

Tim Clausen

List of Publications by Year in descending order

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Version: 2024-02-01

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 | 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 |
| 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. | 7.1 | 2 |
| 3 | Moyamoya disease: diagnosis and interventions. <i>Lancet Neurology</i> , The, 2022, 21, 747-758. | 10.2 | 102 |
| 4 | BacPROTACs mediate targeted protein degradation in bacteria. <i>Cell</i> , 2022, 185, 2338-2353.e18. | 28.9 | 57 |
| 5 | The linear ubiquitin chain assembly complex (LUBAC) generates heterotypic ubiquitin chains. <i>ELife</i> , 2021, 10, . | 6.0 | 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. | 8.0 | 24 |
| 7 | McsB forms a gated kinase chamber to mark aberrant bacterial proteins for degradation. <i>ELife</i> , 2021, 10, . | 6.0 | 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. | 7.1 | 18 |
| 9 | Native Mass Spectrometry Can Effectively Predict PROTAC Efficacy. <i>ACS Central Science</i> , 2020, 6, 1223-1230. | 11.3 | 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, . | 6.0 | 74 |
| 11 | A cross-kingdom conserved ER-phagy receptor maintains endoplasmic reticulum homeostasis during stress. <i>ELife</i> , 2020, 9, . | 6.0 | 139 |
| 12 | Molecular features of the UNC-45 chaperone critical for binding and folding muscle myosin. <i>Nature Communications</i> , 2019, 10, 4781. | 12.8 | 29 |
| 13 | Shaping Striated Muscles with Ubiquitin Proteasome System in Health and Disease. <i>Trends in Molecular Medicine</i> , 2019, 25, 760-774. | 6.7 | 19 |
| 14 | Structure of McsB, a protein kinase for regulated arginine phosphorylation. <i>Nature Chemical Biology</i> , 2019, 15, 510-518. | 8.0 | 36 |
| 15 | UFD-2 is an adaptor-assisted E3 ligase targeting unfolded proteins. <i>Nature Communications</i> , 2018, 9, 484. | 12.8 | 22 |
| 16 | The crystal structure of Deg9 reveals a novel octameric-type HtrA protease. <i>Nature Plants</i> , 2017, 3, 973-982. | 9.3 | 14 |
| 17 | Structural basis for the disaggregase activity and regulation of Hsp104. <i>ELife</i> , 2016, 5, . | 6.0 | 48 |
| 18 | Structural mechanism for the recognition and ubiquitination of a single nucleosome residue by Rad6â€”Bre1. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 10553-10558. | 7.1 | 44 |

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|----|---|------|-----------|
| 19 | Arginine phosphorylation marks proteins for degradation by a Clp protease. <i>Nature</i> , 2016, 539, 48-53. | 27.8 | 168 |
| 20 | Chemical Biology Interrogates Protein Arginine Phosphorylation. <i>Cell Chemical Biology</i> , 2016, 23, 888-890. | 5.2 | 13 |
| 21 | Determinants of amyloid fibril degradation by the PDZ protease HTRA1. <i>Nature Chemical Biology</i> , 2015, 11, 862-869. | 8.0 | 88 |
| 22 | The Nuclear Pore-Associated TREX-2 Complex Employs Mediator to Regulate Gene Expression. <i>Cell</i> , 2015, 162, 1016-1028. | 28.9 | 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. | 3.8 | 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. | 3.8 | 103 |
| 25 | Myosin chaperones. <i>Current Opinion in Structural Biology</i> , 2014, 25, 9-15. | 5.7 | 33 |
| 26 | RNA Specificity and Regulation of Catalysis in the Eukaryotic Polynucleotide Kinase Clp1. <i>Molecular Cell</i> , 2014, 54, 975-986. | 9.7 | 23 |
| 27 | Human CLP1 Mutations Alter tRNA Biogenesis, Affecting Both Peripheral and Central Nervous System Function. <i>Cell</i> , 2014, 157, 636-650. | 28.9 | 189 |
| 28 | Versatile in vitro system to study translocation and functional integration of bacterial outer membrane proteins. <i>Nature Communications</i> , 2014, 5, 5396. | 12.8 | 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. | 28.9 | 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. | 6.4 | 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. | 28.9 | 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. | 7.8 | 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. | 6.6 | 151 |
| 34 | Mutations in the β -Tubulin Gene TUBB5 Cause Microcephaly with Structural Brain Abnormalities. <i>Cell Reports</i> , 2012, 2, 1554-1562. | 6.4 | 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. | 8.2 | 53 |
| 36 | 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 |

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|----|--|------|-----------|
| 37 | Protein Quality Control in the Bacterial Periplasm. <i>Annual Review of Microbiology</i> , 2011, 65, 149-168. | 7.3 | 141 |
| 38 | Augmenting Î²-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 |
| 39 | HTRA proteases: regulated proteolysis in protein quality control. <i>Nature Reviews Molecular Cell Biology</i> , 2011, 12, 152-162. | 37.0 | 416 |
| 40 | 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 |
| 41 | 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 |
| 42 | 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 |
| 43 | 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 |
| 44 | 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 |
| 45 | Conversion of a Regulatory into a Degradative Protease. <i>Journal of Molecular Biology</i> , 2010, 397, 957-966. | 4.2 | 13 |
| 46 | Selectivity profiling of DegP substrates and inhibitors. <i>Bioorganic and Medicinal Chemistry</i> , 2009, 17, 2920-2924. | 3.0 | 34 |
| 47 | 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 |
| 48 | 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 |
| 49 | Structural Basis of Substrate Specificity of Plant 12-Oxophytodienoate Reductases. <i>Journal of Molecular Biology</i> , 2009, 392, 1266-1277. | 4.2 | 46 |
| 50 | Peptidic small molecule activators of the stress sensor DegS. <i>Molecular BioSystems</i> , 2009, 5, 980. | 2.9 | 12 |
| 51 | 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 |
| 52 | Structural basis for the regulated protease and chaperone function of DegP. <i>Nature</i> , 2008, 453, 885-890. | 27.8 | 327 |
| 53 | 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 |
| 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. <i>Genes and Development</i> , 2007, 21, 2659-2670. | 5.9 | 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. | 7.1 | 114 |
| 56 | The Role of Human HtrA1 in Arthritic Disease. Journal of Biological Chemistry, 2006, 281, 6124-6129. | 3.4 | 237 |
| 57 | Molecular Machines for Protein Degradation. , 2005, , 248-287. | | 0 |
| 58 | Molecular Machines for Protein Degradation. ChemBioChem, 2005, 6, 222-256. | 2.6 | 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. | 7.1 | 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. | 3.4 | 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. | 7.1 | 89 |
| 62 | 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 |
| 63 | Crystal Structure of the DegS Stress Sensor. Cell, 2004, 117, 483-494. | 28.9 | 269 |
| 64 | Proteolysis as a Regulatory Mechanism. Annual Review of Genetics, 2004, 38, 709-724. | 7.6 | 183 |
| 65 | Molecular shredders: how proteasomes fulfill their role. Current Opinion in Structural Biology, 2003, 13, 665-673. | 5.7 | 84 |
| 66 | 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. Biological Chemistry, 2003, 384, 373-86. | 2.5 | 94 |
| 67 | Snapshots of the Cystine Lyase C-DES during Catalysis. Journal of Biological Chemistry, 2003, 278, 357-365. | 3.4 | 27 |
| 68 | Structure and Function of Threonine Synthase from Yeast. Journal of Biological Chemistry, 2002, 277, 12396-12405. | 3.4 | 34 |
| 69 | Spectroscopic and Kinetic Analyses Reveal the Pyridoxal 5'-Phosphate Binding Mode and the Catalytic Features of Treponema denticola Cystathionine β -Lyase. Biochemistry, 2002, 41, 9153-9164. | 2.5 | 44 |
| 70 | Enzyme-Ligand Complexes of Pyridoxine 5'-Phosphate Synthase: Implications for Substrate Binding and Catalysis. Journal of Molecular Biology, 2002, 321, 601-612. | 4.2 | 18 |
| 71 | The HtrA Family of Proteases. Molecular Cell, 2002, 10, 443-455. | 9.7 | 597 |
| 72 | Crystal structure of DegP (HtrA) reveals a new protease-chaperone machine. Nature, 2002, 416, 455-459. | 27.8 | 374 |

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| 73 | Crystal structures of cystathionine β -synthase inhibitor complexes rationalize the increased affinity of a novel inhibitor. <i>Journal of Molecular Biology</i> , 2001, 311, 789-801. | 4.2 | 21 |
| 74 | Structural Basis for the Function of Pyridoxine 5 α -Phosphate Synthase. <i>Structure</i> , 2001, 9, 245-253. | 3.3 | 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. | 3.3 | 105 |
| 76 | Crystal Structure of Transcription Factor MalT Domain III. <i>Structure</i> , 2001, 9, 1051-1060. | 3.3 | 39 |
| 77 | The Three-Dimensional Structure of Cystathionine β -Lyase from Arabidopsis and Its Substrate Specificity. <i>Plant Physiology</i> , 2001, 126, 631-642. | 4.8 | 47 |
| 78 | Crystallization and preliminary X-ray crystallographic analysis of PdxJ, the pyridoxine 5 α -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. | 2.5 | 48 |
| 80 | X-ray structure of MalY from Escherichia coli: a pyridoxal 5 α -phosphate-dependent enzyme acting as a modulator in mal gene expression. <i>EMBO Journal</i> , 2000, 19, 831-842. | 7.8 | 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. | 4.2 | 135 |
| 82 | Cloning, Purification and Characterisation of Cystathionine β -Synthase from Nicotiana tabacum. <i>Biological Chemistry</i> , 1999, 380, 1237-42. | 2.5 | 19 |
| 83 | Kinetics and Inhibition of Recombinant Human Cystathionine β -Lyase. <i>Journal of Biological Chemistry</i> , 1999, 274, 12675-12684. | 3.4 | 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 β -synthase from Nicotiana tabacum reveals its substrate and reaction specificity. <i>Journal of Molecular Biology</i> , 1999, 290, 983-996. | 4.2 | 39 |
| 86 | Crystal structure of Escherichia coli cystathionine β -synthase at 1.5 Å... resolution. <i>EMBO Journal</i> , 1998, 17, 6827-6838. | 7.8 | 90 |
| 87 | Cloning, purification, crystallization, and preliminary X-ray diffraction analysis of cystathionine β -synthase from E. coli. <i>FEBS Letters</i> , 1997, 414, 492-496. | 2.8 | 12 |
| 88 | Slow-Binding Inhibition of Escherichia coli Cystathionine β -Lyase by L-Aminoethoxyvinylglycine: A Kinetic and X-ray Study. <i>Biochemistry</i> , 1997, 36, 12633-12643. | 2.5 | 68 |
| 89 | Glutaconate CoA-transferase from Acidaminococcus fermentans: the crystal structure reveals homology with other CoA-transferases. <i>Structure</i> , 1997, 5, 415-426. | 3.3 | 77 |
| 90 | Cloning, purification, and crystallization of Escherichia coli cystathionine β -lyase. <i>FEBS Letters</i> , 1996, 379, 94-96. | 2.8 | 11 |

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| 91 | Crystal Structure of the Pyridoxal-5-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 |
| 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 |