

Michael Ehrmann

List of Publications by Year in descending order

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113
papers

7,870
citations

53751

45
h-index

51562

86
g-index

120
all docs

120
docs citations

120
times ranked

7917
citing authors

#	ARTICLE	IF	CITATIONS
1	An allosteric HTRA1-calpain 2 complex with restricted activation profile. Proceedings of the National Academy of Sciences of the United States of America, 2022, 119, e2113520119.	3.3	2
2	Persister state-directed transitioning and vulnerability in melanoma. Nature Communications, 2022, 13, .	5.8	20
3	PPI-Affinity: A Web Tool for the Prediction and Optimization of Proteinâ€“Peptide and Proteinâ€“Protein Binding Affinity. Journal of Proteome Research, 2022, 21, 1829-1841.	1.8	24
4	Whole-exome sequencing reveals a role of HTRA1 and EGFL8 in brain white matter hyperintensities. Brain, 2021, 144, 2670-2682.	3.7	21
5	From dolastatin 13 to cyanopeptolins, micropeptides, and lyngbyastatins: the chemical biology of Ahp-cyclodepsipeptides. Natural Product Reports, 2020, 37, 163-174.	5.2	24
6	Adoption of a Turn Conformation Drives the Binding Affinity of p53 C-Terminal Domain Peptides to 14-3-3 β . ACS Chemical Biology, 2020, 15, 262-271.	1.6	10
7	Activation by substoichiometric inhibition. Proceedings of the National Academy of Sciences of the United States of America, 2020, 117, 1414-1418.	3.3	18
8	Supramolecular Mechanism of Viral Envelope Disruption by Molecular Tweezers. Journal of the American Chemical Society, 2020, 142, 17024-17038.	6.6	31
9	Native Top-Down Mass Spectrometry and Ion Mobility Spectrometry of the Interaction of Tau Protein with a Molecular Tweezer Assembly Modulator. Journal of the American Society for Mass Spectrometry, 2019, 30, 16-23.	1.2	39
10	The ubiquitinâ€“conjugating enzyme <sc>UBE</sc> 2 <sc>QL</sc> 1 coordinates lysophagy in response to endolysosomal damage. EMBO Reports, 2019, 20, e48014.	2.0	71
11	Chemical Validation of DegS As a Target for the Development of Antibiotics with a Novel Mode of Action. ChemMedChem, 2019, 14, 1074-1078.	1.6	11
12	Identification of Noncatalytic Lysine Residues from Allosteric Circuits via Covalent Probes. ACS Chemical Biology, 2018, 13, 1307-1312.	1.6	10
13	Inactivation of the serine protease HTRA1 inhibits tumor growth by deregulating angiogenesis. Oncogene, 2018, 37, 4260-4272.	2.6	27
14	Identification of the Natural Product Rotihibinâ€“A as a TOR Kinase Signaling Inhibitor by Unbiased Transcriptional Profiling. Chemistry - A European Journal, 2018, 24, 12500-12504.	1.7	5
15	Utilities for Mass Spectrometry Analysis of Proteins (UMSAP): Fast postâ€“processing of mass spectrometry data. Rapid Communications in Mass Spectrometry, 2018, 32, 1659-1667.	0.7	2
16	HTRA1-Dependent Cell Cycle Proteomics. Journal of Proteome Research, 2018, 17, 2679-2694.	1.8	11
17	Tailored protein encapsulation into a DNA host using geometrically organized supramolecular interactions. Nature Communications, 2017, 8, 14472.	5.8	73
18	Tailored Ahpâ€“cyclodepsipeptides as Potent Nonâ€“covalent Serine Protease Inhibitors. Angewandte Chemie - International Edition, 2017, 56, 8555-8558.	7.2	17

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19	MaÃgeschneiderte Ahpâ€Cyclodepsipeptide als potente, nichtâ€kkovalente Serinproteaseâ€Inhibitoren. <i>Angewandte Chemie</i> , 2017, 129, 8675-8679.	1.6	3
20	Small Molecules from Deep within the Gut. <i>ChemBioChem</i> , 2017, 18, 967-968.	1.3	0
21	<scp>VCP</scp> /p97 cooperates with <scp>YOD</scp> 1, <scp>UBXD</scp> 1 and <scp>PLAA</scp> to drive clearance of ruptured lysosomes by autophagy. <i>EMBO Journal</i> , 2017, 36, 135-150.	3.5	259
22	Uptake of the proteins HTRA1 and HTRA2 by cells mediated by calcium phosphate nanoparticles. <i>Beilstein Journal of Nanotechnology</i> , 2017, 8, 381-393.	1.5	17
23	Epigenetic silencing of serine protease HTRA1 drives polyploidy. <i>BMC Cancer</i> , 2016, 16, 399.	1.1	20
24	Reply to Liu et al.: Loss of TGF-Î² signaling in CARASIL pathogenesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, E1694-E1694.	3.3	0
25	Chemical Proteomics versus Leishmaniasis. <i>Chemistry and Biology</i> , 2015, 22, 309-310.	6.2	3
26	Determinants of amyloid fibril degradation by the PDZ protease HTRA1. <i>Nature Chemical Biology</i> , 2015, 11, 862-869.	3.9	88
27	Cerebral small vessel disease-related protease HtrA1 processes latent TGF-Î² binding protein 1 and facilitates TGF-Î² signaling. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 16496-16501.	3.3	114
28	Substrate Occupancy at the Onset of Oligomeric Transitions of DegP. <i>Structure</i> , 2014, 22, 281-290.	1.6	18
29	Identification of a serine protease inhibitor which causes inclusion vacuole reduction and is lethal to <i><scp>C</scp>hlamydia trachomatis</i>. <i>Molecular Microbiology</i> , 2013, 89, 676-689.	1.2	55
30	CtpB Assembles a Gated Protease Tunnel Regulating Cell-Cell Signaling during Spore Formation in <i>Bacillus subtilis</i> . <i>Cell</i> , 2013, 155, 647-658.	13.5	31
31	Diversity of Allosteric Regulation in Proteases. <i>ACS Chemical Biology</i> , 2013, 8, 19-26.	1.6	45
32	Ahp Cyclodepsipeptides: The Impact of the Ahp Residue on the â€œCanonical Inhibitionâ€of S1 Serine Proteases. <i>ChemBioChem</i> , 2013, 14, 1301-1308.	1.3	5
33	MiR-30e and miR-181d control Radial Glia cell proliferation via HtrA1 modulation. <i>Cell Death and Disease</i> , 2012, 3, e360-e360.	2.7	44
34	Detrimental Role for Human High Temperature Requirement Serine Protease A1 (HTRA1) in the Pathogenesis of Intervertebral Disc (IVD) Degeneration. <i>Journal of Biological Chemistry</i> , 2012, 287, 21335-21345.	1.6	57
35	Genetic Analysis of 15 Protein Folding Factors and Proteases of the <i>Escherichia coli</i> Cell Envelope. <i>Journal of Bacteriology</i> , 2012, 194, 3225-3233.	1.0	25
36	<i>E. coli</i> LoiP (YggG), a metalloprotease hydrolyzing Pheâ€Phe bonds. <i>Molecular BioSystems</i> , 2012, 8, 1775.	2.9	17

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37	Newly folded substrates inside the molecular cage of the HtrA chaperone DegQ. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 152-157.	3.6	53
38	Human Serine Protease HTRA1 Positively Regulates Osteogenesis of Human Bone Marrow-derived Mesenchymal Stem Cells and Mineralization of Differentiating Bone-forming Cells Through the Modulation of Extracellular Matrix Protein. <i>Stem Cells</i> , 2012, 30, 2271-2282.	1.4	56
39	Human High Temperature Requirement Serine Protease A1 (HTRA1) Degrades Tau Protein Aggregates. <i>Journal of Biological Chemistry</i> , 2012, 287, 20931-20941.	1.6	103
40	Chemical Biology Approaches Reveal Conserved Features of a C-terminal Processing PDZ Protease. <i>ChemBioChem</i> , 2012, 13, 402-408.	1.3	11
41	Development of a Solid-phase Approach to the Natural Product Class of Ahp-containing Cyclodepsipeptides. <i>European Journal of Organic Chemistry</i> , 2012, 2012, 1616-1625.	1.2	12
42	Peptide Functionalized Polydiacetylene Liposomes Act as a Fluorescent Turn-On Sensor for Bacterial Lipopolysaccharide. <i>Journal of the American Chemical Society</i> , 2011, 133, 9720-9723.	6.6	175
43	Protein Quality Control in the Bacterial Periplasm. <i>Annual Review of Microbiology</i> , 2011, 65, 149-168.	2.9	141
44	Lysine-Specific Molecular Tweezers Are Broad-Spectrum Inhibitors of Assembly and Toxicity of Amyloid Proteins. <i>Journal of the American Chemical Society</i> , 2011, 133, 16958-16969.	6.6	263
45	HTRA proteases: regulated proteolysis in protein quality control. <i>Nature Reviews Molecular Cell Biology</i> , 2011, 12, 152-162.	16.1	416
46	Substrate-induced remodeling of the active site regulates human HTRA1 activity. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 386-388.	3.6	116
47	Structural adaptation of the plant protease Deg1 to repair photosystem II during light exposure. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 728-731.	3.6	85
48	Molecular Adaptation of the DegQ Protease to Exert Protein Quality Control in the Bacterial Cell Envelope. <i>Journal of Biological Chemistry</i> , 2011, 286, 30680-30690.	1.6	55
49	Molecular transformers in the cell: lessons learned from the DegP protease "chaperone". <i>Current Opinion in Structural Biology</i> , 2010, 20, 253-258.	2.6	23
50	Determinants of structural and functional plasticity of a widely conserved protease chaperone complex. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 837-843.	3.6	42
51	The Serine Protease HtrA1 Specifically Interacts and Degrades the Tuberous Sclerosis Complex 2 Protein. <i>Molecular Cancer Research</i> , 2010, 8, 1248-1260.	1.5	41
52	Conversion of a Regulatory into a Degradative Protease. <i>Journal of Molecular Biology</i> , 2010, 397, 957-966.	2.0	13
53	Solid phase total synthesis of the 3-amino-6-hydroxy-2-piperidone (Ahp) cyclodepsipeptide and protease inhibitor Symplocamide A. <i>Chemical Communications</i> , 2010, 46, 8857.	2.2	27
54	Selectivity profiling of DegP substrates and inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2009, 17, 2920-2924.	1.4	34

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55	Structure, function and regulation of the conserved serine proteases DegP and DegS of Escherichia coli. <i>Research in Microbiology</i> , 2009, 160, 660-666.	1.0	56
56	Peptidic small molecule activators of the stress sensor DegS. <i>Molecular BioSystems</i> , 2009, 5, 980.	2.9	12
57	Allosteric Regulation of Proteases. <i>ChemBioChem</i> , 2008, 9, 2920-2928.	1.3	72
58	Allosteric Activation of HtrA Protease DegP by Stress Signals during Bacterial Protein Quality Control. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 1332-1334.	7.2	54
59	Structural basis for the regulated protease and chaperone function of DegP. <i>Nature</i> , 2008, 453, 885-890.	13.7	327
60	HtrA1-dependent proteolysis of TGF- β 2 controls both neuronal maturation and developmental survival. <i>Cell Death and Differentiation</i> , 2008, 15, 1408-1416.	5.0	123
61	Interplay of PDZ and protease domain of DegP ensures efficient elimination of misfolded proteins. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 7702-7707.	3.3	118
62	The serine protease HtrA1 is a novel prognostic factor for human mesothelioma. <i>Pharmacogenomics</i> , 2008, 9, 1069-1077.	0.6	51
63	Regulation of the σ E stress response by DegS: how the PDZ domain keeps the protease inactive in the resting state and allows integration of different OMP-derived stress signals upon folding stress. <i>Genes and Development</i> , 2007, 21, 2659-2670.	2.7	81
64	Determinants of regulated proteolysis in signal transduction. <i>Genes and Development</i> , 2007, 21, 6-10.	2.7	13
65	Target-Directed Proteolysis In Vivo. <i>Methods in Enzymology</i> , 2007, 421, 68-83.	0.4	3
66	Identification of Protein Disulfide Isomerase as a Cardiomyocyte Survival Factor in Ischemic Cardiomyopathy. <i>Journal of the American College of Cardiology</i> , 2007, 50, 1029-1037.	1.2	96
67	Functional characterization of a soluble gp130 isoform and its therapeutic capacity in an experimental model of inflammatory arthritis. <i>Arthritis and Rheumatism</i> , 2006, 54, 1662-1672.	6.7	89
68	The Role of Human HtrA1 in Arthritic Disease. <i>Journal of Biological Chemistry</i> , 2006, 281, 6124-6129.	1.6	237
69	Serine protease HtrA1 modulates chemotherapy-induced cytotoxicity. <i>Journal of Clinical Investigation</i> , 2006, 116, 1994-2004.	3.9	130
70	Identification and Structural Characterisation of Carboxy-Terminal Polypeptides and Antibody Epitopes of Alzheimer's Amyloid Precursor Protein Using High-Resolution Mass Spectrometry. <i>European Journal of Mass Spectrometry</i> , 2005, 11, 547-555.	0.5	17
71	Implications of the serine protease HtrA1 in amyloid precursor protein processing. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 6021-6026.	3.3	188
72	Target-directed proteolysis at the ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2005, 102, 4246-4251.	3.3	25

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73	Characterization of presenilin-amyloid precursor interaction using bacterial expression and two-hybrid systems for human membrane proteins. <i>Molecular Membrane Biology</i> , 2004, 21, 373-383.	2.0	6
74	Crystal Structure of the DegS Stress Sensor. <i>Cell</i> , 2004, 117, 483-494.	13.5	269
75	Proteolysis as a Regulatory Mechanism. <i>Annual Review of Genetics</i> , 2004, 38, 709-724.	3.2	183
76	Context-dependent effects of charged residues in transmembrane segments of MalF-PhoA fusions. <i>Research in Microbiology</i> , 2003, 154, 654-657.	1.0	2
77	SecA-dependent quality control of intracellular protein localization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 13231-13234.	3.3	33
78	The HtrA Family of Proteases. <i>Molecular Cell</i> , 2002, 10, 443-455.	4.5	597
79	Polypeptide binding of Escherichia coli FtsH (HflB). <i>Molecular Microbiology</i> , 2002, 28, 803-812.	1.2	36
80	Crystal structure of DegP (HtrA) reveals a new protease-chaperone machine. <i>Nature</i> , 2002, 416, 455-459.	13.7	374
81	Evidence for coupling of membrane targeting and function of the signal recognition particle (SRP) receptor FtsY. <i>EMBO Reports</i> , 2001, 2, 1040-1046.	2.0	42
82	A Novel Method to Determine the Topology of Peroxisomal Membrane Proteins in Vivo Using the Tobacco Etch Virus Protease. <i>Journal of Biological Chemistry</i> , 2001, 276, 36501-36507.	1.6	26
83	Characterization of Transmembrane Segments 3, 4, and 5 of MalF by Mutational Analysis. <i>Journal of Bacteriology</i> , 2001, 183, 375-381.	1.0	13
84	Synthesis of acyclic 6,7-dihaloquinolone nucleoside analogues as potential antibacterial and antiviral agents. <i>Bioorganic and Medicinal Chemistry</i> , 2000, 8, 1407-1413.	1.4	9
85	Determinants of Translocation and Folding of TreF, a Trehalase of Escherichia coli. <i>Journal of Biological Chemistry</i> , 2000, 275, 23439-23445.	1.6	24
86	Membrane Topology of the Xenobiotic-exporting Subunit, MexB, of the MexA,B-OprM Extrusion Pump in Pseudomonas aeruginosa. <i>Journal of Biological Chemistry</i> , 1999, 274, 10517-10522.	1.6	52
87	Membrane topology of CadA homologous P-type ATPase of Helicobacter pylori as determined by expression of phoA fusions in Escherichia coli and the positive inside rule. <i>Research in Microbiology</i> , 1999, 150, 507-520.	1.0	23
88	A Temperature-Dependent Switch from Chaperone to Protease in a Widely Conserved Heat Shock Protein. <i>Cell</i> , 1999, 97, 339-347.	13.5	692
89	The ABC maltose transporter. <i>Molecular Microbiology</i> , 1998, 29, 685-694.	1.2	114
90	The Protein Translocation Apparatus Contributes to Determining the Topology of an Integral Membrane Protein in Escherichia coli. <i>Journal of Biological Chemistry</i> , 1998, 273, 8419-8424.	1.6	19

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91	Quinolone Nucleosides: 6,7-Dihalo-N ¹ - and ¹ -Glycosyl-4-dihydro-4-oxo-quinoline-3-carboxylic Acids and Derivatives. Synthesis, Antimicrobial and Antiviral Activity. <i>Nucleosides & Nucleotides</i> , 1998, 17, 2255-2266.	0.5	7
92	Biochemical Characterization and Mass Spectrometric Disulfide Bond Mapping of Periplasmic ¹ -Amylase MalS of <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 1997, 272, 22125-22133.	1.6	37
93	TnTIN and TnTAP: Mini-transposons for site-specific proteolysis in vivo. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1997, 94, 13111-13115.	3.3	46
94	Characterization of transmembrane domains 6, 7, and 8 of MalF by mutational analysis. <i>Journal of Bacteriology</i> , 1996, 178, 2255-2262.	1.0	38
95	Characterization of a cytoplasmic trehalase of <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1996, 178, 6250-6257.	1.0	67
96	Site-specific proteolysis of the <i>Escherichia coli</i> SecA protein in vivo. <i>Journal of Bacteriology</i> , 1996, 178, 2986-2988.	1.0	17
97	Synthetic competition between cytoplasmic folding and translocation of a soluble membrane protein domain. <i>Research in Microbiology</i> , 1995, 146, 121-128.	1.0	5
98	Sec-independent translocation of a 100-residue periplasmic N-terminal tail in the <i>E. coli</i> inner membrane protein proW.. <i>EMBO Journal</i> , 1994, 13, 4653-4661.	3.5	62
99	Requirements for translocation of periplasmic domains in polytopic membrane proteins. <i>Journal of Bacteriology</i> , 1994, 176, 4565-4571.	1.0	14
100	The <i>Saccharomyces cerevisiae</i> gene PPH3 encodes a protein phosphatase with properties different from ppx, PP1 and PP2A. <i>Yeast</i> , 1994, 10, 567-578.	0.8	14
101	Decoding signals for membrane protein assembly using alkaline phosphatase fusions.. <i>EMBO Journal</i> , 1991, 10, 2773-2782.	3.5	69
102	Genetic analysis of membrane protein topology by a sandwich gene fusion approach.. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 1990, 87, 7574-7578.	3.3	142
103	Mall, a novel protein involved in regulation of the maltose system of <i>Escherichia coli</i> , is highly homologous to the repressor proteins GalR, CytR, and LacI. <i>Journal of Bacteriology</i> , 1989, 171, 4888-4899.	1.0	72
104	Convenient transfer of lacZ-gene fusions to phage M13 by in vivo recombination and their use for nucleotide sequencing. <i>Gene</i> , 1988, 71, 187-191.	1.0	3
105	Divergent transcription of the sn-glycerol-3-phosphate active transport (glpT) and anaerobic sn-glycerol-3-phosphate dehydrogenase (glpA glpC glpB) genes of <i>Escherichia coli</i> K-12. <i>Journal of Bacteriology</i> , 1987, 169, 526-532.	1.0	42
106	Identification of endogenous inducers of the mal regulon in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1987, 169, 3539-3545.	1.0	60
107	Osmoregulation of the maltose regulon in <i>Escherichia coli</i> . <i>Journal of Bacteriology</i> , 1986, 166, 884-891.	1.0	62
108	Practical Applications for Periplasmic Protein Accumulation. , 0, , 343-360.		2

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109	Periplasmic Expression of Antibody Fragments. , 0, , 361-388.		2
110	Assembly of Integral Membrane Proteins from the Periplasm into the Outer Membrane. , 0, , 30-66.		2
111	Disulfide Bond Formation in the Periplasm. , 0, , 122-140.		4
112	Co-and Posttranslational Protein Targeting to the SecYEG Translocon in <i>Escherichia coli</i> . , 0, , 1-15.		0
113	Periplasmic Proteases and Protease Inhibitors. , 0, , 150-170.		1