

Manajit Hayer-Hartl

List of Publications by Year in Descending Order

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The third column is the impact factor (IF) of the journal, and the fourth column is the number of citations of the article.

95
papers

16,425
citations

47
h-index

128
g-index

136
ext. papers

18,546
ext. citations

22
avg, IF

6.9
L-index

#	Paper	IF	Citations
95	Scaffolding protein CcmM directs multiprotein phase separation in β -carboxysome biogenesis. <i>Nature Structural and Molecular Biology</i> , 2021 , 28, 909-922	17.6	3
94	Bacterial RF3 senses chaperone function in co-translational folding. <i>Molecular Cell</i> , 2021 , 81, 2914-2928.e7	7.6	2
93	Chaperone Machineries of Rubisco - The Most Abundant Enzyme. <i>Trends in Biochemical Sciences</i> , 2020 , 45, 748-763	10.3	16
92	Efficient Catalysis of Protein Folding by GroEL/ES of the Obligate Chaperonin Substrate MetF. <i>Journal of Molecular Biology</i> , 2020 , 432, 2304-2318	6.5	8
91	Bacterial Hsp70 resolves misfolded states and accelerates productive folding of a multi-domain protein. <i>Nature Communications</i> , 2020 , 11, 365	17.4	43
90	Structure and conformational cycle of a bacteriophage-encoded chaperonin. <i>PLoS ONE</i> , 2020 , 15, e0230090	3.9	6
89	Cellular Machineries Devoted to Rubisco [The Most Abundant Enzyme]. <i>FASEB Journal</i> , 2020 , 34, 1-1	0.9	1
88	Dual Functions of a Rubisco Activase in Metabolic Repair and Recruitment to Carboxysomes. <i>Cell</i> , 2020 , 183, 457-473.e20	56.2	9
87	Recent advances in understanding catalysis of protein folding by molecular chaperones. <i>FEBS Letters</i> , 2020 , 594, 2770-2781	3.8	37
86	Rubisco condensate formation by CcmM in β -carboxysome biogenesis. <i>Nature</i> , 2019 , 566, 131-135	50.4	102
85	Crystal structure of phosphoribulokinase from <i>Synechococcus</i> sp. strain PCC 6301. <i>Acta Crystallographica Section F, Structural Biology Communications</i> , 2019 , 75, 278-289	1.1	5
84	The Hsp70 Chaperone System Stabilizes a Thermo-sensitive Subproteome in <i>E. coli</i> . <i>Cell Reports</i> , 2019 , 28, 1335-1345.e6	10.6	20
83	Improved recombinant expression and purification of functional plant Rubisco. <i>FEBS Letters</i> , 2019 , 593, 611-621	3.8	20
82	GroEL Ring Separation and Exchange in the Chaperonin Reaction. <i>Cell</i> , 2018 , 172, 605-617.e11	56.2	33
81	Complex Chaperone Dependence of Rubisco Biogenesis. <i>Biochemistry</i> , 2018 , 57, 3210-3216	3.2	29
80	Pathway of Actin Folding Directed by the Eukaryotic Chaperonin TRiC. <i>Cell</i> , 2018 , 174, 1507-1521.e16	56.2	36
79	Tc toxin activation requires unfolding and refolding of a β -propeller. <i>Nature</i> , 2018 , 563, 209-213	50.4	24

78	Biogenesis and Metabolic Maintenance of Rubisco. <i>Annual Review of Plant Biology</i> , 2017 , 68, 29-60	30.7	126
77	From chaperonins to Rubisco assembly and metabolic repair. <i>Protein Science</i> , 2017 , 26, 2324-2333	6.3	17
76	Mechanism of Enzyme Repair by the AAA Chaperone Rubisco Activase. <i>Molecular Cell</i> , 2017 , 67, 744-756	16.6	30
75	Plant RuBisCo assembly in with five chloroplast chaperones including BSD2. <i>Science</i> , 2017 , 358, 1272-1278	39.3	112
74	Rubisco Activases: AAA+ Chaperones Adapted to Enzyme Repair. <i>Frontiers in Molecular Biosciences</i> , 2017 , 4, 20	5.6	38
73	Soluble Oligomers of PolyQ-Expanded Huntingtin Target a Multiplicity of Key Cellular Factors. <i>Molecular Cell</i> , 2016 , 63, 951-64	17.6	115
72	In vivo aspects of protein folding and quality control. <i>Science</i> , 2016 , 353, aac4354	33.3	726
71	Failure of RQC machinery causes protein aggregation and proteotoxic stress. <i>Nature</i> , 2016 , 531, 191-5	50.4	129
70	Structure of human heat-shock transcription factor 1 in complex with DNA. <i>Nature Structural and Molecular Biology</i> , 2016 , 23, 140-6	17.6	62
69	The GroEL-GroES Chaperonin Machine: A Nano-Cage for Protein Folding. <i>Trends in Biochemical Sciences</i> , 2016 , 41, 62-76	10.3	205
68	Structure and mechanism of the Rubisco-assembly chaperone Raf1. <i>Nature Structural and Molecular Biology</i> , 2015 , 22, 720-8	17.6	45
67	Chaperonin-Assisted Protein Folding: Relative Population of Asymmetric and Symmetric GroEL:GroES Complexes. <i>Journal of Molecular Biology</i> , 2015 , 427, 2244-55	6.5	29
66	Degradation of potent Rubisco inhibitor by selective sugar phosphatase. <i>Nature Plants</i> , 2015 , 1, 14002	11.5	30
65	Role of auxiliary proteins in Rubisco biogenesis and function. <i>Nature Plants</i> , 2015 , 1, 15065	11.5	68
64	Structural Analysis of the Rubisco-Assembly Chaperone RbcX-II from <i>Chlamydomonas reinhardtii</i> . <i>PLoS ONE</i> , 2015 , 10, e0135448	3.7	11
63	Opposing effects of folding and assembly chaperones on evolvability of Rubisco. <i>Nature Chemical Biology</i> , 2015 , 11, 148-55	11.7	67
62	Role of small subunit in mediating assembly of red-type form I Rubisco. <i>Journal of Biological Chemistry</i> , 2015 , 290, 1066-74	5.4	23
61	Interplay of acetyltransferase EP300 and the proteasome system in regulating heat shock transcription factor 1. <i>Cell</i> , 2014 , 156, 975-85	56.2	106

60	Active cage mechanism of chaperonin-assisted protein folding demonstrated at single-molecule level. <i>Journal of Molecular Biology</i> , 2014 , 426, 2739-54	6.5	41
59	GroEL/ES chaperonin modulates the mechanism and accelerates the rate of TIM-barrel domain folding. <i>Cell</i> , 2014 , 157, 922-934	56.2	92
58	The first chaperonin. <i>Nature Reviews Molecular Cell Biology</i> , 2013 , 14, 611	48.7	3
57	PolyQ proteins interfere with nuclear degradation of cytosolic proteins by sequestering the Sis1p chaperone. <i>Cell</i> , 2013 , 154, 134-45	56.2	255
56	Molecular chaperone functions in protein folding and proteostasis. <i>Annual Review of Biochemistry</i> , 2013 , 82, 323-55	29.1	937
55	DnaK functions as a central hub in the E. coli chaperone network. <i>Cell Reports</i> , 2012 , 1, 251-64	10.6	233
54	Chaperonin cofactors, Cpn10 and Cpn20, of green algae and plants function as hetero-oligomeric ring complexes. <i>Journal of Biological Chemistry</i> , 2012 , 287, 20471-81	5.4	39
53	Structure of green-type Rubisco activase from tobacco. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 1366-70	17.6	89
52	Amyloid-like aggregates sequester numerous metastable proteins with essential cellular functions. <i>Cell</i> , 2011 , 144, 67-78	56.2	520
51	Molecular chaperones in protein folding and proteostasis. <i>Nature</i> , 2011 , 475, 324-32	50.4	2147
50	Structure and function of the AAA+ protein CbbX, a red-type Rubisco activase. <i>Nature</i> , 2011 , 479, 194-9	50.4	117
49	Crystal structure of a chaperone-bound assembly intermediate of form I Rubisco. <i>Nature Structural and Molecular Biology</i> , 2011 , 18, 875-80	17.6	50
48	Coupled chaperone action in folding and assembly of hexadecameric Rubisco. <i>Nature</i> , 2010 , 463, 197-203	50.4	143
47	Protein folding in the cytoplasm and the heat shock response. <i>Cold Spring Harbor Perspectives in Biology</i> , 2010 , 2, a004390	10.2	270
46	Chaperonin-catalyzed rescue of kinetically trapped states in protein folding. <i>Cell</i> , 2010 , 142, 112-22	56.2	111
45	Role of Molecular Chaperones in Protein Folding 2010 , 47-72		3
44	Differential substrate specificity of group I and group II chaperonins in the archaeon <i>Methanosarcina mazei</i> . <i>Molecular Microbiology</i> , 2009 , 74, 1152-68	4.1	38
43	Converging concepts of protein folding in vitro and in vivo. <i>Nature Structural and Molecular Biology</i> , 2009 , 16, 574-81	17.6	827

42	Essential role of the chaperonin folding compartment in vivo. <i>EMBO Journal</i> , 2008 , 27, 1458-68	13	58
41	Monitoring protein conformation along the pathway of chaperonin-assisted folding. <i>Cell</i> , 2008 , 133, 1425-32	56.2	139
40	SnapShot: molecular chaperones, Part I. <i>Cell</i> , 2007 , 128, 212	56.2	47
39	SnapShot: molecular chaperones, Part II. <i>Cell</i> , 2007 , 128, 412	56.2	30
38	Structure and function of RbcX, an assembly chaperone for hexadecameric Rubisco. <i>Cell</i> , 2007 , 129, 1189-200	56.2	107
37	A simple semiempirical model for the effect of molecular confinement upon the rate of protein folding. <i>Biochemistry</i> , 2006 , 45, 13356-60	3.2	44
36	Structural features of the GroEL-GroES nano-cage required for rapid folding of encapsulated protein. <i>Cell</i> , 2006 , 125, 903-14	56.2	244
35	Structural basis for subunit assembly in UDP-glucose pyrophosphorylase from <i>Saccharomyces cerevisiae</i> . <i>Journal of Molecular Biology</i> , 2006 , 364, 551-60	6.5	33
34	Real-time observation of trigger factor function on translating ribosomes. <i>Nature</i> , 2006 , 444, 455-60	50.4	175
33	How to orient the functional GroEL-SR1 mutant for atomic force microscopy investigations. <i>Biochemical and Biophysical Research Communications</i> , 2005 , 328, 477-83	3.4	10
32	Proteome-wide analysis of chaperonin-dependent protein folding in <i>Escherichia coli</i> . <i>Cell</i> , 2005 , 122, 209-20	56.2	515
31	Functional characterization of an archaeal GroEL/GroES chaperonin system: significance of substrate encapsulation. <i>Journal of Biological Chemistry</i> , 2004 , 279, 1090-9	5.4	25
30	A mobile loop order-disorder transition modulates the speed of chaperonin cycling. <i>Protein Science</i> , 2004 , 13, 2139-48	6.3	16
29	Cellular toxicity of polyglutamine expansion proteins: mechanism of transcription factor deactivation. <i>Molecular Cell</i> , 2004 , 15, 95-105	17.6	349
28	Function of trigger factor and DnaK in multidomain protein folding: increase in yield at the expense of folding speed. <i>Cell</i> , 2004 , 117, 199-209	56.2	172
27	Coexistence of group I and group II chaperonins in the archaeon <i>Methanosarcina mazei</i> . <i>Journal of Biological Chemistry</i> , 2003 , 278, 33256-67	5.4	56
26	The protein import motor of mitochondria: a targeted molecular ratchet driving unfolding and translocation. <i>EMBO Journal</i> , 2002 , 21, 3659-71	13	91
25	Structural plasticity and noncovalent substrate binding in the GroEL apical domain. A study using electrospray ionization mass spectrometry and fluorescence binding studies. <i>Journal of Biological Chemistry</i> , 2002 , 277, 33115-26	5.4	28

24	Molecular chaperones as modulators of polyglutamine protein aggregation and toxicity. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2002 , 99 Suppl 4, 16412-8	11.5	190
23	Molecular chaperones in the cytosol: from nascent chain to folded protein. <i>Science</i> , 2002 , 295, 1852-8	33.3	2738
22	Geldanamycin activates a heat shock response and inhibits huntingtin aggregation in a cell culture model of Huntington ^Q disease. <i>Human Molecular Genetics</i> , 2001 , 10, 1307-15	5.6	346
21	Nitric oxide inhibits the cochaperone activity of the RING finger-like protein DnaJ. <i>Nitric Oxide - Biology and Chemistry</i> , 2001 , 5, 289-95	5	10
20	Dual function of protein confinement in chaperonin-assisted protein folding. <i>Cell</i> , 2001 , 107, 223-33	56.2	253
19	Prevention of rhodanese aggregation by the chaperonin GroEL. <i>Methods in Molecular Biology</i> , 2000 , 140, 111-5	1.4	7
18	Hsp70 and hsp40 chaperones can inhibit self-assembly of polyglutamine proteins into amyloid-like fibrils. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2000 , 97, 7841-6	11.5	541
17	Refolding of bovine mitochondrial rhodanese by chaperonins GroEL and GroES. <i>Methods in Molecular Biology</i> , 2000 , 140, 117-26	1.4	11
16	Assay of malate dehydrogenase. A substrate for the E. coli chaperonins GroEL and GroES. <i>Methods in Molecular Biology</i> , 2000 , 140, 127-32	1.4	15
15	On the role of symmetrical and asymmetrical chaperonin complexes in assisted protein folding. <i>Biological Chemistry</i> , 1999 , 380, 531-40	4.5	18
14	The oligomeric structure of GroEL/GroES is required for biologically significant chaperonin function in protein folding. <i>Nature Structural Biology</i> , 1998 , 5, 977-85		60
13	Crystal structure of the nucleotide exchange factor GrpE bound to the ATPase domain of the molecular chaperone DnaK. <i>Science</i> , 1997 , 276, 431-5	33.3	424
12	What is the molten globule?. <i>Nature Structural Biology</i> , 1995 , 2, 10-1		26
11	Asymmetrical interaction of GroEL and GroES in the ATPase cycle of assisted protein folding. <i>Science</i> , 1995 , 269, 836-41	33.3	143
10	Functional significance of symmetrical versus asymmetrical GroEL-GroES chaperonin complexes. <i>Science</i> , 1995 , 269, 832-6	33.3	80
9	Interaction of two complementary fragments of the bovine spinal cord myelin basic protein with phosphatidylglycerol bilayers, studied by ² H and ³¹ P NMR spectroscopy. <i>Biochemistry</i> , 1993 , 32, 9709-13	3.2	8
8	A comment on: The aromatic amino acid content of the bacterial chaperone protein groEL (cpn60): evidence for the presence of a single tryptophan ^Q by N.C. Price, S.M. Kelly, S. Wood and A. auf der Mauer (1991) FEBS Lett. 292, 9-12. <i>FEBS Letters</i> , 1993 , 320, 83-4; discussion 85	3.8	17
7	Successive action of DnaK, DnaJ and GroEL along the pathway of chaperone-mediated protein folding. <i>Nature</i> , 1992 , 356, 683-9	50.4	905

6	Interactions of phospholipids with the mitochondrial cytochrome-c reductase studied by spin-label ESR and NMR spectroscopy. <i>FEBS Journal</i> , 1992 , 209, 423-30		44
5	Molecular species of cardiolipin in relation to other mitochondrial phospholipids. Is there an acyl specificity of the interaction between cardiolipin and the ADP/ATP carrier?. <i>FEBS Journal</i> , 1991 , 199, 459-66		59
4	The monensin-mediated transport of sodium ions through phospholipid bilayers studied by ²³ Na-NMR spectroscopy. <i>Biochimica Et Biophysica Acta - Biomembranes</i> , 1985 , 817, 313-7	3.8	76
3	Shift reagents for ³⁹ K Nmr. <i>Inorganica Chimica Acta</i> , 1984 , 92, L37-L39	2.7	5
2	Measurement of intracellular potassium ion concentrations by n.m.r. <i>Biochemical Journal</i> , 1983 , 210, 961-3	3.8	54
1	Dual Role of a Rubisco Activase in Metabolic Repair and Carboxysome Organization		3