

KÃ¼rÅad Turgay

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6682717/publications.pdf>

Version: 2024-02-01

45
papers

3,404
citations

172457

29
h-index

254184

43
g-index

60
all docs

60
docs citations

60
times ranked

2698
citing authors

#	ARTICLE	IF	CITATIONS
1	Exploring a potential Achilles heel of <i>Mycobacterium tuberculosis</i> : defining the ClpC1 interactome. FEBS Journal, 2021, 288, 95-98.	4.7	2
2	Structural Basis for Regulation of the Opposing (p)ppGpp Synthetase and Hydrolase within the Stringent Response Orchestrator Rel. Cell Reports, 2020, 32, 108157.	6.4	39
3	The alarmones (p)ppGpp are part of the heat shock response of <i>Bacillus subtilis</i> . PLoS Genetics, 2020, 16, e1008275.	3.5	52
4	Xenogeneic modulation of the ClpCP protease of <i>Bacillus subtilis</i> by a phage-encoded adaptor-like protein. Journal of Biological Chemistry, 2019, 294, 17501-17511.	3.4	9
5	Recent Advances and Current Trends in Nucleotide Second Messenger Signaling in Bacteria. Journal of Molecular Biology, 2019, 431, 908-927.	4.2	41
6	Spx, a versatile regulator of the <i>Bacillus subtilis</i> stress response. Current Genetics, 2019, 65, 871-876.	1.7	14
7	YocM a small heat shock protein can protect <i>Bacillus subtilis</i> cells during salt stress. Molecular Microbiology, 2019, 111, 423-440.	2.5	18
8	Structural changes of TasA in biofilm formation of <i>Bacillus subtilis</i> . Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, 3237-3242.	7.1	97
9	Spx, the central regulator of the heat and oxidative stress response in <i>B. subtilis</i> , can repress transcription of translation-related genes. Molecular Microbiology, 2018, 111, 514-533.	2.5	20
10	Dysregulating ClpP: From Antibiotics to Anticancer?. Cell Chemical Biology, 2018, 25, 929-930.	5.2	6
11	Structural insight into protein-aided bacterial biofilm formation. Acta Crystallographica Section A: Foundations and Advances, 2018, 74, e206-e206.	0.1	0
12	Structure of the <i>Bacillus subtilis</i> hibernating 100S ribosome reveals the basis for 70S dimerization. EMBO Journal, 2017, 36, 2061-2072.	7.8	74
13	Functional Diversity of AAA+ Protease Complexes in <i>Bacillus subtilis</i> . Frontiers in Molecular Biosciences, 2017, 4, 44.	3.5	42
14	Regulatory coiled-coil domains promote head-to-head assemblies of AAA+ chaperones essential for tunable activity control. ELife, 2017, 6, .	6.0	32
15	Structural insight into protein-aided bacterial biofilm formation. Acta Crystallographica Section A: Foundations and Advances, 2017, 73, C391-C391.	0.1	0
16	Role of Hsp100/Clp Protease Complexes in Controlling the Regulation of Motility in <i>Bacillus subtilis</i> . Frontiers in Microbiology, 2016, 7, 315.	3.5	16
17	Exploring the diversity of protein modifications: special bacterial phosphorylation systems. FEMS Microbiology Reviews, 2016, 40, 398-417.	8.6	100
18	The role of thiol oxidative stress response in heat-induced protein aggregate formation during thermotolerance in <i>Bacillus subtilis</i> . Molecular Microbiology, 2014, 91, 1036-1052.	2.5	55

#	ARTICLE	IF	CITATIONS
19	The key to unlock the Hsp100/Clp protein degradation machines of <i>Mycobacterium</i> . <i>Molecular Microbiology</i> , 2014, 93, 583-586.	2.5	1
20	General and Regulatory Proteolysis in <i>Bacillus subtilis</i> . <i>Sub-Cellular Biochemistry</i> , 2013, 66, 73-103.	2.4	14
21	Global impact of protein arginine phosphorylation on the physiology of <i>Bacillus subtilis</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2012, 109, 7451-7456.	7.1	133
22	The antibiotic ADEP reprogrammes ClpP, switching it from a regulated to an uncontrolled protease. <i>EMBO Molecular Medicine</i> , 2009, 1, 37-49.	6.9	196
23	Adapting the machine: adaptor proteins for Hsp100/Clp and AAA+ proteases. <i>Nature Reviews Microbiology</i> , 2009, 7, 589-599.	28.6	232
24	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
25	Chaperone-protease systems in regulation and protein quality control in <i>Bacillus subtilis</i> . <i>Research in Microbiology</i> , 2009, 160, 637-644.	2.1	46
26	Proteolysis in prokaryotes – from molecular machines to a systems perspective. <i>Research in Microbiology</i> , 2009, 160, 615-617.	2.1	4
27	Roles of the two ClpC ATP binding sites in the regulation of competence and the stress response. <i>Molecular Microbiology</i> , 2008, 42, 717-727.	2.5	19
28	Conserved residues in the N-domain of the AAA+ chaperone ClpA regulate substrate recognition and unfolding. <i>FEBS Journal</i> , 2008, 275, 1400-1410.	4.7	24
29	Protein disaggregation by the AAA+ chaperone ClpB involves partial threading of looped polypeptide segments. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 641-650.	8.2	139
30	Localization of general and regulatory proteolysis in <i>Bacillus subtilis</i> cells. <i>Molecular Microbiology</i> , 2008, 70, 682-694.	2.5	48
31	The tyrosine kinase McsB is a regulated adaptor protein for ClpCP. <i>EMBO Journal</i> , 2007, 26, 2061-2070.	7.8	95
32	Adaptor protein controlled oligomerization activates the AAA+ protein ClpC. <i>EMBO Journal</i> , 2006, 25, 1481-1491.	7.8	127
33	Cyanobacterial ClpC/HSP100 Protein Displays Intrinsic Chaperone Activity. <i>Journal of Biological Chemistry</i> , 2006, 281, 5468-5475.	3.4	46
34	A tyrosine kinase and its activator control the activity of the CtsR heat shock repressor in <i>B. subtilis</i> . <i>EMBO Journal</i> , 2005, 24, 3435-3445.	7.8	108
35	A New Tyrosine Phosphorylation Mechanism Involved in Signal Transduction in <i>Bacillus subtilis</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2005, 9, 182-188.	1.0	43
36	Broad yet high substrate specificity: the challenge of AAA+ proteins. <i>Journal of Structural Biology</i> , 2004, 146, 90-98.	2.8	45

#	ARTICLE	IF	CITATIONS
37	MecA, an adaptor protein necessary for ClpC chaperone activity. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 2306-2311.	7.1	139
38	AAA+ proteins and substrate recognition, it all depends on their partner in crime. FEBS Letters, 2002, 529, 6-10.	2.8	193
39	The N- and C-terminal domains of MecA recognize different partners in the competence molecular switch. Molecular Microbiology, 1999, 33, 886-894.	2.5	76
40	Competence in Bacillus subtilis is controlled by regulated proteolysis of a transcription factor. EMBO Journal, 1998, 17, 6730-6738.	7.8	314
41	Physical identification of a chromosomal locus encoding biosynthetic genes for the lipopeptide calcium-dependent antibiotic (CDA) of Streptomyces coelicolor A3(2). Microbiology (United Kingdom), 1998, 144, 193-199.	1.8	58
42	Biochemical characterization of a molecular switch involving the heat shock protein ClpC, which controls the activity of ComK, the competence transcription factor of Bacillus subtilis.. Genes and Development, 1997, 11, 119-128.	5.9	186
43	ThegtcRSoperon coding for two-component system regulatory proteins is located adjacent to the grs operon of Bacillus brevis. DNA Sequence, 1995, 5, 283-290.	0.7	11
44	Four homologous domains in the primary structure of GrsB are related to domains in a superfamily of adenylate-forming enzymes. Molecular Microbiology, 1992, 6, 529-546.	2.5	246
45	Role of Proteolysis and Chaperones in Stress Response and Regulation. , 0, , 75-90.		4