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	Structural basis of prokaryotic ubiquitin-like protein engagement and translocation by the mycobacterial Mpa-proteasome complex. Nature Communications, 2022, 13, 276.	12.8	9
2	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
3	Antibacterial peptide CyclomarinA creates toxicity by deregulating the Mycobacterium tuberculosis ClpC1â€"ClpP1P2 protease. Journal of Biological Chemistry, 2022, 298, 102202.	3.4	18
4	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
5	Survival in Hostile Conditions: Pupylation and the Proteasome in Actinobacterial Stress Response Pathways. Frontiers in Molecular Biosciences, 2021, 8, 685757.	3.5	11
6	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
7	Transcriptional control of mycobacterial DNA damage response by sigma adaptation. Science Advances, 2021, 7, eabl4064.	10.3	10
8	Toxic Activation of an AAA+ Protease by the Antibacterial Drug Cyclomarin A. Cell Chemical Biology, 2019, 26, 1169-1179.e4.	5.2	36
9	Structure and functional implications of WYL domain-containing bacterial DNA damage response regulator PafBC. Nature Communications, 2019, 10, 4653.	12.8	23
10	Protein post-translational modifications in bacteria. Nature Reviews Microbiology, 2019, 17, 651-664.	28.6	223
11	Pupylated proteins are subject to broad proteasomal degradation specificity and differential depupylation. PLoS ONE, 2019, 14, e0215439.	2.5	5
12	The Bacterial Proteasome at the Core of Diverse Degradation Pathways. Frontiers in Molecular Biosciences, 2019, 6, 23.	3.5	33
13	Prokaryotic ubiquitin-like protein remains intrinsically disordered when covalently attached to proteasomal target proteins. BMC Structural Biology, 2018, 17, 1.	2.3	17
14	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
15	Cdc48-like protein of actinobacteria (Cpa) is a novel proteasome interactor in mycobacteria and related organisms. ELife, 2018, 7, .	6.0	17
16	Depupylase Dop Requires Inorganic Phosphate in the Active Site for Catalysis. Journal of Biological Chemistry, 2017, 292, 4044-4053.	3.4	15
17	Prokaryotic Ubiquitin-Like Protein and Its Ligase/Deligase Enyzmes. Journal of Molecular Biology, 2017, 429, 3486-3499.	4.2	17
18	Mycobacterium smegmatis PafBC is involved in regulation of DNA damage response. Scientific Reports, 2017, 7, 13987.	3.3	34

#	Article	IF	Citations
19	Structural Analysis of the Bacterial Proteasome Activator Bpa in Complex with the 20S Proteasome. Structure, 2016, 24, 2138-2151.	3.3	22
20	Pupylation-dependent and -independent proteasomal degradation in mycobacteria. Biomolecular Concepts, 2015, 6, 285-301.	2.2	11
21	The Mycobacterium tuberculosis ClpP1P2 Protease Interacts Asymmetrically with Its ATPase Partners ClpX and ClpC1. PLoS ONE, 2015, 10, e0125345.	2.5	61
22	Bacterial Proteasome Activator Bpa (Rv3780) Is a Novel Ring-Shaped Interactor of the Mycobacterial Proteasome. PLoS ONE, 2014, 9, e114348.	2.5	29
23	Pupylation as a signal for proteasomal degradation in bacteria. Biochimica Et Biophysica Acta - Molecular Cell Research, 2014, 1843, 103-113.	4.1	67
24	Chaperone-Proteases of Mycobacteria. , 2014, , 419-444.		8
25	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
26	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
27	Activity of the Mycobacterial Proteasomal ATPase Mpa Is Reversibly Regulated by Pupylation. Journal of Biological Chemistry, 2012, 287, 7907-7914.	3.4	38
28	The pupylation pathway and its role in mycobacteria. BMC Biology, 2012, 10, 95.	3.8	54
29	Structures of Pup ligase PafA and depupylase Dop from the prokaryotic ubiquitin-like modification pathway. Nature Communications, 2012, 3, 1014.	12.8	58
30	Solution Structure and Activation Mechanism of Ubiquitin-Like Small Archaeal Modifier Proteins. Journal of Molecular Biology, 2011, 405, 1040-1055.	4.2	29
31	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
32	Deletion of dop in Mycobacterium smegmatis abolishes pupylation of protein substrates in vivo. Molecular Microbiology, 2010, 75, 744-754.	2.5	65
33	The mycobacterial Mpaâ€“proteasome unfolds and degrades pupylated substrates by engaging Pup's N-terminus. EMBO Journal, 2010, 29, 1262-1271.	7.8	108
34	Dop functions as a depupylase in the prokaryotic ubiquitinâ€like modification pathway. EMBO Reports, 2010, 11, 791-797.	4.5	90
35	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
36	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

#	Article	IF	Citations
37	Both ATPase Domains of ClpA Are Critical for Processing of Stable Protein Structures. Journal of Biological Chemistry, 2009, 284, 31441-31452.	3.4	47
38	Controlled destruction: AAA+ ATPases in protein degradation from bacteria to eukaryotes. Current Opinion in Structural Biology, 2009, 19, 209-217.	5.7	119
39	Optimal Efficiency of ClpAP and ClpXP Chaperone-Proteases Is Achieved by Architectural Symmetry. Structure, 2009, 17, 508-516.	3.3	32
40	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
41	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
42	Clp chaperoneâ€“proteases: structure and function. Research in Microbiology, 2009, 160, 618-628.	2.1	104
43	Studying chaperoneâ€“proteases using a real-time approach based on FRET. Journal of Structural Biology, 2009, 168, 267-277.	2.8	22
44	The Alternating Power Stroke of a 6-Cylinder AAA Protease Chaperone Engine. Molecular Cell, 2009, 35, 545-547.	9.7	4
45	Structural basis of enzyme encapsulation into a bacterial nanocompartment. Nature Structural and Molecular Biology, 2008, 15, 939-947.	8.2	347
46	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
47	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
48	Assembly Pathway of an AAA+ Protein:â€‰ Tracking ClpA and ClpAP Complex Formation in Real Time. Biochemistry, 2007, 46, 6183-6193.	2.5	37
49	Characterization of a new AAA+ protein from archaea. Journal of Structural Biology, 2006, 156, 120-129.	2.8	4
50	Pilus chaperones represent a new type of protein-folding catalyst. Nature, 2004, 431, 329-333.	27.8	102
51	Thermotolerance Requires Refolding of Aggregated Proteins by Substrate Translocation through the Central Pore of ClpB. Cell, 2004, 119, 653-665.	28.9	433
52	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
53	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
54	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

#	Article	IF	Citations
55	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
56	Global unfolding of a substrate protein by the Hsp100 chaperone ClpA. Nature, 1999, 401, 90-93.	27.8	408
57	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
58	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
59	Protein architecture, dynamics and allostery in tryptophan synthase channeling. Trends in Biochemical Sciences, 1997, 22, 22-27.	7.5	115
60	Kinetic Isotope Effects as a Probe of the Î²-Elimination Reaction Catalyzed byO-Acetylserine Sulfhydrylaseâ€. Biochemistry, 1996, 35, 6358-6365.	2.5	35
61	Formation of the Î±-Aminoacrylate Intermediate Limits the Overall Reaction Catalyzed byO-Acetylserine Sulfhydrylaseâ€. Biochemistry, 1996, 35, 4776-4783.	2.5	63
62	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
63	The roles of Na+ and K+ in pyridoxal phosphate enzyme catalysis. Coordination Chemistry Reviews, 1995, 144, 147-197.	18.8	48
64	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
65	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