Attachment of the N-Domains to the ClpA Ring Body Allows their Use On Demand. Journal of Molecular Biology, 2008, 378, 412-424.	4.2	24
45	Structure and functional implications of WYL domain-containing bacterial DNA damage response regulator PafBC. Nature Communications, 2019, 10, 4653.	12.8	23
46	Intersubunit Cross-talk in Pyridoxal 5â€²-Phosphate Synthase, Coordinated by the C Terminus of the Synthase Subunit. Journal of Biological Chemistry, 2009, 284, 7706-7718.	3.4	22
47	Studying chaperoneâ€“proteases using a real-time approach based on FRET. Journal of Structural Biology, 2009, 168, 267-277.	2.8	22
48	FixK₂, a key regulator in Bradyrhizobium japonicum, is a substrate for the protease ClpAP in vitro. FEBS Letters, 2013, 587, 88-93.	2.8	22
49	Structural Analysis of the Bacterial Proteasome Activator Bpa in Complex with the 20S Proteasome. Structure, 2016, 24, 2138-2151.	3.3	22
50	Genomeâ€wide interaction screen for MycobacteriumÂtuberculosis ClpCP protease reveals toxinâ€“antitoxin systems as a major substrate class. FEBS Journal, 2021, 288, 99-114.	4.7	22
51	Antibacterial peptide CyclomarinA creates toxicity by deregulating the Mycobacterium tuberculosis ClpC1â€“ClpP1P2 protease. Journal of Biological Chemistry, 2022, 298, 102202.	3.4	18
52	Prokaryotic Ubiquitin-Like Protein and Its Ligase/Deligase Enyzmes. Journal of Molecular Biology, 2017, 429, 3486-3499.	4.2	17
53	Prokaryotic ubiquitin-like protein remains intrinsically disordered when covalently attached to proteasomal target proteins. BMC Structural Biology, 2018, 17, 1.	2.3	17
54	Cdc48-like protein of actinobacteria (Cpa) is a novel proteasome interactor in mycobacteria and related organisms. ELife, 2018, 7, .	6.0	17

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55	Depupylase Dop Requires Inorganic Phosphate in the Active Site for Catalysis. Journal of Biological Chemistry, 2017, 292, 4044-4053.	3.4	15
56	Pupylation-dependent and -independent proteasomal degradation in mycobacteria. Biomolecular Concepts, 2015, 6, 285-301.	2.2	11
57	Survival in Hostile Conditions: Pupylation and the Proteasome in Actinobacterial Stress Response Pathways. Frontiers in Molecular Biosciences, 2021, 8, 685757.	3.5	11
58	Transcriptional control of mycobacterial DNA damage response by sigma adaptation. Science Advances, 2021, 7, eabl4064.	10.3	10
59	Structural basis of prokaryotic ubiquitin-like protein engagement and translocation by the mycobacterial Mpa-proteasome complex. Nature Communications, 2022, 13, 276.	12.8	9
60	Chaperone-Proteases of Mycobacteria. , 2014, , 419-444.		8
61	Pupylated proteins are subject to broad proteasomal degradation specificity and differential depupylation. PLoS ONE, 2019, 14, e0215439.	2.5	5
62	Targeted protein degradation: from small molecules to complex organellesâ€”a Keystone Symposia report. Annals of the New York Academy of Sciences, 2022, 1510, 79-99.	3.8	5
63	Characterization of a new AAA+ protein from archaea. Journal of Structural Biology, 2006, 156, 120-129.	2.8	4
64	The Alternating Power Stroke of a 6-Cylinder AAA Protease Chaperone Engine. Molecular Cell, 2009, 35, 545-547.	9.7	4
65	Structures of prokaryotic ubiquitin-like protein Pup in complex with depupylase Dop reveal the mechanism of catalytic phosphate formation. Nature Communications, 2021, 12, 6635.	12.8	3