

Tim Clausen

List of Publications by Year in descending order

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92
papers

8,299
citations

44069

48
h-index

48315

88
g-index

161
all docs

161
docs citations

161
times ranked

8694
citing authors

#	ARTICLE	IF	CITATIONS
1	The HtrA Family of Proteases. <i>Molecular Cell</i> , 2002, 10, 443-455.	9.7	597
2	HTRA proteases: regulated proteolysis in protein quality control. <i>Nature Reviews Molecular Cell Biology</i> , 2011, 12, 152-162.	37.0	416
3	Crystal Structure of the Pyridoxal-5-P-phosphate Dependent Cystathionine β -lyase from <i>Escherichia coli</i> at 1.83 Å... <i>Journal of Molecular Biology</i> , 1996, 262, 202-224.	4.2	402
4	Crystal structure of DegP (HtrA) reveals a new protease-chaperone machine. <i>Nature</i> , 2002, 416, 455-459.	27.8	374
5	Structural basis for the regulated protease and chaperone function of DegP. <i>Nature</i> , 2008, 453, 885-890.	27.8	327
6	Crystal Structure of the DegS Stress Sensor. <i>Cell</i> , 2004, 117, 483-494.	28.9	269
7	The Role of Human HtrA1 in Arthritic Disease. <i>Journal of Biological Chemistry</i> , 2006, 281, 6124-6129.	3.4	237
8	Human CLP1 Mutations Alter tRNA Biogenesis, Affecting Both Peripheral and Central Nervous System Function. <i>Cell</i> , 2014, 157, 636-650.	28.9	189
9	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.	7.1	188
10	Proteolysis as a Regulatory Mechanism. <i>Annual Review of Genetics</i> , 2004, 38, 709-724.	7.6	183
11	Molecular Machines for Protein Degradation. <i>ChemBioChem</i> , 2005, 6, 222-256.	2.6	176
12	Arginine phosphorylation marks proteins for degradation by a Clp protease. <i>Nature</i> , 2016, 539, 48-53.	27.8	168
13	Mutations in the β -Tubulin Gene TUBB5 Cause Microcephaly with Structural Brain Abnormalities. <i>Cell Reports</i> , 2012, 2, 1554-1562.	6.4	162
14	McsB Is a Protein Arginine Kinase That Phosphorylates and Inhibits the Heat-Shock Regulator CtsR. <i>Science</i> , 2009, 324, 1323-1327.	12.6	151
15	Stress-Induced GSK3 Regulates the Redox Stress Response by Phosphorylating Glucose-6-Phosphate Dehydrogenase in <i>Arabidopsis</i> . <i>Plant Cell</i> , 2012, 24, 3380-3392.	6.6	151
16	Protein Quality Control in the Bacterial Periplasm. <i>Annual Review of Microbiology</i> , 2011, 65, 149-168.	7.3	141
17	A cross-kingdom conserved ER-phagy receptor maintains endoplasmic reticulum homeostasis during stress. <i>ELife</i> , 2020, 9, .	6.0	139
18	Crystal structure of a NifS-like protein from <i>Thermotoga maritima</i> : implications for iron sulphur cluster assembly. <i>Journal of Molecular Biology</i> , 2000, 297, 451-464.	4.2	135

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19	A structural basis for kinetochore recruitment of the Ndc80 complex via two distinct centromere receptors. <i>EMBO Journal</i> , 2013, 32, 409-423.	7.8	128
20	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.	7.1	118
21	The 1.3 Å... Crystal Structure of the Flavoprotein YqjM Reveals a Novel Class of Old Yellow Enzymes. <i>Journal of Biological Chemistry</i> , 2005, 280, 27904-27913.	3.4	116
22	Substrate-induced remodeling of the active site regulates human HTRA1 activity. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 386-388.	8.2	116
23	Crystal structure of 12-oxophytodienoate reductase 3 from tomato: Self-inhibition by dimerization. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 14337-14342.	7.1	114
24	HtrA proteases have a conserved activation mechanism that can be triggered by distinct molecular cues. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 844-852.	8.2	112
25	X-Ray Structure of 12-Oxophytodienoate Reductase 1 Provides Structural Insight into Substrate Binding and Specificity within the Family of OYE. <i>Structure</i> , 2001, 9, 419-429.	3.3	105
26	Human High Temperature Requirement Serine Protease A1 (HTRA1) Degrades Tau Protein Aggregates. <i>Journal of Biological Chemistry</i> , 2012, 287, 20931-20941.	3.4	103
27	Quantitative Phosphoproteomics Reveals the Role of Protein Arginine Phosphorylation in the Bacterial Stress Response. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 537-550.	3.8	103
28	Moyamoya disease: diagnosis and interventions. <i>Lancet Neurology</i> , The, 2022, 21, 747-758.	10.2	102
29	The Nuclear Pore-Associated TREX-2 Complex Employs Mediator to Regulate Gene Expression. <i>Cell</i> , 2015, 162, 1016-1028.	28.9	99
30	Kinetics and Inhibition of Recombinant Human Cystathionine β -Lyase. <i>Journal of Biological Chemistry</i> , 1999, 274, 12675-12684.	3.4	98
31	Determinants of Enzymatic Specificity in the Cys-Met-Metabolism PLP-Dependent Enzyme Family: Crystal Structure of Cystathionine β -Lyase from Yeast and Intrafamilial Structure Comparison. <i>Biological Chemistry</i> , 2003, 384, 373-86.	2.5	94
32	The Myosin Chaperone UNC-45 Is Organized in Tandem Modules to Support Myofilament Formation in <i>C.Ælegans</i> . <i>Cell</i> , 2013, 152, 183-195.	28.9	94
33	Crystal structure of Escherichia coli cystathionine β -synthase at 1.5 Å... resolution. <i>EMBO Journal</i> , 1998, 17, 6827-6838.	7.8	90
34	Crystal structure of the p14/MP1 scaffolding complex: How a twin couple attaches mitogen-activated protein kinase signaling to late endosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2004, 101, 10984-10989.	7.1	89
35	Determinants of amyloid fibril degradation by the PDZ protease HTRA1. <i>Nature Chemical Biology</i> , 2015, 11, 862-869.	8.0	88
36	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.	8.2	85

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37	Molecular shredders: how proteasomes fulfill their role. <i>Current Opinion in Structural Biology</i> , 2003, 13, 665-673.	5.7	84
38	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.	5.9	81
39	Glutaconate CoA-transferase from <i>Acidaminococcus fermentans</i> : the crystal structure reveals homology with other CoA-transferases. <i>Structure</i> , 1997, 5, 415-426.	3.3	77
40	Augmenting σ^E -Augmentation: Structural Basis of How BamB Binds BamA and May Support Folding of Outer Membrane Proteins. <i>Journal of Molecular Biology</i> , 2011, 406, 659-666.	4.2	77
41	Moyamoya disease factor RNF213 is a giant E3 ligase with a dynein-like core and a distinct ubiquitin-transfer mechanism. <i>ELife</i> , 2020, 9, .	6.0	74
42	Slow-Binding Inhibition of <i>Escherichia coli</i> Cystathionine β -Lyase by L-Aminoethoxyvinylglycine: A Kinetic and X-ray Study. <i>Biochemistry</i> , 1997, 36, 12633-12643.	2.5	68
43	BacPROTACs mediate targeted protein degradation in bacteria. <i>Cell</i> , 2022, 185, 2338-2353.e18.	28.9	57
44	Structure, function and regulation of the conserved serine proteases DegP and DegS of <i>Escherichia coli</i> . <i>Research in Microbiology</i> , 2009, 160, 660-666.	2.1	56
45	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.	3.4	55
46	Allosteric Activation of HtrA Protease DegP by Stress Signals during Bacterial Protein Quality Control. <i>Angewandte Chemie - International Edition</i> , 2008, 47, 1332-1334.	13.8	54
47	Newly folded substrates inside the molecular cage of the HtrA chaperone DegQ. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 152-157.	8.2	53
48	Structural Basis for Recognizing Phosphoarginine and Evolving Residue-Specific Protein Phosphatases in Gram-Positive Bacteria. <i>Cell Reports</i> , 2013, 3, 1832-1839.	6.4	52
49	Chasing Phosphoarginine Proteins: Development of a Selective Enrichment Method Using a Phosphatase Trap. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1953-1964.	3.8	52
50	Characterization of recombinant <i>Arabidopsis thaliana</i> threonine synthase. <i>FEBS Journal</i> , 1999, 263, 212-221.	0.2	48
51	A new mechanism for the control of a prokaryotic transcriptional regulator: antagonistic binding of positive and negative effectors. <i>Molecular Microbiology</i> , 2000, 35, 765-776.	2.5	48
52	Structural basis for the disaggregase activity and regulation of Hsp104. <i>ELife</i> , 2016, 5, .	6.0	48
53	The Three-Dimensional Structure of Cystathionine β -Lyase from <i>Arabidopsis</i> and Its Substrate Specificity. <i>Plant Physiology</i> , 2001, 126, 631-642.	4.8	47
54	Structural Basis of Substrate Specificity of Plant 12-Oxophytodienoate Reductases. <i>Journal of Molecular Biology</i> , 2009, 392, 1266-1277.	4.2	46

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55	Involvement of Tyr24 and Trp108 in Substrate Binding and Substrate Specificity of Glycolate Oxidase. FEBS Journal, 1995, 228, 408-416.	0.2	45
56	X-ray structure of MalY from Escherichia coli: a pyridoxal 5â€²-phosphate-dependent enzyme acting as a modulator in mal gene expression. EMBO Journal, 2000, 19, 831-842.	7.8	44
57	Spectroscopic and Kinetic Analyses Reveal the Pyridoxal 5â€²-Phosphate Binding Mode and the Catalytic Features of Treponema denticola Cystalysin. Biochemistry, 2002, 41, 9153-9164.	2.5	44
58	Structural mechanism for the recognition and ubiquitination of a single nucleosome residue by Rad6 and Bre1. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 10553-10558.	7.1	44
59	The crystal structure of cystathionine Î³-synthase from Nicotiana tabacum reveals its substrate and reaction specificity. Journal of Molecular Biology, 1999, 290, 983-996.	4.2	39
60	Crystal Structure of Transcription Factor MalT Domain III. Structure, 2001, 9, 1051-1060.	3.3	39
61	The linear ubiquitin chain assembly complex (LUBAC) generates heterotypic ubiquitin chains. ELife, 2021, 10, .	6.0	38
62	Native Mass Spectrometry Can Effectively Predict PROTAC Efficacy. ACS Central Science, 2020, 6, 1223-1230.	11.3	37
63	Structure of McsB, a protein kinase for regulated arginine phosphorylation. Nature Chemical Biology, 2019, 15, 510-518.	8.0	36
64	Structure and Function of Threonine Synthase from Yeast. Journal of Biological Chemistry, 2002, 277, 12396-12405.	3.4	34
65	Selectivity profiling of DegP substrates and inhibitors. Bioorganic and Medicinal Chemistry, 2009, 17, 2920-2924.	3.0	34
66	Myosin chaperones. Current Opinion in Structural Biology, 2014, 25, 9-15.	5.7	33
67	CtpB Assembles a Gated Protease Tunnel Regulating Cell-Cell Signaling during Spore Formation in Bacillus subtilis. Cell, 2013, 155, 647-658.	28.9	31
68	Molecular features of the UNC-45 chaperone critical for binding and folding muscle myosin. Nature Communications, 2019, 10, 4781.	12.8	29
69	Structural Basis for the Function of Pyridoxine 5â€²-Phosphate Synthase. Structure, 2001, 9, 245-253.	3.3	27
70	Snapshots of the Cystine Lyase C-DES during Catalysis. Journal of Biological Chemistry, 2003, 278, 357-365.	3.4	27
71	Structural and functional impairment of an Old Yellow Enzyme homologue upon affinity tag incorporation. Protein Expression and Purification, 2004, 36, 280-291.	1.3	27
72	Versatile in vitro system to study translocation and functional integration of bacterial outer membrane proteins. Nature Communications, 2014, 5, 5396.	12.8	24

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73	HUWE1 employs a giant substrate-binding ring to feed and regulate its HECT E3 domain. <i>Nature Chemical Biology</i> , 2021, 17, 1084-1092.	8.0	24
74	Molecular transformers in the cell: lessons learned from the DegP proteaseâ€“chaperone. <i>Current Opinion in Structural Biology</i> , 2010, 20, 253-258.	5.7	23
75	RNA Specificity and Regulation of Catalysis in the Eukaryotic Polynucleotide Kinase Clp1. <i>Molecular Cell</i> , 2014, 54, 975-986.	9.7	23
76	UFD-2 is an adaptor-assisted E3 ligase targeting unfolded proteins. <i>Nature Communications</i> , 2018, 9, 484.	12.8	22
77	Crystal structures of cystathionine Î³-synthase inhibitor complexes rationalize the increased affinity of a novel inhibitor. <i>Journal of Molecular Biology</i> , 2001, 311, 789-801.	4.2	21
78	Cloning, Purification and Characterisation of Cystathionine Î³-Synthase from <i>Nicotiana tabacum</i> . <i>Biological Chemistry</i> , 1999, 380, 1237-42.	2.5	19
79	Shaping Striated Muscles with Ubiquitin Proteasome System in Health and Disease. <i>Trends in Molecular Medicine</i> , 2019, 25, 760-774.	6.7	19
80	Enzymeâ€“ligand Complexes of Pyridoxine 5â€“Phosphate Synthase: Implications for Substrate Binding and Catalysis. <i>Journal of Molecular Biology</i> , 2002, 321, 601-612.	4.2	18
81	Activation by substoichiometric inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1414-1418.	7.1	18
82	The crystal structure of Deg9 reveals a novel octameric-type HtrA protease. <i>Nature Plants</i> , 2017, 3, 973-982.	9.3	14
83	Conversion of a Regulatory into a Degradative Protease. <i>Journal of Molecular Biology</i> , 2010, 397, 957-966.	4.2	13
84	Chemical Biology Interrogates Protein Arginine Phosphorylation. <i>Cell Chemical Biology</i> , 2016, 23, 888-890.	5.2	13
85	Cloning, purification, crystallization, and preliminary X-ray diffraction analysis of cystathionine Î³-synthase from <i>E. coli</i> . <i>FEBS Letters</i> , 1997, 414, 492-496.	2.8	12
86	Peptidic small molecule activators of the stress sensor DegS. <i>Molecular BioSystems</i> , 2009, 5, 980.	2.9	12
87	Cloning, purification, and crystallization of <i>Escherichia coli</i> cystathionine Î²-lyase. <i>FEBS Letters</i> , 1996, 379, 94-96.	2.8	11
88	McsB forms a gated kinase chamber to mark aberrant bacterial proteins for degradation. <i>ELife</i> , 2021, 10, .	6.0	11
89	Crystallization and preliminary X-ray crystallographic analysis of PdxJ, the pyridoxine 5â€“phosphate synthesizing enzyme. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1045-1048.	2.5	7
90	Targeted protein degradation: from small molecules to complex organellesâ€“a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2022, 1510, 79-99.	3.8	5

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91	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.	7.1	2
92	Molecular Machines for Protein Degradation. , 2005, , 248-287.		0