

Thomas Becker

List of Publications by Year in descending order

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Version: 2024-02-01

37
papers

4,303
citations

201674

27
h-index

395702

33
g-index

45
all docs

45
docs citations

45
times ranked

5471
citing authors

#	ARTICLE	IF	CITATIONS
1	Structural basis for translational shutdown and immune evasion by the Nsp1 protein of SARS-CoV-2. <i>Science</i> , 2020, 369, 1249-1255.	12.6	635
2	Cryo-EM structure of the ribosome-â€œSecYE complex in the membrane environment. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 614-621.	8.2	264
3	Structure of Monomeric Yeast and Mammalian Sec61 Complexes Interacting with the Translating Ribosome. <i>Science</i> , 2009, 326, 1369-1373.	12.6	263
4	Ubiquitination of stalled ribosome triggers ribosome-associated quality control. <i>Nature Communications</i> , 2017, 8, 159.	12.8	249
5	Collided ribosomes form a unique structural interface to induce Hel2â€œdriven quality controlâ€œpathways. <i>EMBO Journal</i> , 2019, 38, .	7.8	232
6	Structural basis of highly conserved ribosome recycling in eukaryotes and archaea. <i>Nature</i> , 2012, 482, 501-506.	27.8	210
7	Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-â€œ resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19748-19753.	7.1	196
8	Structures of the Sec61 complex engaged in nascent peptide translocation or membrane insertion. <i>Nature</i> , 2014, 506, 107-110.	27.8	186
9	The Ccr4-Not complex monitors the translating ribosome for codon optimality. <i>Science</i> , 2020, 368, .	12.6	180
10	Structural basis for coupling protein transport and N-glycosylation at the mammalian endoplasmic reticulum. <i>Science</i> , 2018, 360, 215-219.	12.6	177
11	Structure of the no-go mRNA decay complex Dom34â€œHbs1 bound to a stalled 80S ribosome. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 715-720.	8.2	150
12	Structure of the mammalian oligosaccharyl-transferase complex in the native ER protein translocon. <i>Nature Communications</i> , 2014, 5, 3072.	12.8	127
13	Molecular mechanism of translational stalling by inhibitory codon combinations and poly(A) tracts. <i>EMBO Journal</i> , 2020, 39, e103365.	7.8	113
14	The cryo-EM structure of a ribosome-â€œSki2-Ski3-Ski8 helicase complex. <i>Science</i> , 2016, 354, 1431-1433.	12.6	108
15	Structural Basis for Translational Stalling by Human Cytomegalovirus and Fungal Arginine Attenuator Peptide. <i>Molecular Cell</i> , 2010, 40, 138-146.	9.7	106
16	Structure of the hypusinylated eukaryotic translation factor eIF-5A bound to the ribosome. <i>Nucleic Acids Research</i> , 2016, 44, 1944-1951.	14.5	106
17	Cryoelectron Microscopic Structures of Eukaryotic Translation Termination Complexes Containing eRF1-eRF3 or eRF1-ABCE1. <i>Cell Reports</i> , 2014, 8, 59-65.	6.4	105
18	Structure of a human translation termination complex. <i>Nucleic Acids Research</i> , 2015, 43, 8615-8626.	14.5	99

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19	RQT complex dissociates ribosomes collided on endogenous RQC substrate SDD1. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 323-332.	8.2	97
20	Ribosomeâ€™NatA architecture reveals that rRNA expansion segments coordinate N-terminal acetylation. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 35-39.	8.2	79
21	Parallel Structural Evolution of Mitochondrial Ribosomes and OXPHOS Complexes. <i>Genome Biology and Evolution</i> , 2015, 7, 1235-1251.	2.5	77
22	Structure of the 40Sâ€™ABCE1 post-splitting complex in ribosome recycling and translation initiation. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 453-460.	8.2	77
23	Cryo-EM structure of a late pre-40S ribosomal subunit from <i>Saccharomyces cerevisiae</i> . <i>ELife</i> , 2017, 6, .	6.0	77
24	Structure of the 80S ribosomeâ€™Xrn1 nuclease complex. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 275-280.	8.2	62
25	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. <i>PLoS Biology</i> , 2020, 18, e3000780.	5.6	56
26	Sucrose sensing through nascent peptideâ€™mediated ribosome stalling at the stop codon of <i>Arabidopsis ZIP11</i> <u>ORF2</u>. <i>FEBS Letters</i> , 2017, 591, 1266-1277.	2.8	46
27	A structural inventory of native ribosomal ABCE1â€™43S preâ€™initiation complexes. <i>EMBO Journal</i> , 2021, 40, e105179.	7.8	35
28	Architecture of the active postâ€™translational Sec translocon. <i>EMBO Journal</i> , 2021, 40, e105643.	7.8	33
29	Structure of the Bcs1 AAA-ATPase suggests an airlock-like translocation mechanism for folded proteins. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 142-149.	8.2	32
30	Structure of the ribosome post-recycling complex probed by chemical cross-linking and mass spectrometry. <i>Nature Communications</i> , 2016, 7, 13248.	12.8	27
31	Molecular analysis of the ribosome recycling factor <u>ABCE1</u> bound to the 30S postâ€™splitting complex. <i>EMBO Journal</i> , 2020, 39, e103788.	7.8	24
32	Structure of the translating <i>Neurospora</i> ribosome arrested by cycloheximide. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	18
33	Structural basis of <u>L</u>-tryptophan-dependent inhibition of release factor 2 by the TnaC arrest peptide. <i>Nucleic Acids Research</i> , 2021, 49, 9539-9547.	14.5	12
34	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. , 2020, 18, e3000780.		0
35	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. , 2020, 18, e3000780.		0
36	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. , 2020, 18, e3000780.		0

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37	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. , 2020, 18, e3000780.		0