

Sukyeong Lee

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/11000183/publications.pdf>

Version: 2024-02-01

38
papers

2,292
citations

394421

19
h-index

361022

35
g-index

39
all docs

39
docs citations

39
times ranked

2103
citing authors

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 1 | Thermotolerance Requires Refolding of Aggregated Proteins by Substrate Translocation through the Central Pore of ClpB. <i>Cell</i> , 2004, 119, 653-665. | 28.9 | 433 |
| 2 | The Structure of ClpB. <i>Cell</i> , 2003, 115, 229-240. | 28.9 | 422 |
| 3 | Identification of a protein binding site on the surface of the alphavirus nucleocapsid and its implication in virus assembly. <i>Structure</i> , 1996, 4, 531-541. | 3.3 | 159 |
| 4 | M Domains Couple the ClpB Threading Motor with the DnaK Chaperone Activity. <i>Molecular Cell</i> , 2007, 25, 247-260. | 9.7 | 153 |
| 5 | Visualizing the ATPase Cycle in a Protein Disaggregating Machine: Structural Basis for Substrate Binding by ClpB. <i>Molecular Cell</i> , 2007, 25, 261-271. | 9.7 | 112 |
| 6 | Heat shock protein (Hsp) 70 is an activator of the Hsp104 motor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 8513-8518. | 7.1 | 101 |
| 7 | An Intersubunit Signaling Network Coordinates ATP Hydrolysis by m-AAA Proteases. <i>Molecular Cell</i> , 2009, 35, 574-585. | 9.7 | 96 |
| 8 | The ClpB/Hsp104 molecular chaperone is a protein disaggregating machine. <i>Journal of Structural Biology</i> , 2004, 146, 99-105. | 2.8 | 91 |
| 9 | Structure of Semliki Forest virus core protein. , 1997, 27, 345-359. | | 89 |
| 10 | CryoEM structure of Hsp104 and its mechanistic implication for protein disaggregation. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 8135-8140. | 7.1 | 82 |
| 11 | Structural Analysis of Sindbis Virus Capsid Mutants Involving Assembly and Catalysis. <i>Journal of Molecular Biology</i> , 1996, 262, 151-167. | 4.2 | 58 |
| 12 | Electron Cryomicroscopy Structure of a Membrane-anchored Mitochondrial AAA Protease. <i>Journal of Biological Chemistry</i> , 2011, 286, 4404-4411. | 3.4 | 54 |
| 13 | Structural basis for intersubunit signaling in a protein disaggregating machine. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 12515-12520. | 7.1 | 43 |
| 14 | Mitochondrial Hsp90 is a ligand-activated molecular chaperone coupling ATP binding to dimer closure through a coiled-coil intermediate. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, 2952-2957. | 7.1 | 42 |
| 15 | Molecular Chaperones in Protein Quality Control. <i>BMB Reports</i> , 2005, 38, 259-265. | 2.4 | 42 |
| 16 | Molecular chaperones: guardians of the proteome in normal and disease states. <i>F1000Research</i> , 2015, 4, 1448. | 1.6 | 39 |
| 17 | Cryo-EM Structures of the Hsp104 Protein Disaggregase Captured in the ATP Conformation. <i>Cell Reports</i> , 2019, 26, 29-36.e3. | 6.4 | 36 |
| 18 | Probing the potential glycoprotein binding site of sindbis virus capsid protein with dioxane and model building. <i>Proteins: Structure, Function and Bioinformatics</i> , 1998, 33, 311-317. | 2.6 | 24 |

| # | ARTICLE | IF | CITATIONS |
|----|--|------|-----------|
| 19 | A biallelic pathogenic variant in the <scp><i>OGDH</i></scp> gene results in a neurological disorder with features of a mitochondrial disease. <i>Journal of Inherited Metabolic Disease</i> , 2021, 44, 388-400. | 3.6 | 24 |
| 20 | Development of Novel Epoxyketone-Based Proteasome Inhibitors as a Strategy To Overcome Cancer Resistance to Carfilzomib and Bortezomib. <i>Journal of Medicinal Chemistry</i> , 2019, 62, 4444-4455. | 6.4 | 20 |
| 21 | LMP2 Inhibitors as a Potential Treatment for Alzheimer's Disease. <i>Journal of Medicinal Chemistry</i> , 2020, 63, 3763-3783. | 6.4 | 19 |
| 22 | Functional analysis of conserved cis- and trans-elements in the Hsp104 protein disaggregating machine. <i>Journal of Structural Biology</i> , 2012, 179, 172-180. | 2.8 | 18 |
| 23 | 2.4-Å resolution crystal structure of human TRAP1_{NM}, the Hsp90 paralog in the mitochondrial matrix. <i>Acta Crystallographica Section D: Structural Biology</i> , 2016, 72, 904-911. | 2.3 | 16 |
| 24 | Functional interpretation of ATAD3A variants in neuro-mitochondrial phenotypes. <i>Genome Medicine</i> , 2021, 13, 55. | 8.2 | 16 |
| 25 | Functional cooperativity between the trigger factor chaperone and the ClpXP proteolytic complex. <i>Nature Communications</i> , 2021, 12, 281. | 12.8 | 16 |
| 26 | Overlapping and Specific Functions of the Hsp104 N Domain Define Its Role in Protein Disaggregation. <i>Scientific Reports</i> , 2017, 7, 11184. | 3.3 | 15 |
| 27 | Structural determinants for protein unfolding and translocation by the Hsp104 protein disaggregase. <i>Bioscience Reports</i> , 2017, 37, . | 2.4 | 15 |
| 28 | Structural Elements Regulating AAA+ Protein Quality Control Machines. <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 27. | 3.5 | 13 |
| 29 | The Mitochondrial Protease LonP1 Promotes Proteasome Inhibitor Resistance in Multiple Myeloma. <i>Cancers</i> , 2021, 13, 843. | 3.7 | 12 |
| 30 | Bi-allelic variants in OGDHL cause a neurodevelopmental spectrum disease featuring epilepsy, hearing loss, visual impairment, and ataxia. <i>American Journal of Human Genetics</i> , 2021, 108, 2368-2384. | 6.2 | 12 |
| 31 | Macrocyclic Immunoproteasome Inhibitors as a Potential Therapy for Alzheimer's Disease. <i>Journal of Medicinal Chemistry</i> , 2021, 64, 10934-10950. | 6.4 | 7 |
| 32 | Crystallization and preliminary X-ray crystallographic analysis of the Hsp100 chaperone ClpB from <i>Thermus thermophilus</i> . <i>Acta Crystallographica Section D: Biological Crystallography</i> , 2003, 59, 2334-2336. | 2.5 | 6 |
| 33 | Crystal Structure of the YcjX Stress Protein Reveals a Ras-Like GTP-Binding Protein. <i>Journal of Molecular Biology</i> , 2019, 431, 3179-3190. | 4.2 | 3 |
| 34 | Structural insights into the oligomerization of FtsH periplasmic domain from <i>Thermotoga maritima</i> . <i>Biochemical and Biophysical Research Communications</i> , 2018, 495, 1201-1207. | 2.1 | 2 |
| 35 | Crystallization and preliminary X-ray crystallographic analysis of a 40-kDa N-terminal fragment of the yeast prion-remodeling factor Hsp104. <i>Acta Crystallographica Section F: Structural Biology Communications</i> , 2007, 63, 784-786. | 0.7 | 1 |
| 36 | Atomic Structure of the <i>Leishmania</i> spp . Hsp100 N-Domain. <i>Proteins: Structure, Function and Bioinformatics</i> , 2022, , . | 2.6 | 1 |

| # | ARTICLE | IF | CITATIONS |
|----|--|-----|-----------|
| 37 | Three-dimensional Structure of a Prion-remodeling Machine. FASEB Journal, 2009, 23, 672.3. | 0.5 | 0 |
| 38 | The M-domain controls the Hsp104 protein disaggregating activity. FASEB Journal, 2011, 25, . | 0.5 | 0 |