

# Tim Clausen

## List of Publications by Year in descending order

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92  
papers

8,299  
citations

43973

48  
h-index

48187

88  
g-index

161  
all docs

161  
docs citations

161  
times ranked

8694  
citing authors

#	ARTICLE	IF	CITATIONS
1	Targeted protein degradation: from small molecules to complex organelles – a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2022, 1510, 79-99.	1.8	5
2	An allosteric HTRA1-calpain 2 complex with restricted activation profile. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2113520119.	3.3	2
3	Moyamoya disease: diagnosis and interventions. <i>Lancet Neurology</i> , The, 2022, 21, 747-758.	4.9	102
4	BacPROTACs mediate targeted protein degradation in bacteria. <i>Cell</i> , 2022, 185, 2338-2353.e18.	13.5	57
5	The linear ubiquitin chain assembly complex (LUBAC) generates heterotypic ubiquitin chains. <i>ELife</i> , 2021, 10, .	2.8	38
6	HUWE1 employs a giant substrate-binding ring to feed and regulate its HECT E3 domain. <i>Nature Chemical Biology</i> , 2021, 17, 1084-1092.	3.9	24
7	McsB forms a gated kinase chamber to mark aberrant bacterial proteins for degradation. <i>ELife</i> , 2021, 10, .	2.8	11
8	Activation by substoichiometric inhibition. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 1414-1418.	3.3	18
9	Native Mass Spectrometry Can Effectively Predict PROTAC Efficacy. <i>ACS Central Science</i> , 2020, 6, 1223-1230.	5.3	37
10	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, .	2.8	74
11	A cross-kingdom conserved ER-phagy receptor maintains endoplasmic reticulum homeostasis during stress. <i>ELife</i> , 2020, 9, .	2.8	139
12	Molecular features of the UNC-45 chaperone critical for binding and folding muscle myosin. <i>Nature Communications</i> , 2019, 10, 4781.	5.8	29
13	Shaping Striated Muscles with Ubiquitin Proteasome System in Health and Disease. <i>Trends in Molecular Medicine</i> , 2019, 25, 760-774.	3.5	19
14	Structure of McsB, a protein kinase for regulated arginine phosphorylation. <i>Nature Chemical Biology</i> , 2019, 15, 510-518.	3.9	36
15	UFD-2 is an adaptor-assisted E3 ligase targeting unfolded proteins. <i>Nature Communications</i> , 2018, 9, 484.	5.8	22
16	The crystal structure of Deg9 reveals a novel octameric-type HtrA protease. <i>Nature Plants</i> , 2017, 3, 973-982.	4.7	14
17	Structural basis for the disaggregase activity and regulation of Hsp104. <i>ELife</i> , 2016, 5, .	2.8	48
18	Structural mechanism for the recognition and ubiquitination of a single nucleosome residue by Rad6 – Bre1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10553-10558.	3.3	44

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19	Arginine phosphorylation marks proteins for degradation by a Clp protease. <i>Nature</i> , 2016, 539, 48-53.	13.7	168
20	Chemical Biology Interrogates Protein Arginine Phosphorylation. <i>Cell Chemical Biology</i> , 2016, 23, 888-890.	2.5	13
21	Determinants of amyloid fibril degradation by the PDZ protease HTRA1. <i>Nature Chemical Biology</i> , 2015, 11, 862-869.	3.9	88
22	The Nuclear Pore-Associated TREX-2 Complex Employs Mediator to Regulate Gene Expression. <i>Cell</i> , 2015, 162, 1016-1028.	13.5	99
23	Chasing Phosphoarginine Proteins: Development of a Selective Enrichment Method Using a Phosphatase Trap. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 1953-1964.	2.5	52
24	Quantitative Phosphoproteomics Reveals the Role of Protein Arginine Phosphorylation in the Bacterial Stress Response. <i>Molecular and Cellular Proteomics</i> , 2014, 13, 537-550.	2.5	103
25	Myosin chaperones. <i>Current Opinion in Structural Biology</i> , 2014, 25, 9-15.	2.6	33
26	RNA Specificity and Regulation of Catalysis in the Eukaryotic Polynucleotide Kinase Clp1. <i>Molecular Cell</i> , 2014, 54, 975-986.	4.5	23
27	Human CLP1 Mutations Alter tRNA Biogenesis, Affecting Both Peripheral and Central Nervous System Function. <i>Cell</i> , 2014, 157, 636-650.	13.5	189
28	Versatile in vitro system to study translocation and functional integration of bacterial outer membrane proteins. <i>Nature Communications</i> , 2014, 5, 5396.	5.8	24
29	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.	13.5	94
30	Structural Basis for Recognizing Phosphoarginine and Evolving Residue-Specific Protein Phosphatases in Gram-Positive Bacteria. <i>Cell Reports</i> , 2013, 3, 1832-1839.	2.9	52
31	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
32	A structural basis for kinetochore recruitment of the Ndc80 complex via two distinct centromere receptors. <i>EMBO Journal</i> , 2013, 32, 409-423.	3.5	128
33	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.	3.1	151
34	Mutations in the $\beta$ -Tubulin Gene TUBB5 Cause Microcephaly with Structural Brain Abnormalities. <i>Cell Reports</i> , 2012, 2, 1554-1562.	2.9	162
35	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
36	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

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37	Protein Quality Control in the Bacterial Periplasm. Annual Review of Microbiology, 2011, 65, 149-168.	2.9	141
38	Augmenting Î²-Augmentation: Structural Basis of How BamB Binds BamA and May Support Folding of Outer Membrane Proteins. Journal of Molecular Biology, 2011, 406, 659-666.	2.0	77
39	HTRA proteases: regulated proteolysis in protein quality control. Nature Reviews Molecular Cell Biology, 2011, 12, 152-162.	16.1	416
40	Substrate-induced remodeling of the active site regulates human HTRA1 activity. Nature Structural and Molecular Biology, 2011, 18, 386-388.	3.6	116
41	Structural adaptation of the plant protease Deg1 to repair photosystem II during light exposure. Nature Structural and Molecular Biology, 2011, 18, 728-731.	3.6	85
42	Molecular Adaptation of the DegQ Protease to Exert Protein Quality Control in the Bacterial Cell Envelope. Journal of Biological Chemistry, 2011, 286, 30680-30690.	1.6	55
43	Molecular transformers in the cell: lessons learned from the DegP proteaseâ€™chaperone. Current Opinion in Structural Biology, 2010, 20, 253-258.	2.6	23
44	HtrA proteases have a conserved activation mechanism that can be triggered by distinct molecular cues. Nature Structural and Molecular Biology, 2010, 17, 844-852.	3.6	112
45	Conversion of a Regulatory into a Degradative Protease. Journal of Molecular Biology, 2010, 397, 957-966.	2.0	13
46	Selectivity profiling of DegP substrates and inhibitors. Bioorganic and Medicinal Chemistry, 2009, 17, 2920-2924.	1.4	34
47	McsB Is a Protein Arginine Kinase That Phosphorylates and Inhibits the Heat-Shock Regulator CtsR. Science, 2009, 324, 1323-1327.	6.0	151
48	Structure, function and regulation of the conserved serine proteases DegP and DegS of Escherichia coli. Research in Microbiology, 2009, 160, 660-666.	1.0	56
49	Structural Basis of Substrate Specificity of Plant 12-Oxophytodienoate Reductases. Journal of Molecular Biology, 2009, 392, 1266-1277.	2.0	46
50	Peptidic small molecule activators of the stress sensor DegS. Molecular BioSystems, 2009, 5, 980.	2.9	12
51	Allosteric Activation of HtrA Protease DegP by Stress Signals during Bacterial Protein Quality Control. Angewandte Chemie - International Edition, 2008, 47, 1332-1334.	7.2	54
52	Structural basis for the regulated protease and chaperone function of DegP. Nature, 2008, 453, 885-890.	13.7	327
53	Interplay of PDZ and protease domain of DegP ensures efficient elimination of misfolded proteins. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 7702-7707.	3.3	118
54	Regulation of the Î¶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. Genes and Development, 2007, 21, 2659-2670.	2.7	81

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55	Crystal structure of 12-oxophytodienoate reductase 3 from tomato: Self-inhibition by dimerization. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 14337-14342.	3.3	114
56	The Role of Human HtrA1 in Arthritic Disease. Journal of Biological Chemistry, 2006, 281, 6124-6129.	1.6	237
57	Molecular Machines for Protein Degradation. , 2005, , 248-287.		0
58	Molecular Machines for Protein Degradation. ChemBioChem, 2005, 6, 222-256.	1.3	176
59	Implications of the serine protease HtrA1 in amyloid precursor protein processing. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 6021-6026.	3.3	188
60	The 1.3 Å... Crystal Structure of the Flavoprotein YqjM Reveals a Novel Class of Old Yellow Enzymes. Journal of Biological Chemistry, 2005, 280, 27904-27913.	1.6	116
61	Crystal structure of the p14/MP1 scaffolding complex: How a twin couple attaches mitogen-activated protein kinase signaling to late endosomes. Proceedings of the National Academy of Sciences of the United States of America, 2004, 101, 10984-10989.	3.3	89
62	Structural and functional impairment of an Old Yellow Enzyme homologue upon affinity tag incorporation. Protein Expression and Purification, 2004, 36, 280-291.	0.6	27
63	Crystal Structure of the DegS Stress Sensor. Cell, 2004, 117, 483-494.	13.5	269
64	Proteolysis as a Regulatory Mechanism. Annual Review of Genetics, 2004, 38, 709-724.	3.2	183
65	Molecular shredders: how proteasomes fulfill their role. Current Opinion in Structural Biology, 2003, 13, 665-673.	2.6	84
66	Determinants of Enzymatic Specificity in the Cys-Met-Metabolism PLP-Dependent Enzyme Family: Crystal Structure of Cystathionine $\beta$ -Lyase from Yeast and Intrafamilial Structure Comparison. Biological Chemistry, 2003, 384, 373-86.	1.2	94
67	Snapshots of the Cystine Lyase C-DES during Catalysis. Journal of Biological Chemistry, 2003, 278, 357-365.	1.6	27
68	Structure and Function of Threonine Synthase from Yeast. Journal of Biological Chemistry, 2002, 277, 12396-12405.	1.6	34
69	Spectroscopic and Kinetic Analyses Reveal the Pyridoxal 5'-Phosphate Binding Mode and the Catalytic Features of Treponema denticola Cystathionine $\beta$ -Lyase. Biochemistry, 2002, 41, 9153-9164.	1.2	44
70	Enzyme-Ligand Complexes of Pyridoxine 5'-Phosphate Synthase: Implications for Substrate Binding and Catalysis. Journal of Molecular Biology, 2002, 321, 601-612.	2.0	18
71	The HtrA Family of Proteases. Molecular Cell, 2002, 10, 443-455.	4.5	597
72	Crystal structure of DegP (HtrA) reveals a new protease-chaperone machine. Nature, 2002, 416, 455-459.	13.7	374

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73	Crystal structures of cystathionine $\beta$ -synthase inhibitor complexes rationalize the increased affinity of a novel inhibitor. <i>Journal of Molecular Biology</i> , 2001, 311, 789-801.	2.0	21
74	Structural Basis for the Function of Pyridoxine 5 $\alpha$ -Phosphate Synthase. <i>Structure</i> , 2001, 9, 245-253.	1.6	27
75	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.	1.6	105
76	Crystal Structure of Transcription Factor MalT Domain III. <i>Structure</i> , 2001, 9, 1051-1060.	1.6	39
77	The Three-Dimensional Structure of Cystathionine $\beta$ -Lyase from Arabidopsis and Its Substrate Specificity. <i>Plant Physiology</i> , 2001, 126, 631-642.	2.3	47
78	Crystallization and preliminary X-ray crystallographic analysis of PdxJ, the pyridoxine 5 $\alpha$ -phosphate synthesizing enzyme. <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2000, 56, 1045-1048.	2.5	7
79	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.	1.2	48
80	X-ray structure of MalY from Escherichia coli: a pyridoxal 5 $\alpha$ -phosphate-dependent enzyme acting as a modulator in mal gene expression. <i>EMBO Journal</i> , 2000, 19, 831-842.	3.5	44
81	Crystal structure of a NifS-like protein from Thermotoga maritima: implications for iron sulphur cluster assembly. <i>Journal of Molecular Biology</i> , 2000, 297, 451-464.	2.0	135
82	Cloning, Purification and Characterisation of Cystathionine $\beta$ -Synthase from Nicotiana tabacum. <i>Biological Chemistry</i> , 1999, 380, 1237-42.	1.2	19
83	Kinetics and Inhibition of Recombinant Human Cystathionine $\beta$ -Lyase. <i>Journal of Biological Chemistry</i> , 1999, 274, 12675-12684.	1.6	98
84	Characterization of recombinant Arabidopsis thaliana threonine synthase. <i>FEBS Journal</i> , 1999, 263, 212-221.	0.2	48
85	The crystal structure of cystathionine $\beta$ -synthase from Nicotiana tabacum reveals its substrate and reaction specificity. <i>Journal of Molecular Biology</i> , 1999, 290, 983-996.	2.0	39
86	Crystal structure of Escherichia coli cystathionine $\beta$ -synthase at 1.5 Å... resolution. <i>EMBO Journal</i> , 1998, 17, 6827-6838.	3.5	90
87	Cloning, purification, crystallization, and preliminary X-ray diffraction analysis of cystathionine $\beta$ -synthase from E. coli. <i>FEBS Letters</i> , 1997, 414, 492-496.	1.3	12
88	Slow-Binding Inhibition of Escherichia coli Cystathionine $\beta$ -Lyase by L-Aminoethoxyvinylglycine: A Kinetic and X-ray Study. <i>Biochemistry</i> , 1997, 36, 12633-12643.	1.2	68
89	Glutaconate CoA-transferase from Acidaminococcus fermentans: the crystal structure reveals homology with other CoA-transferases. <i>Structure</i> , 1997, 5, 415-426.	1.6	77
90	Cloning, purification, and crystallization of Escherichia coli cystathionine $\beta$ -lyase. <i>FEBS Letters</i> , 1996, 379, 94-96.	1.3	11

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91	Crystal Structure of the Pyridoxal-5-phosphate Dependent Cystathionine $\beta$ -lyase from <i>Escherichia coli</i> at 1.83 Å... <i>Journal of Molecular Biology</i> , 1996, 262, 202-224.	2.0	402
92	Involvement of Tyr24 and Trp108 in Substrate Binding and Substrate Specificity of Glycolate Oxidase. <i>FEBS Journal</i> , 1995, 228, 408-416.	0.2	45