

Axel Mogk

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/8940285/publications.pdf>

Version: 2024-02-01

75
papers

9,660
citations

34105

52
h-index

69250

77
g-index

82
all docs

82
docs citations

82
times ranked

7850
citing authors

#	ARTICLE	IF	CITATIONS
1	The Diverse Functions of Small Heat Shock Proteins in the Proteostasis Network. <i>Journal of Molecular Biology</i> , 2022, 434, 167157.	4.2	53
2	Antibacterial peptide CyclomarinA creates toxicity by deregulating the <i>Mycobacterium tuberculosis</i> ClpC1-ClpP1P2 protease. <i>Journal of Biological Chemistry</i> , 2022, 298, 102202.	3.4	18
3	A recently isolated human commensal <i>Escherichia coli</i> ST10 clone member mediates enhanced thermotolerance and tetrathionate respiration on a P1 phage-derived IncY plasmid. <i>Molecular Microbiology</i> , 2021, 115, 255-271.	2.5	21
4	Basic mechanism of the autonomous ClpG disaggregase. <i>Journal of Biological Chemistry</i> , 2021, 296, 100460.	3.4	9
5	Resisting the Heat: Bacterial Disaggregases Rescue Cells From Devastating Protein Aggregation. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 681439.	3.5	7
6	The HSP110/HSP70 disaggregation system generates spreading-competent toxic α -synuclein species. <i>EMBO Journal</i> , 2020, 39, e103954.	7.8	53
7	Disassembly of Tau fibrils by the human Hsp70 disaggregation machinery generates small seeding-competent species. <i>Journal of Biological Chemistry</i> , 2020, 295, 9676-9690.	3.4	103
8	Chaperone-Mediated Protein Disaggregation Triggers Proteolytic Clearance of Intra-nuclear Protein Inclusions. <i>Cell Reports</i> , 2020, 31, 107680.	6.4	43
9	Processive extrusion of polypeptide loops by a Hsp100 disaggregase. <i>Nature</i> , 2020, 578, 317-320.	27.8	92
10	Toxic Activation of an AAA+ Protease by the Antibacterial Drug Cyclomarin A. <i>Cell Chemical Biology</i> , 2019, 26, 1169-1179.e4.	5.2	36
11	Cellular sequestrases maintain basal Hsp70 capacity ensuring balanced proteostasis. <i>Nature Communications</i> , 2019, 10, 4851.	12.8	49
12	Two-Step Activation Mechanism of the ClpB Disaggregase for Sequential Substrate Threading by the Main ATPase Motor. <i>Cell Reports</i> , 2019, 27, 3433-3446.e4.	6.4	46
13	Cellular Functions and Mechanisms of Action of Small Heat Shock Proteins. <i>Annual Review of Microbiology</i> , 2019, 73, 89-110.	7.3	127
14	ClpG Provides Increased Heat Resistance by Acting as Superior Disaggregase. <i>Biomolecules</i> , 2019, 9, 815.	4.0	14
15	Cellular Handling of Protein Aggregates by Disaggregation Machines. <i>Molecular Cell</i> , 2018, 69, 214-226.	9.7	280
16	A prion-like domain in Hsp42 drives chaperone-facilitated aggregation of misfolded proteins. <i>Journal of Cell Biology</i> , 2018, 217, 1269-1285.	5.2	57
17	Stand-alone ClpG disaggregase confers superior heat tolerance to bacteria. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E273-E282.	7.1	37
18	Role of sHsps in organizing cytosolic protein aggregation and disaggregation. <i>Cell Stress and Chaperones</i> , 2017, 22, 493-502.	2.9	92

#	ARTICLE	IF	CITATIONS
19	Hsp70 displaces small heat shock proteins from aggregates to initiate protein refolding. <i>EMBO Journal</i> , 2017, 36, 783-796.	7.8	120
20	Structural pathway of regulated substrate transfer and threading through an Hsp100 disaggregase. <i>Science Advances</i> , 2017, 3, e1701726.	10.3	112
21	Mutant Analysis Reveals Allosteric Regulation of ClpB Disaggregase. <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 6.	3.5	8
22	Regulatory coiled-coil domains promote head-to-head assemblies of AAA+ chaperones essential for tunable activity control. <i>ELife</i> , 2017, 6, .	6.0	32
23	Small heat shock proteins sequester misfolding proteins in near-native conformation for cellular protection and efficient refolding. <i>Nature Communications</i> , 2016, 7, 13673.	12.8	147
24	Bacterial and Yeast AAA + Disaggregases ClpB and Hsp104 Operate through Conserved Mechanism Involving Cooperation with Hsp70. <i>Journal of Molecular Biology</i> , 2016, 428, 4378-4391.	4.2	22
25	Cooperation of Hsp70 and Hsp100 chaperone machines in protein disaggregation. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 22.	3.5	140
26	Prolonged starvation drives reversible sequestration of lipid biosynthetic enzymes and organelle reorganization in <i>Saccharomyces cerevisiae</i> . <i>Molecular Biology of the Cell</i> , 2015, 26, 1601-1615.	2.1	59
27	Spatially Organized Aggregation of Misfolded Proteins as Cellular Stress Defense Strategy. <i>Journal of Molecular Biology</i> , 2015, 427, 1564-1574.	4.2	164
28	Compartment-specific aggregases direct distinct nuclear and cytoplasmic aggregate deposition. <i>EMBO Journal</i> , 2015, 34, 778-797.	7.8	243
29	Systemic control of protein synthesis through sequestration of translation and ribosome biogenesis factors during severe heat stress. <i>FEBS Letters</i> , 2015, 589, 3654-3664.	2.8	55
30	Human Hsp70 Disaggregase Reverses Parkinson's-Linked α -Synuclein Amyloid Fibrils. <i>Molecular Cell</i> , 2015, 59, 781-793.	9.7	336
31	Structure of the VipA/B Type VI Secretion Complex Suggests a Contraction-State-Specific Recycling Mechanism. <i>Cell Reports</i> , 2014, 8, 20-30.	6.4	74
32	Type VI Secretion System Helps Find a Niche. <i>Cell Host and Microbe</i> , 2014, 16, 5-6.	11.0	22
33	Head-to-tail interactions of the coiled-coil domains regulate ClpB activity and cooperation with Hsp70 in protein disaggregation. <i>ELife</i> , 2014, 3, e02481.	6.0	111
34	Coordination of Translational Control and Protein Homeostasis during Severe Heat Stress. <i>Current Biology</i> , 2013, 23, 2452-2462.	3.9	191
35	Deadly syringes: type VI secretion system activities in pathogenicity and interbacterial competition. <i>Current Opinion in Microbiology</i> , 2013, 16, 52-58.	5.1	92
36	ClpV recycles VipA tubules and prevents non-productive tubule formation to ensure efficient type VI protein secretion. <i>Molecular Microbiology</i> , 2013, 87, 1013-1028.	2.5	132

#	ARTICLE	IF	CITATIONS
37	Mechanism of Hsp104/ClpB inhibition by prion curing Guanidinium hydrochloride. FEBS Letters, 2013, 587, 810-817.	2.8	20
38	Hsp70 proteins bind Hsp100 regulatory M domains to activate AAA+ disaggregase at aggregate surfaces. Nature Structural and Molecular Biology, 2012, 19, 1347-1355.	8.2	152
39	Hsp70 targets Hsp100 chaperones to substrates for protein disaggregation and prion fragmentation. Journal of Cell Biology, 2012, 198, 387-404.	5.2	196
40	Chaperone networks in protein disaggregation and prion propagation. Journal of Structural Biology, 2012, 179, 152-160.	2.8	121
41	A tightly regulated molecular toggle controls AAA+ disaggregase. Nature Structural and Molecular Biology, 2012, 19, 1338-1346.	8.2	124
42	Hsp42 is required for sequestration of protein aggregates into deposition sites in <i>Saccharomyces cerevisiae</i> . Journal of Cell Biology, 2011, 195, 617-629.	5.2	233
43	Integrating Protein Homeostasis Strategies in Prokaryotes. Cold Spring Harbor Perspectives in Biology, 2011, 3, a004366-a004366.	5.5	82
44	Molecular Basis for the Unique Role of the AAA+ Chaperone ClpV in Type VI Protein Secretion. Journal of Biological Chemistry, 2011, 286, 30010-30021.	3.4	95
45	Cooperative and independent activities of Sgt2 and Get5 in the targeting of tail-anchored proteins. Biological Chemistry, 2011, 392, 601-8.	2.5	28
46	Tubules and donuts: a type VI secretion story. Molecular Microbiology, 2010, 76, 815-821.	2.5	141
47	Quantitative and spatio-temporal features of protein aggregation in Escherichia coli and consequences on protein quality control and cellular ageing. EMBO Journal, 2010, 29, 910-923.	7.8	241
48	Cellular strategies for controlling protein aggregation. Nature Reviews Molecular Cell Biology, 2010, 11, 777-788.	37.0	785
49	Towards a unifying mechanism for ClpB/Hsp104-mediated protein disaggregation and prion propagation This paper is one of a selection of papers published in this special issue entitled 8th International Conference on AAA Proteins and has undergone the Journal's usual peer review process.. Biochemistry and Cell Biology, 2010, 88, 63-75.	2.0	56
50	The Yeast AAA ⁺ Chaperone Hsp104 Is Part of a Network That Links the Actin Cytoskeleton with the Inheritance of Damaged Proteins. Molecular and Cellular Biology, 2009, 29, 3738-3745.	2.3	66
51	The antibiotic ADEP reprogrammes ClpP, switching it from a regulated to an uncontrolled protease. EMBO Molecular Medicine, 2009, 1, 37-49.	6.9	196
52	Remodelling of VipA/VipB tubules by ClpV-mediated threading is crucial for type VI protein secretion. EMBO Journal, 2009, 28, 315-325.	7.8	288
53	Protein disaggregation by the AAA+ chaperone ClpB involves partial threading of looped polypeptide segments. Nature Structural and Molecular Biology, 2008, 15, 641-650.	8.2	139
54	Substrate threading through the central pore of the Hsp104 chaperone as a common mechanism for protein disaggregation and prion propagation. Molecular Microbiology, 2008, 68, 87-97.	2.5	171

#	ARTICLE	IF	CITATIONS
55	Common and specific mechanisms of AAA+ proteins involved in protein quality control. <i>Biochemical Society Transactions</i> , 2008, 36, 120-125.	3.4	70
56	M Domains Couple the ClpB Threading Motor with the DnaK Chaperone Activity. <i>Molecular Cell</i> , 2007, 25, 247-260.	9.7	153
57	Chaperone-based procedure to increase yields of soluble recombinant proteins produced in <i>E. coli</i> . <i>BMC Biotechnology</i> , 2007, 7, 32.	3.3	231
58	Adaptor protein controlled oligomerization activates the AAA+ protein ClpC. <i>EMBO Journal</i> , 2006, 25, 1481-1491.	7.8	127
59	Novel insights into the mechanism of chaperone-assisted protein disaggregation. <i>Biological Chemistry</i> , 2005, 386, 739-44.	2.5	92
60	ClpV, a unique Hsp100/Clp member of pathogenic proteobacteria. <i>Biological Chemistry</i> , 2005, 386, 1115-27.	2.5	78
61	Substrate recognition by the AAA+ chaperone ClpB. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 607-615.	8.2	219
62	Molecular Chaperones: Structure of a Protein Disaggregase. <i>Current Biology</i> , 2004, 14, R78-R80.	3.9	64
63	Unscrambling an egg: protein disaggregation by AAA+ proteins. <i>Microbial Cell Factories</i> , 2004, 3, 1.	4.0	80
64	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
65	Solubilization of aggregated proteins by ClpB/DnaK relies on the continuous extraction of unfolded polypeptides. <i>FEBS Letters</i> , 2004, 578, 351-356.	2.8	76
66	Broad yet high substrate specificity: the challenge of AAA+ proteins. <i>Journal of Structural Biology</i> , 2004, 146, 90-98.	2.8	45
67	Small heat shock proteins, ClpB and the DnaK system form a functional triade in reversing protein aggregation. <i>Molecular Microbiology</i> , 2003, 50, 585-595.	2.5	342
68	Poly-L-lysine enhances the protein disaggregation activity of ClpB. <i>FEBS Letters</i> , 2003, 553, 125-130.	2.8	14
69	Roles of Individual Domains and Conserved Motifs of the AAA+ Chaperone ClpB in Oligomerization, ATP Hydrolysis, and Chaperone Activity. <i>Journal of Biological Chemistry</i> , 2003, 278, 17615-17624.	3.4	222
70	MecA, an adaptor protein necessary for ClpC chaperone activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 2306-2311.	7.1	139
71	Refolding of Substrates Bound to Small Hsps Relies on a Disaggregation Reaction Mediated Most Efficiently by ClpB/DnaK. <i>Journal of Biological Chemistry</i> , 2003, 278, 31033-31042.	3.4	243
72	Characterization of a Trap Mutant of the AAA+ Chaperone ClpB. <i>Journal of Biological Chemistry</i> , 2003, 278, 32608-32617.	3.4	140

#	ARTICLE	IF	CITATIONS
73	AAA+ proteins and substrate recognition, it all depends on their partner in crime. FEBS Letters, 2002, 529, 6-10.	2.8	193
74	Genetic dissection of the roles of chaperones and proteases in protein folding and degradation in the Escherichia coli cytosol. Molecular Microbiology, 2001, 40, 397-413.	2.5	302
75	Role of Region C in Regulation of the Heat Shock Gene-Specific Sigma Factor of <i>Escherichia coli</i> , ³² . Journal of Bacteriology, 1999, 181, 3552-3561.	2.2	45