

Bernd Bukau

List of Publications by Year in descending order

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159
papers

25,307
citations

3933

88
h-index

7348

152
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174
all docs

174
docs citations

174
times ranked

16342
citing authors

#	ARTICLE	IF	CITATIONS
1	The Hsp70 and Hsp60 Chaperone Machines. <i>Cell</i> , 1998, 92, 351-366.	28.9	2,634
2	Molecular Chaperones and Protein Quality Control. <i>Cell</i> , 2006, 125, 443-451.	28.9	1,352
3	Cellular strategies for controlling protein aggregation. <i>Nature Reviews Molecular Cell Biology</i> , 2010, 11, 777-788.	37.0	785
4	The Hsp70 chaperone network. <i>Nature Reviews Molecular Cell Biology</i> , 2019, 20, 665-680.	37.0	721
5	Trigger factor and DnaK cooperate in folding of newly synthesized proteins. <i>Nature</i> , 1999, 400, 693-696.	27.8	465
6	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
7	The ribosome as a platform for co-translational processing, folding and targeting of newly synthesized proteins. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 589-597.	8.2	420
8	Selective Ribosome Profiling Reveals the Cotranslational Chaperone Action of Trigger Factor In Vivo. <i>Cell</i> , 2011, 147, 1295-1308.	28.9	419
9	Getting Newly Synthesized Proteins into Shape. <i>Cell</i> , 2000, 101, 119-122.	28.9	406
10	Regulation of the Escherichia coli heat-shock response. <i>Molecular Microbiology</i> , 1993, 9, 671-680.	2.5	365
11	Trigger factor in complex with the ribosome forms a molecular cradle for nascent proteins. <i>Nature</i> , 2004, 431, 590-596.	27.8	347
12	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
13	Human Hsp70 Disaggregase Reverses Parkinson's-Linked α -Synuclein Amyloid Fibrils. <i>Molecular Cell</i> , 2015, 59, 781-793.	9.7	336
14	Multistep mechanism of substrate binding determines chaperone activity of Hsp70. <i>Nature Structural Biology</i> , 2000, 7, 586-593.	9.7	335
15	Crucial HSP70 co-chaperone complex unlocks metazoan protein disaggregation. <i>Nature</i> , 2015, 524, 247-251.	27.8	320
16	L23 protein functions as a chaperone docking site on the ribosome. <i>Nature</i> , 2002, 419, 171-174.	27.8	309
17	Genetic dissection of the roles of chaperones and proteases in protein folding and degradation in the Escherichia coli cytosol. <i>Molecular Microbiology</i> , 2001, 40, 397-413.	2.5	302
18	Metazoan Hsp70 machines use Hsp110 to power protein disaggregation. <i>EMBO Journal</i> , 2012, 31, 4221-4235.	7.8	284

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19	Cellular Handling of Protein Aggregates by Disaggregation Machines. <i>Molecular Cell</i> , 2018, 69, 214-226.	9.7	280
20	ClpS, a Substrate Modulator of the ClpAP Machine. <i>Molecular Cell</i> , 2002, 9, 673-683.	9.7	270
21	Cotranslational assembly of protein complexes in eukaryotes revealed by ribosome profiling. <i>Nature</i> , 2018, 561, 268-272.	27.8	266
22	The N-end rule pathway for regulated proteolysis: prokaryotic and eukaryotic strategies. <i>Trends in Cell Biology</i> , 2007, 17, 165-172.	7.9	258
23	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
24	Chaperone network in the yeast cytosol: Hsp110 is revealed as an Hsp70 nucleotide exchange factor. <i>EMBO Journal</i> , 2006, 25, 2510-2518.	7.8	243
25	Compartment-specific aggregases direct distinct nuclear and cytoplasmic aggregate deposition. <i>EMBO Journal</i> , 2015, 34, 778-797.	7.8	243
26	Quantitative and spatio-temporal features of protein aggregation in <i>Escherichia coli</i> and consequences on protein quality control and cellular ageing. <i>EMBO Journal</i> , 2010, 29, 910-923.	7.8	241
27	Nucleotide-induced Conformational Changes in the ATPase and Substrate Binding Domains of the DnaK Chaperone Provide Evidence for Interdomain Communication. <i>Journal of Biological Chemistry</i> , 1995, 270, 16903-16910.	3.4	233
28	Hsp42 is required for sequestration of protein aggregates into deposition sites in <i>Saccharomyces cerevisiae</i> . <i>Journal of Cell Biology</i> , 2011, 195, 617-629.	5.2	233
29	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
30	Substrate recognition by the AAA+ chaperone ClpB. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 607-615.	8.2	219
31	Structure and function of the molecular chaperone Trigger Factor. <i>Biochimica Et Biophysica Acta - Molecular Cell Research</i> , 2010, 1803, 650-661.	4.1	210
32	The Second Step of ATP Binding to DnaK Induces Peptide Release. <i>Journal of Molecular Biology</i> , 1996, 263, 657-670.	4.2	209
33	Size-dependent Disaggregation of Stable Protein Aggregates by the DnaK Chaperone Machinery. <i>Journal of Biological Chemistry</i> , 2000, 275, 21107-21113.	3.4	207
34	Tuning of chaperone activity of Hsp70 proteins by modulation of nucleotide exchange. <i>Nature Structural Biology</i> , 2001, 8, 427-432.	9.7	205
35	Allosteric Regulation of Hsp70 Chaperones Involves a Conserved Interdomain Linker. <i>Journal of Biological Chemistry</i> , 2006, 281, 38705-38711.	3.4	196
36	Hsp70 targets Hsp100 chaperones to substrates for protein disaggregation and prion fragmentation. <i>Journal of Cell Biology</i> , 2012, 198, 387-404.	5.2	196

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37	Coordination of Translational Control and Protein Homeostasis during Severe Heat Stress. <i>Current Biology</i> , 2013, 23, 2452-2462.	3.9	191
38	Levels of DnaK and DnaJ provide tight control of heat shock gene expression and protein repair in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 1998, 30, 567-581.	2.5	185
39	Mechanics of Hsp70 chaperones enables differential interaction with client proteins. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 345-351.	8.2	181
40	Trigger Factor and DnaK possess overlapping substrate pools and binding specificities. <i>Molecular Microbiology</i> , 2003, 47, 1317-1328.	2.5	174
41	Substrate threading through the central pore of the Hsp104 chaperone as a common mechanism for protein disaggregation and prion propagation. <i>Molecular Microbiology</i> , 2008, 68, 87-97.	2.5	171
42	Alternative modes of client binding enable functional plasticity of Hsp70. <i>Nature</i> , 2016, 539, 448-451.	27.8	167
43	Allosteric Regulation of Hsp70 Chaperones by a Proline Switch. <i>Molecular Cell</i> , 2006, 21, 359-367.	9.7	166
44	Spatially Organized Aggregation of Misfolded Proteins as Cellular Stress Defense Strategy. <i>Journal of Molecular Biology</i> , 2015, 427, 1564-1574.	4.2	164
45	Functional Analysis of Hsp70 Inhibitors. <i>PLoS ONE</i> , 2013, 8, e78443.	2.5	160
46	Operon structure and cotranslational subunit association direct protein assembly in bacteria. <i>Science</i> , 2015, 350, 678-680.	12.6	160
47	The growing world of small heat shock proteins: from structure to functions. <i>Cell Stress and Chaperones</i> , 2017, 22, 601-611.	2.9	158
48	Profiling Ssb-Nascent Chain Interactions Reveals Principles of Hsp70-Assisted Folding. <i>Cell</i> , 2017, 170, 298-311.e20.	28.9	154
49	M Domains Couple the ClpB Threading Motor with the DnaK Chaperone Activity. <i>Molecular Cell</i> , 2007, 25, 247-260.	9.7	153
50	Molecular dissection of amyloid disaggregation by human HSP70. <i>Nature</i> , 2020, 587, 483-488.	27.8	153
51	Hsp70 proteins bind Hsp100 regulatory M domains to activate AAA+ disaggregase at aggregate surfaces. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1347-1355.	8.2	152
52	Molecular Basis for Regulation of the Heat Shock Transcription Factor σ 32 by the DnaK and DnaJ Chaperones. <i>Molecular Cell</i> , 2008, 32, 347-358.	9.7	151
53	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
54	Bag-1M Accelerates Nucleotide Release for Human Hsc70 and Hsp70 and Can Act Concentration-dependent as Positive and Negative Cofactor. <i>Journal of Biological Chemistry</i> , 2001, 276, 32538-32544.	3.4	146

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55	Molecular mechanism and structure of Trigger Factor bound to the translating ribosome. <i>EMBO Journal</i> , 2008, 27, 1622-1632.	7.8	142
56	Hsp110 Is a Nucleotide-activated Exchange Factor for Hsp70. <i>Journal of Biological Chemistry</i> , 2008, 283, 8877-8884.	3.4	142
57	Substrate Shuttling Between the DnaK and GroEL Systems Indicates a Chaperone Network Promoting Protein Folding. <i>Journal of Molecular Biology</i> , 1996, 261, 328-333.	4.2	140
58	Characterization of a Trap Mutant of the AAA+ Chaperone ClpB. <i>Journal of Biological Chemistry</i> , 2003, 278, 32608-32617.	3.4	140
59	Cooperation of Hsp70 and Hsp100 chaperone machines in protein disaggregation. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 22.	3.5	140
60	HSP40 proteins use class-specific regulation to drive HSP70 functional diversity. <i>Nature</i> , 2020, 587, 489-494.	27.8	140
61	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
62	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
63	Mechanisms of Cotranslational Maturation of Newly Synthesized Proteins. <i>Annual Review of Biochemistry</i> , 2019, 88, 337-364.	11.1	138
64	Substrate Specificity of the SecB Chaperone. <i>Journal of Biological Chemistry</i> , 1999, 274, 34219-34225.	3.4	137
65	Translation suppression promotes stress granule formation and cell survival in response to cold shock. <i>Molecular Biology of the Cell</i> , 2012, 23, 3786-3800.	2.1	137
66	Co-translational mechanisms of protein maturation. <i>Current Opinion in Structural Biology</i> , 2014, 24, 24-33.	5.7	128
67	Cellular Functions and Mechanisms of Action of Small Heat Shock Proteins. <i>Annual Review of Microbiology</i> , 2019, 73, 89-110.	7.3	127
68	Investigation of the Interaction between DnaK and DnaJ by Surface Plasmon Resonance Spectroscopy. <i>Journal of Molecular Biology</i> , 1999, 289, 1131-1144.	4.2	126
69	Global profiling of SRP interaction with nascent polypeptides. <i>Nature</i> , 2016, 536, 219-223.	27.8	125
70	A conserved loop in the ATPase domain of the DnaK chaperone is essential for stable binding of GrpE. <i>Nature Structural and Molecular Biology</i> , 1994, 1, 95-101.	8.2	124
71	A tightly regulated molecular toggle controls AAA+ disaggregase. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1338-1346.	8.2	124
72	Chaperone networks in protein disaggregation and prion propagation. <i>Journal of Structural Biology</i> , 2012, 179, 152-160.	2.8	121

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73	Hsp70 displaces small heat shock proteins from aggregates to initiate protein refolding. <i>EMBO Journal</i> , 2017, 36, 783-796.	7.8	120
74	Heat shock regulation in the ftsH null mutant of <i>Escherichia coli</i> : dissection of stability and activity control mechanisms of sigma32 in vivo. <i>Molecular Microbiology</i> , 1998, 30, 583-593.	2.5	118
75	Reshaping of the conformational search of a protein by the chaperone trigger factor. <i>Nature</i> , 2013, 500, 98-101.	27.8	118
76	Structural analysis of the adaptor protein ClpS in complex with the N-terminal domain of ClpA. <i>Nature Structural Biology</i> , 2002, 9, 906-911.	9.7	115
77	Selective ribosome profiling as a tool for studying the interaction of chaperones and targeting factors with nascent polypeptide chains and ribosomes. <i>Nature Protocols</i> , 2013, 8, 2212-2239.	12.0	112
78	Structural pathway of regulated substrate transfer and threading through an Hsp100 disaggregase. <i>Science Advances</i> , 2017, 3, e1701726.	10.3	112
79	Molecular Basis for Interactions of the DnaK Chaperone with Substrates. <i>Biological Chemistry</i> , 2000, 381, 877-85.	2.5	111
80	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
81	Pathways of allosteric regulation in Hsp70 chaperones. <i>Nature Communications</i> , 2015, 6, 8308.	12.8	110
82	Chaperone-Assisted Folding of Newly Synthesized Proteins in the Cytosol. <i>Critical Reviews in Biochemistry and Molecular Biology</i> , 2004, 39, 261-277.	5.2	109
83	Protein Disaggregation in Multicellular Organisms. <i>Trends in Biochemical Sciences</i> , 2018, 43, 285-300.	7.5	103
84	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
85	Metazoan Hsp70-based protein disaggregases: emergence and mechanisms. <i>Frontiers in Molecular Biosciences</i> , 2015, 2, 57.	3.5	101
86	Selective 40S Footprinting Reveals Cap-Tethered Ribosome Scanning in Human Cells. <i>Molecular Cell</i> , 2020, 79, 561-574.e5.	9.7	96
87	Trigger Factor Peptidyl-prolyl cis/trans Isomerase Activity Is Not Essential for the Folding of Cytosolic Proteins in <i>Escherichia coli</i> . <i>Journal of Biological Chemistry</i> , 2004, 279, 14165-14170.	3.4	94
88	Concerted Action of the Ribosome and the Associated Chaperone Trigger Factor Confines Nascent Polypeptide Folding. <i>Molecular Cell</i> , 2012, 48, 63-74.	9.7	94
89	A peptide deformylase-ribosome complex reveals mechanism of nascent chain processing. <i>Nature</i> , 2008, 452, 108-111.	27.8	93
90	The Amino-terminal 118 Amino Acids of <i>Escherichia coli</i> Trigger Factor Constitute a Domain That Is Necessary and Sufficient for Binding to Ribosomes. <i>Journal of Biological Chemistry</i> , 1997, 272, 21865-21871.	3.4	92

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91	Novel insights into the mechanism of chaperone-assisted protein disaggregation. <i>Biological Chemistry</i> , 2005, 386, 739-44.	2.5	92
92	Role of sHsps in organizing cytosolic protein aggregation and disaggregation. <i>Cell Stress and Chaperones</i> , 2017, 22, 493-502.	2.9	92
93	Processive extrusion of polypeptide loops by a Hsp100 disaggregase. <i>Nature</i> , 2020, 578, 317-320.	27.8	92
94	Three-State Equilibrium of <i>Escherichia coli</i> Trigger Factor. <i>Biological Chemistry</i> , 2002, 383, 1611-9.	2.5	90
95	SecA Interacts with Ribosomes in Order to Facilitate Posttranslational Translocation in Bacteria. <i>Molecular Cell</i> , 2011, 41, 343-353.	9.7	90
96	Dynamics of Trigger Factor Interaction with Translating Ribosomes. <i>Journal of Biological Chemistry</i> , 2008, 283, 4124-4132.	3.4	82
97	Integrating Protein Homeostasis Strategies in Prokaryotes. <i>Cold Spring Harbor Perspectives in Biology</i> , 2011, 3, a004366-a004366.	5.5	82
98	The C-terminal Domain of <i>Escherichia coli</i> Trigger Factor Represents the Central Module of Its Chaperone Activity. <i>Journal of Biological Chemistry</i> , 2006, 281, 31963-31971.	3.4	81
99	Interactions between nascent proteins translated by adjacent ribosomes drive homomer assembly. <i>Science</i> , 2021, 371, 57-64.	12.6	80
100	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
101	ClpS is the recognition component for <i>Escherichia coli</i> substrates of the N-end rule degradation pathway. <i>Molecular Microbiology</i> , 2009, 72, 506-517.	2.5	76
102	Trigger Factor Forms a Protective Shield for Nascent Polypeptides at the Ribosome. <i>Journal of Biological Chemistry</i> , 2006, 281, 6539-6545.	3.4	75
103	Identification of the prolyl isomerase domain of <i>Escherichia coli</i> trigger factor. <i>FEBS Letters</i> , 1996, 385, 67-71.	2.8	74
104	Trigger Factor Reduces the Force Exerted on the Nascent Chain by a Cotranslationally Folding Protein. <i>Journal of Molecular Biology</i> , 2016, 428, 1356-1364.	4.2	74
105	Incomplete proteasomal degradation of green fluorescent proteins in the context of tandem fluorescent protein timers. <i>Molecular Biology of the Cell</i> , 2016, 27, 360-370.	2.1	72
106	Insights into the structural dynamics of the Hsp110-Hsp70 interaction reveal the mechanism for nucleotide exchange activity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2008, 105, 16519-16524.	7.1	70
107	Common and specific mechanisms of AAA+ proteins involved in protein quality control. <i>Biochemical Society Transactions</i> , 2008, 36, 120-125.	3.4	70
108	Hsp110 Chaperones Regulate Prion Formation and Propagation in <i>S. cerevisiae</i> by Two Discrete Activities. <i>PLoS ONE</i> , 2008, 3, e1763.	2.5	69

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109	The Yeast AAA ⁺ Chaperone Hsp104 Is Part of a Network That Links the Actin Cytoskeleton with the Inheritance of Damaged Proteins. <i>Molecular and Cellular Biology</i> , 2009, 29, 3738-3745.	2.3	66
110	GPD1 Specifically Marks Dormant Glioma Stem Cells with a Distinct Metabolic Profile. <i>Cell Stem Cell</i> , 2019, 25, 241-257.e8.	11.1	66
111	Modulation of substrate specificity of the DnaK chaperone by alteration of a hydrophobic arch. <i>Journal of Molecular Biology</i> , 2000, 304, 245-251.	4.2	65
112	Modulation of Amyloid States by Molecular Chaperones. <i>Cold Spring Harbor Perspectives in Biology</i> , 2019, 11, a033969.	5.5	63
113	Human and yeast Hsp110 chaperones exhibit functional differences. <i>FEBS Letters</i> , 2006, 580, 168-174.	2.8	62
114	Evolution of an intricate J-protein network driving protein disaggregation in eukaryotes. <i>ELife</i> , 2017, 6, .	6.0	60
115	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
116	SecA Cotranslationally Interacts with Nascent Substrate Proteins <i>In Vivo</i> . <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	59
117	Dynamic enzyme docking to the ribosome coordinates N-terminal processing with polypeptide folding. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 843-850.	8.2	58
118	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
119	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.. <i>Biochemistry and Cell Biology</i> , 2010, 88, 63-75.	2.0	56
120	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
121	<i>In vivo</i> properties of the disaggregase function of Hsp70 proteins and Hsc70 in <i>Caenorhabditis elegans</i> stress and aging. <i>Aging Cell</i> , 2017, 16, 1414-1424.	6.7	53
122	The HSP110/HSP70 disaggregation system generates spreading-competent toxic α -synuclein species. <i>EMBO Journal</i> , 2020, 39, e103954.	7.8	53
123	The Diverse Functions of Small Heat Shock Proteins in the Proteostasis Network. <i>Journal of Molecular Biology</i> , 2022, 434, 167157.	4.2	53
124	Functional Dissection of Trigger Factor and DnaK: Interactions with Nascent Polypeptides and Thermally Denatured Proteins. <i>Biological Chemistry</i> , 2001, 382, 1235-43.	2.5	51
125	Mapping Temperature-induced Conformational Changes in the Escherichia coli Heat Shock Transcription Factor σ 32 by Amide Hydrogen Exchange. <i>Journal of Biological Chemistry</i> , 2003, 278, 51415-51421.	3.4	50
126	Cellular sequestrases maintain basal Hsp70 capacity ensuring balanced proteostasis. <i>Nature Communications</i> , 2019, 10, 4851.	12.8	49

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127	The Endoplasmic Reticulum Grp170 Acts as a Nucleotide Exchange Factor of Hsp70 via a Mechanism Similar to That of the Cytosolic Hsp110. <i>Journal of Biological Chemistry</i> , 2010, 285, 12445-12453.	3.4	46
128	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
129	Structure-Function Analysis of HscC, the <i>Escherichia coli</i> Member of a Novel Subfamily of Specialized Hsp70 Chaperones. <i>Journal of Biological Chemistry</i> , 2002, 277, 41060-41069.	3.4	45
130	Accurate prediction of cellular co-translational folding indicates proteins can switch from post- to co-translational folding. <i>Nature Communications</i> , 2016, 7, 10341.	12.8	45
131	Role of Region C in Regulation of the Heat Shock Gene-Specific Sigma Factor of <i>Escherichia coli</i> , σ^{32} . <i>Journal of Bacteriology</i> , 1999, 181, 3552-3561.	2.2	45
132	Chaperone-Mediated Protein Disaggregation Triggers Proteolytic Clearance of Intra-nuclear Protein Inclusions. <i>Cell Reports</i> , 2020, 31, 107680.	6.4	43
133	Large-scale purification of ribosome nascent chain complexes for biochemical and structural studies. <i>FEBS Letters</i> , 2009, 583, 2407-2413.	2.8	41
134	Functional diversity between HSP70 paralogs caused by variable interactions with specific co-chaperones. <i>Journal of Biological Chemistry</i> , 2020, 295, 7301-7316.	3.4	39
135	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
136	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
137	Structural analysis of a signal peptide inside the ribosome tunnel by DNP MAS NMR. <i>Science Advances</i> , 2016, 2, e1600379.	10.3	33
138	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
139	Principles of general and regulatory proteolysis by AAA+ proteases in <i>Escherichia coli</i> . <i>Research in Microbiology</i> , 2009, 160, 629-636.	2.1	31
140	Substrate binding by the yeast Hsp110 nucleotide exchange factor and molecular chaperone Sse1 is not obligate for its biological activities. <i>Molecular Biology of the Cell</i> , 2017, 28, 2066-2075.	2.1	31
141	Hormesis enables cells to handle accumulating toxic metabolites during increased energy flux. <i>Redox Biology</i> , 2017, 13, 674-686.	9.0	31
142	Physical Origins of Codon Positions That Strongly Influence Cotranslational Folding: A Framework for Controlling Nascent-Protein Folding. <i>Journal of the American Chemical Society</i> , 2016, 138, 1180-1195.	13.7	27
143	Bacterial ribosome collision sensing by a MutS DNA repair ATPase paralogue. <i>Nature</i> , 2022, 603, 509-514.	27.8	27
144	N \pm -terminal acetylation of proteins by NatA and NatB serves distinct physiological roles in <i>Saccharomyces cerevisiae</i> . <i>Cell Reports</i> , 2021, 34, 108711.	6.4	26

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145	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
146	Mechanism of Hsp104/ClpB inhibition by prion curing Guanidinium hydrochloride. <i>FEBS Letters</i> , 2013, 587, 810-817.	2.8	20
147	Monitoring Protein Misfolding by Site-Specific Labeling of Proteins In Vivo. <i>PLoS ONE</i> , 2014, 9, e99395.	2.5	20
148	Poly-L-lysine enhances the protein disaggregation activity of ClpB. <i>FEBS Letters</i> , 2003, 553, 125-130.	2.8	14
149	Cooperative amyloid fibre binding and disassembly by the Hsp70 disaggregase. <i>EMBO Journal</i> , 2022, 41, .	7.8	14
150	The C-terminal Domain of Escherichia coli Trigger Factor Represents the Central Module of Its Chaperone Activity. <i>Journal of Biological Chemistry</i> , 2006, 281, 31963-31971.	3.4	10
151	Pairs of amino acids at the P- and A-sites of the ribosome predictably and causally modulate translation-elongation rates. <i>Journal of Molecular Biology</i> , 2020, 432, 166696.	4.2	9
152	The C-terminal tail of the bacterial translocation ATPase SecA modulates its activity. <i>ELife</i> , 2019, 8, .	6.0	9
153	Mitochondria Tether Protein Trash to Rejuvenate Cellular Environments. <i>Cell</i> , 2014, 159, 471-472.	28.9	8
154	Mutant Analysis Reveals Allosteric Regulation of ClpB Disaggregase. <i>Frontiers in Molecular Biosciences</i> , 2017, 4, 6.	3.5	8
155	Nucleotide Exchange Factors for Hsp70 Chaperones. <i>Methods in Molecular Biology</i> , 2018, 1709, 179-188.	0.9	7
156	Role for ribosome-associated complex and stress-seventy subfamily B (RAC-Ssb) in integral membrane protein translation. <i>Journal of Biological Chemistry</i> , 2017, 292, 19610-19627.	3.4	4
157	Translational Regulation of Pmt1 and Pmt2 by Bfr1 Affects Unfolded Protein O-Mannosylation. <i>International Journal of Molecular Sciences</i> , 2019, 20, 6220.	4.1	4
158	Combinations of slow-translating codon clusters can increase mRNA half-life in <i>Saccharomyces cerevisiae</i> . <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	2
159	Finding nascent proteins the right home. <i>Science</i> , 2015, 348, 182-183.	12.6	1