

# Günter Kramer

## List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/1222210/publications.pdf>

Version: 2024-02-01

57  
papers

5,043  
citations

101543

36  
h-index

144013

57  
g-index

69  
all docs

69  
docs citations

69  
times ranked

4590  
citing authors

#	ARTICLE	IF	CITATIONS
1	Protein chain collapse modulation and folding stimulation by GroEL-ES. <i>Science Advances</i> , 2022, 8, eabl6293.	10.3	14
2	Bacterial ribosome collision sensing by a MutS DNA repair ATPase paralogue. <i>Nature</i> , 2022, 603, 509-514.	27.8	27
3	Protein Synthesis in the Developing Neocortex at Near-Atomic Resolution Reveals Ebp1-Mediated Neuronal Proteostasis at the 60S Tunnel Exit. <i>Molecular Cell</i> , 2021, 81, 304-322.e16.	9.7	27
4	Interactions between nascent proteins translated by adjacent ribosomes drive homomer assembly. <i>Science</i> , 2021, 371, 57-64.	12.6	80
5	N <sup>1</sup> -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
6	Mechanisms of Cotranslational Protein Maturation in Bacteria. <i>Frontiers in Molecular Biosciences</i> , 2021, 8, 689755.	3.5	20
7	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
8	The Anti-Aggregation Holdase Hsp33 Promotes the Formation of Folded Protein Structures. <i>Biophysical Journal</i> , 2020, 118, 85-95.	0.5	27
9	DENR promotes translation reinitiation via ribosome recycling to drive expression of oncogenes including ATF4. <i>Nature Communications</i> , 2020, 11, 4676.	12.8	58
10	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
11	Selective 40S Footprinting Reveals Cap-Tethered Ribosome Scanning in Human Cells. <i>Molecular Cell</i> , 2020, 79, 561-574.e5.	9.7	96
12	Condensation of Ded1p Promotes a Translational Switch from Housekeeping to Stress Protein Production. <i>Cell</i> , 2020, 181, 818-831.e19.	28.9	130
13	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
14	Monitoring Cell-Type-Specific Gene Expression Using Ribosome Profiling In Vivo During Cardiac Hemodynamic Stress. <i>Circulation Research</i> , 2019, 125, 431-448.	4.5	56
15	Selective ribosome profiling to study interactions of translating ribosomes in yeast. <i>Nature Protocols</i> , 2019, 14, 2279-2317.	12.0	28
16	A chemical kinetic basis for measuring translation initiation and elongation rates from ribosome profiling data. <i>PLoS Computational Biology</i> , 2019, 15, e1007070.	3.2	50
17	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
18	Mechanisms of Cotranslational Maturation of Newly Synthesized Proteins. <i>Annual Review of Biochemistry</i> , 2019, 88, 337-364.	11.1	138

#	ARTICLE	IF	CITATIONS
19	The C-terminal tail of the bacterial translocation ATPase SecA modulates its activity. <i>ELife</i> , 2019, 8, .	6.0	9
20	Protein Folding Mediated by Trigger Factor and Hsp70: New Insights from Single-Molecule Approaches. <i>Journal of Molecular Biology</i> , 2018, 430, 438-449.	4.2	29
21	Evolutionarily-Encoded Translation Kinetics Coordinate Co-Translational SSB Chaperone Binding in Yeast. <i>Biophysical Journal</i> , 2018, 114, 395a.	0.5	1
22	Cotranslational assembly of protein complexes in eukaryotes revealed by ribosome profiling. <i>Nature</i> , 2018, 561, 268-272.	27.8	266
23	SecA Cotranslationally Interacts with Nascent Substrate Proteins <i>in Vivo</i> . <i>Journal of Bacteriology</i> , 2017, 199, .	2.2	59
24	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
25	Profiling Ssb-Nascent Chain Interactions Reveals Principles of Hsp70-Assisted Folding. <i>Cell</i> , 2017, 170, 298-311.e20.	28.9	154
26	Analyzing the Complex Regulatory Landscape of Hfq – an Integrative, Multi-Omics Approach. <i>Frontiers in Microbiology</i> , 2017, 8, 1784.	3.5	17
27	Structural analysis of a signal peptide inside the ribosome tunnel by DNP MAS NMR. <i>Science Advances</i> , 2016, 2, e1600379.	10.3	33
28	Global profiling of SRP interaction with nascent polypeptides. <i>Nature</i> , 2016, 536, 219-223.	27.8	125
29	Alternative modes of client binding enable functional plasticity of Hsp70. <i>Nature</i> , 2016, 539, 448-451.	27.8	167
30	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
31	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
32	Finding nascent proteins the right home. <i>Science</i> , 2015, 348, 182-183.	12.6	1
33	Operon structure and cotranslational subunit association direct protein assembly in bacteria. <i>Science</i> , 2015, 350, 678-680.	12.6	160
34	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
35	Monitoring Protein Misfolding by Site-Specific Labeling of Proteins <i>In Vivo</i> . <i>PLoS ONE</i> , 2014, 9, e99395.	2.5	20
36	Chaperone Action at the Single-Molecule Level. <i>Chemical Reviews</i> , 2014, 114, 660-676.	47.7	51

#	ARTICLE	IF	CITATIONS
37	Co-translational mechanisms of protein maturation. <i>Current Opinion in Structural Biology</i> , 2014, 24, 24-33.	5.7	128
38	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
39	Reshaping of the conformational search of a protein by the chaperone trigger factor. <i>Nature</i> , 2013, 500, 98-101.	27.8	118
40	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
41	Genome-scale Co-evolutionary Inference Identifies Functions and Clients of Bacterial Hsp90. <i>PLoS Genetics</i> , 2013, 9, e1003631.	3.5	27
42	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
43	Selective Ribosome Profiling Reveals the Cotranslational Chaperone Action of Trigger Factor In Vivo. <i>Cell</i> , 2011, 147, 1295-1308.	28.9	419
44	SecA Interacts with Ribosomes in Order to Facilitate Posttranslational Translocation in Bacteria. <i>Molecular Cell</i> , 2011, 41, 343-353.	9.7	90
45	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
46	Large-scale purification of ribosome-nascent chain complexes for biochemical and structural studies. <i>FEBS Letters</i> , 2009, 583, 2407-2413.	2.8	41
47	Spatially and kinetically resolved changes in the conformational dynamics of the Hsp90 chaperone machine. <i>EMBO Journal</i> , 2009, 28, 602-613.	7.8	126
48	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
49	A peptide deformylase-ribosome complex reveals mechanism of nascent chain processing. <i>Nature</i> , 2008, 452, 108-111.	27.8	93
50	Dissecting functional similarities of ribosome-associated chaperones from <i>Saccharomyces cerevisiae</i> and <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2005, 57, 357-365.	2.5	19
51	Dimerization of the Human E3 Ligase CHIP via a Coiled-coil Domain Is Essential for Its Activity. <i>Journal of Biological Chemistry</i> , 2004, 279, 2673-2678.	3.4	105
52	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
53	Trigger Factor and DnaK possess overlapping substrate pools and binding specificities. <i>Molecular Microbiology</i> , 2003, 47, 1317-1328.	2.5	174
54	Three-State Equilibrium of <i>Escherichia coli</i> Trigger Factor. <i>Biological Chemistry</i> , 2002, 383, 1611-9.	2.5	90

#	ARTICLE	IF	CITATIONS
55	L23 protein functions as a chaperone docking site on the ribosome. <i>Nature</i> , 2002, 419, 171-174.	27.8	309
56	Mechanism of regulation of the bifunctional histidine kinase NtrB in <i>Escherichia coli</i> . <i>Journal of Molecular Microbiology and Biotechnology</i> , 2002, 4, 229-33.	1.0	18
57	Binding specificity of <i>Escherichia coli</i> trigger factor. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2001, 98, 14244-14249.	7.1	164