

Judith Frydman

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/3168433/publications.pdf>

Version: 2024-02-01

80
papers

8,019
citations

57758

44
h-index

71685

76
g-index

96
all docs

96
docs citations

96
times ranked

10206
citing authors

#	ARTICLE	IF	CITATIONS
1	Misfolded proteins partition between two distinct quality control compartments. <i>Nature</i> , 2008, 454, 1088-1095.	27.8	835
2	Diverse Cellular Functions of the Hsp90 Molecular Chaperone Uncovered Using Systems Approaches. <i>Cell</i> , 2007, 131, 121-135.	28.9	437
3	Systematic Functional Prioritization of Protein Posttranslational Modifications. <i>Cell</i> , 2012, 150, 413-425.	28.9	375
4	Lysosome activation clears aggregates and enhances quiescent neural stem cell activation during aging. <i>Science</i> , 2018, 359, 1277-1283.	12.6	374
5	The role of mutational robustness in RNA virus evolution. <i>Nature Reviews Microbiology</i> , 2013, 11, 327-336.	28.6	306
6	Spatial sequestration of misfolded proteins by a dynamic chaperone pathway enhances cellular fitness during stress. <i>Nature Cell Biology</i> , 2013, 15, 1231-1243.	10.3	281
7	The Molecular Architecture of the Eukaryotic Chaperonin TRiC/CCT. <i>Structure</i> , 2012, 20, 814-825.	3.3	261
8	Evolutionary constraints on chaperone-mediated folding provide an antiviral approach refractory to development of drug resistance. <i>Genes and Development</i> , 2007, 21, 195-205.	5.9	246
9	Folding and Quality Control of the VHL Tumor Suppressor Proceed through Distinct Chaperone Pathways. <i>Cell</i> , 2005, 121, 739-748.	28.9	237
10	Systems Analyses Reveal Two Chaperone Networks with Distinct Functions in Eukaryotic Cells. <i>Cell</i> , 2006, 124, 75-88.	28.9	227
11	Mechanisms and Functions of Spatial Protein Quality Control. <i>Annual Review of Biochemistry</i> , 2017, 86, 97-122.	11.1	225
12	Chemical cross-linking/mass spectrometry targeting acidic residues in proteins and protein complexes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2014, 111, 9455-9460.	7.1	213
13	Local slowdown of translation by nonoptimal codons promotes nascent-chain recognition by SRP in vivo. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 1100-1105.	8.2	202
14	Mechanism of folding chamber closure in a group II chaperonin. <i>Nature</i> , 2010, 463, 379-383.	27.8	196
15	The Mechanism and Function of Group II Chaperonins. <i>Journal of Molecular Biology</i> , 2015, 427, 2919-2930.	4.2	158
16	4.0-Å resolution cryo-EM structure of the mammalian chaperonin TRiC/CCT reveals its unique subunit arrangement. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4967-4972.	7.1	152
17	Parkinson's Disease Genes VPS35 and EIF4G1 Interact Genetically and Converge on α -Synuclein. <i>Neuron</i> , 2015, 85, 76-87.	8.1	149
18	Cotranslational signal-independent SRP preloading during membrane targeting. <i>Nature</i> , 2016, 536, 224-228.	27.8	148

#	ARTICLE	IF	CITATIONS
19	Sorting out the trash: the spatial nature of eukaryotic protein quality control. <i>Current Opinion in Cell Biology</i> , 2014, 26, 139-146.	5.4	143
20	State of the Science: An Update on Renal Cell Carcinoma. <i>Molecular Cancer Research</i> , 2012, 10, 859-880.	3.4	142
21	Distinct proteostasis circuits cooperate in nuclear and cytoplasmic protein quality control. <i>Nature</i> , 2018, 563, 407-411.	27.8	141
22	A Direct Regulatory Interaction between Chaperonin TRiC and Stress-Responsive Transcription Factor HSF1. <i>Cell Reports</i> , 2014, 9, 955-966.	6.4	135
23	The Structural Basis of Substrate Recognition by the Eukaryotic Chaperonin TRiC/CCT. <i>Cell</i> , 2014, 159, 1042-1055.	28.9	131
24	Proteostatic Control of Telomerase Function through TRiC-Mediated Folding of TCAB1. <i>Cell</i> , 2014, 159, 1389-1403.	28.9	126
25	The Chaperonin TRiC/CCT Associates with Prefoldin through a Conserved Electrostatic Interface Essential for Cellular Proteostasis. <i>Cell</i> , 2019, 177, 751-765.e15.	28.9	98
26	Nascent Polypeptide Domain Topology and Elongation Rate Direct the Cotranslational Hierarchy of Hsp70 and TRiC/CCT. <i>Molecular Cell</i> , 2019, 75, 1117-1130.e5.	9.7	93
27	Mechanism of lid closure in the eukaryotic chaperonin TRiC/CCT. <i>Nature Structural and Molecular Biology</i> , 2008, 15, 746-753.	8.2	91
28	Ageing exacerbates ribosome pausing to disrupt cotranslational proteostasis. <i>Nature</i> , 2022, 601, 637-642.	27.8	91
29	A ribosome-anchored chaperone network that facilitates eukaryotic ribosome biogenesis. <i>Journal of Cell Biology</i> , 2010, 189, 69-81.	5.2	87
30	Modulation of STAT3 Folding and Function by TRiC/CCT Chaperonin. <i>PLoS Biology</i> , 2014, 12, e1001844.	5.6	84
31	Zika Virus Dependence on Host Hsp70 Provides a Protective Strategy against Infection and Disease. <i>Cell Reports</i> , 2019, 26, 906-920.e3.	6.4	81
32	Symmetry-free cryo-EM structures of the chaperonin TRiC along its ATPase-driven conformational cycle. <i>EMBO Journal</i> , 2012, 31, 720-730.	7.8	80
33	TRiC's tricks inhibit huntingtin aggregation. <i>ELife</i> , 2013, 2, e00710.	6.0	73
34	Actin mutations in hypertrophic and dilated cardiomyopathy cause inefficient protein folding and perturbed filament formation. <i>FEBS Journal</i> , 2005, 272, 2037-2049.	4.7	71
35	Crystal Structures of a Group II Chaperonin Reveal the Open and Closed States Associated with the Protein Folding Cycle. <i>Journal of Biological Chemistry</i> , 2010, 285, 27958-27966.	3.4	66
36	Differentiation Drives Widespread Rewiring of the Neural Stem Cell Chaperone Network. <i>Molecular Cell</i> , 2020, 78, 329-345.e9.	9.7	66

#	ARTICLE	IF	CITATIONS
37	Hsp90 shapes protein and RNA evolution to balance trade-offs between protein stability and aggregation. <i>Nature Communications</i> , 2018, 9, 1781.	12.8	64
38	The ATP-powered gymnastics of TRiC/CCT: an asymmetric protein folding machine with a symmetric origin story. <i>Current Opinion in Structural Biology</i> , 2019, 55, 50-58.	5.7	62
39	Control of the structural landscape and neuronal proteotoxicity of mutant Huntingtin by domains flanking the polyQ tract. <i>ELife</i> , 2016, 5, .	6.0	62
40	Exogenous delivery of chaperonin subunit fragment ApiCCT1 modulates mutant Huntingtin cellular phenotypes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2013, 110, 3077-3082.	7.1	60
41	Multi-scale 3D Cryo-Correlative Microscopy for Vitrified Cells. <i>Structure</i> , 2020, 28, 1231-1237.e3.	3.3	60
42	Hsp90 Inhibitors Exhibit Resistance-Free Antiviral Activity against Respiratory Syncytial Virus. <i>PLoS ONE</i> , 2013, 8, e56762.	2.5	54
43	Cryo-EM Structure of a Group II Chaperonin in the Prehydrolysis ATP-Bound State Leading to Lid Closure. <i>Structure</i> , 2011, 19, 633-639.	3.3	52
44	Trivalent Arsenic Inhibits the Functions of Chaperonin Complex. <i>Genetics</i> , 2010, 186, 725-734.	2.9	51
45	Subdiffraction Imaging of Huntingtin Protein Aggregates by Fluorescence Blink Microscopy and Atomic Force Microscopy. <i>ChemPhysChem</i> , 2011, 12, 2387-2390.	2.1	47
46	The TRiC chaperonin controls reovirus replication through outer-capsid folding. <i>Nature Microbiology</i> , 2018, 3, 481-493.	13.3	47
47	The Hsp90 mosaic: a picture emerges. <i>Nature Structural and Molecular Biology</i> , 2009, 16, 2-6.	8.2	40
48	Delayed emergence of subdiffraction-sized mutant huntingtin fibrils following inclusion body formation. <i>Quarterly Reviews of Biophysics</i> , 2016, 49, e2.	5.7	39
49	The Cotranslational Contacts between Ribosome-bound Nascent Polypeptides and the Subunits of the Hetero-oligomeric Chaperonin TRiC Probed by Photocross-linking. <i>Journal of Biological Chemistry</i> , 2005, 280, 28118-28126.	3.4	36
50	Proteostasis in Viral Infection: Unfolding the Complex Virus-Chaperone Interplay. <i>Cold Spring Harbor Perspectives in Biology</i> , 2020, 12, a034090.	5.5	36
51	A defective viral genome strategy elicits broad protective immunity against respiratory viruses. <i>Cell</i> , 2021, 184, 6037-6051.e14.	28.9	33
52	Interplay between Chaperones and Protein Disorder Promotes the Evolution of Protein Networks. <i>PLoS Computational Biology</i> , 2014, 10, e1003674.	3.2	31
53	A Viral Protein Restricts Drosophila RNAi Immunity by Regulating Argonaute Activity and Stability. <i>Cell Host and Microbe</i> , 2018, 24, 542-557.e9.	11.0	31
54	Dual Role of Ribosome-Binding Domain of NAC as a Potent Suppressor of Protein Aggregation and Aging-Related Proteinopathies. <i>Molecular Cell</i> , 2019, 74, 729-741.e7.	9.7	31

#	ARTICLE	IF	CITATIONS
55	Principles of dengue virus evolvability derived from genotype-fitness maps in human and mosquito cells. <i>ELife</i> , 2021, 10, .	6.0	30
56	Structural and functional dissection of reovirus capsid folding and assembly by the prefoldin-TRiC/CCT chaperone network. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	30
57	Cotranslational Mechanisms of Protein Biogenesis and Complex Assembly in Eukaryotes. <i>Annual Review of Biomedical Data Science</i> , 2022, 5, 67-94.	6.5	27
58	Directionality of Polypeptide Transfer in the Mitochondrial Pathway of Chaperone-Mediated Protein Folding. <i>Biological Chemistry</i> , 1998, 379, 301-310.	2.5	26
59	Heterozygous Yeast Deletion Collection Screens Reveal Essential Targets of Hsp90. <i>PLoS ONE</i> , 2011, 6, e28211.	2.5	26
60	Multivalent contacts of the Hsp70 Ssb contribute to its architecture on ribosomes and nascent chain interaction. <i>Nature Communications</i> , 2016, 7, 13695.	12.8	25
61	Cryo-electron tomography provides topological insights into mutant huntingtin exon 1 and polyQ aggregates. <i>Communications Biology</i> , 2021, 4, 849.	4.4	19
62	Hardware-based anti-Brownian electrokinetic trap (ABEL trap) for single molecules: control loop simulations and application to ATP binding stoichiometry in multi-subunit enzymes. <i>Proceedings of SPIE</i> , 2008, 7038, 1-12.	0.8	18
63	Huntingtin's N-Terminus Rearrangements in the Presence of Membranes: A Joint Spectroscopic and Computational Perspective. <i>ACS Chemical Neuroscience</i> , 2019, 10, 472-481.	3.5	18
64	Cotranslational prolyl hydroxylation is essential for flavivirus biogenesis. <i>Nature</i> , 2021, 596, 558-564.	27.8	18
65	An information theoretic framework reveals a tunable allosteric network in group II chaperonins. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 726-733.	8.2	14
66	Small molecule C381 targets the lysosome to reduce inflammation and ameliorate disease in models of neurodegeneration. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2022, 119, e2121609119.	7.1	14
67	Disease-related Huntingtin seeding activities in cerebrospinal fluids of Huntington's disease patients. <i>Scientific Reports</i> , 2020, 10, 20295.	3.3	10
68	Where chaperones and nascent polypeptides meet. <i>Nature Structural Biology</i> , 2002, 9, 716-718.	9.7	9
69	CryoEM reveals the stochastic nature of individual ATP binding events in a group II chaperonin. <i>Nature Communications</i> , 2021, 12, 4754.	12.8	9
70	Dynamics and clustering of IRE1 \pm during ER stress. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2020, 117, 3352-3354.	7.1	8
71	The Dynamic Conformational Cycle of the Group I Chaperonin C-Termini Revealed via Molecular Dynamics Simulation. <i>PLoS ONE</i> , 2015, 10, e0117724.	2.5	8
72	Methods for measuring misfolded protein clearance in the budding yeast <i>Saccharomyces cerevisiae</i> . <i>Methods in Enzymology</i> , 2019, 619, 27-45.	1.0	7

#	ARTICLE	IF	CITATIONS
73	Native mass spectrometry analyses of chaperonin complex TRiC/CCT reveal subunit N-terminal processing and re-association patterns. <i>Scientific Reports</i> , 2021, 11, 13084.	3.3	7
74	Monitoring Actin Folding: Purification Protocols for Labeled Proteins and Binding to DNase I-Sepharose Beads. , 2000, 140, 161-167.		6
75	Targeted protein degradation: from small molecules to complex organelles—a Keystone Symposia report. <i>Annals of the New York Academy of Sciences</i> , 2022, 1510, 79-99.	3.8	5
76	Dosage compensation plans: protein aggregation provides additional insurance against aneuploidy. <i>Genes and Development</i> , 2019, 33, 1027-1030.	5.9	3
77	Time-Resolved Measurement of the ATP-Dependent Motion of the Group II Chaperonin by Diffracted Electron Tracking. <i>International Journal of Molecular Sciences</i> , 2018, 19, 950.	4.1	2
78	Polyglutamine Flanking Regions in Huntingtin Highlight Key Structural Intermediates Relevant for Molecular Chaperone Interaction and Huntington's Disease Pathogenesis. <i>Biophysical Journal</i> , 2014, 106, 682a.	0.5	0
79	Sorting Out the JUNQ: the Spatial Nature of Protein Quality Control. <i>Microscopy and Microanalysis</i> , 2017, 23, 994-995.	0.4	0
80	REP-X: An Evolution-guided Strategy for the Rational Design of Cysteine-less Protein Variants. <i>Scientific Reports</i> , 2020, 10, 2193.	3.3	0