

Sukyeong Lee

List of Publications by Year in descending order

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38
papers

2,292
citations

394421

19
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361022

35
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39
all docs

39
docs citations

39
times ranked

2103
citing authors

#	ARTICLE	IF	CITATIONS
1	Atomic Structure of the Leishmania spp . Hsp100 Nê€Domain. Proteins: Structure, Function and Bioinformatics, 2022, , .	2.6	1
2	A biallelic pathogenic variant in the <scp><i>OGDH</i></scp> gene results in a neurological disorder with features of a mitochondrial disease. Journal of Inherited Metabolic Disease, 2021, 44, 388-400.	3.6	24
3	The Mitochondrial Protease LonP1 Promotes Proteasome Inhibitor Resistance in Multiple Myeloma. Cancers, 2021, 13, 843.	3.7	12
4	Functional interpretation of ATAD3A variants in neuro-mitochondrial phenotypes. Genome Medicine, 2021, 13, 55.	8.2	16
5	Macrocyclic Immunoproteasome Inhibitors as a Potential Therapy for Alzheimerê€™s Disease. Journal of Medicinal Chemistry, 2021, 64, 10934-10950.	6.4	7
6	Functional cooperativity between the trigger factor chaperone and the ClpXP proteolytic complex. Nature Communications, 2021, 12, 281.	12.8	16
7	Bi-allelic variants in OGDHL cause a neurodevelopmental spectrum disease featuring epilepsy, hearing loss, visual impairment, and ataxia. American Journal of Human Genetics, 2021, 108, 2368-2384.	6.2	12
8	LMP2 Inhibitors as a Potential Treatment for Alzheimerê€™s Disease. Journal of Medicinal Chemistry, 2020, 63, 3763-3783.	6.4	19
9	Crystal Structure of the YcjX Stress Protein Reveals a Ras-Like GTP-Binding Protein. Journal of Molecular Biology, 2019, 431, 3179-3190.	4.2	3
10	Development of Novel Epoxyketone-Based Proteasome Inhibitors as a Strategy To Overcome Cancer Resistance to Carfilzomib and Bortezomib. Journal of Medicinal Chemistry, 2019, 62, 4444-4455.	6.4	20
11	Cryo-EM Structures of the Hsp104 Protein Disaggregase Captured in the ATP Conformation. Cell Reports, 2019, 26, 29-36.e3.	6.4	36
12	Structural insights into the oligomerization of FtsH periplasmic domain from Thermotoga maritima. Biochemical and Biophysical Research Communications, 2018, 495, 1201-1207.	2.1	2
13	Overlapping and Specific Functions of the Hsp104 N Domain Define Its Role in Protein Disaggregation. Scientific Reports, 2017, 7, 11184.	3.3	15
14	Structural Elements Regulating AAA+ Protein Quality Control Machines. Frontiers in Molecular Biosciences, 2017, 4, 27.	3.5	13
15	Structural determinants for protein unfolding and translocation by the Hsp104 protein disaggregase. Bioscience Reports, 2017, 37, .	2.4	15
16	2.4ê€Å... resolution crystal structure of human TRAP1_{NM}, the Hsp90 paralog in the mitochondrial matrix. Acta Crystallographica Section D: Structural Biology, 2016, 72, 904-911.	2.3	16
17	Mitochondrial Hsp90 is a ligand-activated molecular chaperone coupling ATP binding to dimer closure through a coiled-coil intermediate. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, 2952-2957.	7.1	42
18	Molecular chaperones: guardians of the proteome in normal and disease states. F1000Research, 2015, 4, 1448.	1.6	39

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19	Heat shock protein (Hsp) 70 is an activator of the Hsp104 motor. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8513-8518.	7.1	101
20	Structural basis for intersubunit signaling in a protein disaggregating machine. Proceedings of the National Academy of Sciences of the United States of America, 2012, 109, 12515-12520.	7.1	43
21	Functional analysis of conserved cis- and trans-elements in the Hsp104 protein disaggregating machine. Journal of Structural Biology, 2012, 179, 172-180.	2.8	18
22	Electron Cryomicroscopy Structure of a Membrane-anchored Mitochondrial AAA Protease. Journal of Biological Chemistry, 2011, 286, 4404-4411.	3.4	54
23	The M ϵ domain controls the Hsp104 protein disaggregating activity. FASEB Journal, 2011, 25, .	0.5	0
24	CryoEM structure of Hsp104 and its mechanistic implication for protein disaggregation. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 8135-8140.	7.1	82
25	An Intersubunit Signaling Network Coordinates ATP Hydrolysis by m-AAA Proteases. Molecular Cell, 2009, 35, 574-585.	9.7	96
26	Three-dimensional Structure of a Prion-remodeling Machine. FASEB Journal, 2009, 23, 672.3.	0.5	0
27	M Domains Couple the ClpB Threading Motor with the DnaK Chaperone Activity. Molecular Cell, 2007, 25, 247-260.	9.7	153
28	Visualizing the ATPase Cycle in a Protein Disaggregating Machine: Structural Basis for Substrate Binding by ClpB. Molecular Cell, 2007, 25, 261-271.	9.7	112
29	Crystallization and preliminary X-ray crystallographic analysis of a 40-kDa N-terminal fragment of the yeast prion-remodeling factor Hsp104. Acta Crystallographica Section F: Structural Biology Communications, 2007, 63, 784-786.	0.7	1
30	Molecular Chaperones in Protein Quality Control. BMB Reports, 2005, 38, 259-265.	2.4	42
31	Thermotolerance Requires Refolding of Aggregated Proteins by Substrate Translocation through the Central Pore of ClpB. Cell, 2004, 119, 653-665.	28.9	433
32	The ClpB/Hsp104 molecular chaperone is a protein disaggregating machine. Journal of Structural Biology, 2004, 146, 99-105.	2.8	91
33	Crystallization and preliminary X-ray crystallographic analysis of the Hsp100 chaperone ClpB from Thermus thermophilus. Acta Crystallographica Section D: Biological Crystallography, 2003, 59, 2334-2336.	2.5	6
34	The Structure of ClpB. Cell, 2003, 115, 229-240.	28.9	422
35	Probing the potential glycoprotein binding site of sindbis virus capsid protein with dioxane and model building. Proteins: Structure, Function and Bioinformatics, 1998, 33, 311-317.	2.6	24
36	Structure of Semliki Forest virus core protein. , 1997, 27, 345-359.		89

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37	Structural Analysis of Sindbis Virus Capsid Mutants Involving Assembly and Catalysis. <i>Journal of Molecular Biology</i> , 1996, 262, 151-167.	4.2	58
38	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