

Otto Berninghausen

List of Publications by Year in descending order

Source: <https://exaly.com/author-pdf/6824015/publications.pdf>

Version: 2024-02-01

62
papers

6,294
citations

71102

41
h-index

133252

59
g-index

73
all docs

73
docs citations

73
times ranked

7173
citing authors

#	ARTICLE	IF	CITATIONS
1	Inhibition of SRP-dependent protein secretion by the bacterial alarmone (p)ppGpp. Nature Communications, 2022, 13, 1069.	12.8	16
2	Ribosome collisions induce mRNA cleavage and ribosome rescue in bacteria. Nature, 2022, 603, 503-508.	27.8	50
3	Structure of the Maturing 90S Pre-ribosome in Association with the RNA Exosome. Molecular Cell, 2021, 81, 293-303.e4.	9.7	36
4	Structure of Gcn1 bound to stalled and colliding 80S ribosomes. Proceedings of the National Academy of Sciences of the United States of America, 2021, 118, .	7.1	79
5	A distinct assembly pathway of the human 39S late pre-mitoribosome. Nature Communications, 2021, 12, 4544.	12.8	27
6	Structural basis of <sc>l</sc>-tryptophan-dependent inhibition of release factor 2 by the TnaC arrest peptide. Nucleic Acids Research, 2021, 49, 9539-9547.	14.5	12
7	A structural inventory of native ribosomal ABCE1â€43S preâ€initiation complexes. EMBO Journal, 2021, 40, e105179.	7.8	35
8	Architecture of the active postâ€translational Sec translocon. EMBO Journal, 2021, 40, e105643.	7.8	33
9	Molecular mechanism of translational stalling by inhibitory codon combinations and poly(A) tracts. EMBO Journal, 2020, 39, e103365.	7.8	113
10	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. PLoS Biology, 2020, 18, e3000780.	5.6	56
11	Construction of the Central Protuberance and L1 Stalk during 60S Subunit Biogenesis. Molecular Cell, 2020, 79, 615-628.e5.	9.7	48
12	Structural basis for translational shutdown and immune evasion by the Nsp1 protein of SARS-CoV-2. Science, 2020, 369, 1249-1255.	12.6	635
13	Structural basis for the final steps of human 40S ribosome maturation. Nature, 2020, 587, 683-687.	27.8	52
14	90 <i>S</i> pre-ribosome transformation into the primordial 40 <i>S</i> subunit. Science, 2020, 369, 1470-1476.	12.6	59
15	Molecular analysis of the ribosome recycling factor <sc>ABCE</sc> 1 bound to the 30S postâ€splitting complex. EMBO Journal, 2020, 39, e103788.	7.8	24
16	Structure of the Bcs1 AAA-ATPase suggests an airlock-like translocation mechanism for folded proteins. Nature Structural and Molecular Biology, 2020, 27, 142-149.	8.2	32
17	The Ccr4-Not complex monitors the translating ribosome for codon optimality. Science, 2020, 368, .	12.6	180
18	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. , 2020, 18, e3000780.		0

#	ARTICLE	IF	CITATIONS
19	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. , 2020, 18, e3000780.		0
20	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. , 2020, 18, e3000780.		0
21	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. , 2020, 18, e3000780.		0
22	Thermophile 90S Pre-ribosome Structures Reveal the Reverse Order of Co-transcriptional 18S rRNA Subdomain Integration. <i>Molecular Cell</i> , 2019, 75, 1256-1269.e7.	9.7	48
23	Partially inserted nascent chain unzips the lateral gate of the Sec translocon. <i>EMBO Reports</i> , 2019, 20, e48191.	4.5	39
24	Structure and function of Vms1 and Arb1 in RQC and mitochondrial proteome homeostasis. <i>Nature</i> , 2019, 570, 538-542.	27.8	63
25	Structure of the 80S ribosome-Xrn1 nuclease complex. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 275-280.	8.2	62
26	Ribosome-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
27	Structural and mutational analysis of the ribosome-arresting human XBP1u. <i>ELife</i> , 2019, 8, .	6.0	51
28	Structural basis for coupling protein transport and N-glycosylation at the mammalian endoplasmic reticulum. <i>Science</i> , 2018, 360, 215-219.	12.6	177
29	Structure of a hibernating 100S ribosome reveals an inactive conformation of the ribosomal protein S1. <i>Nature Microbiology</i> , 2018, 3, 1115-1121.	13.3	92
30	Visualizing late states of human 40S ribosomal subunit maturation. <i>Nature</i> , 2018, 558, 249-253.	27.8	118
31	Structure of the <i>Bacillus subtilis</i> hibernating 100S ribosome reveals the basis for 70S dimerization. <i>EMBO Journal</i> , 2017, 36, 2061-2072.	7.8	74
32	Structural basis for ArfA-RF2-mediated translation termination on mRNAs lacking stop codons. <i>Nature</i> , 2017, 541, 546-549.	27.8	39
33	Structure of the 40S-ABCE1 post-splitting complex in ribosome recycling and translation initiation. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 453-460.	8.2	77
34	3.2-Å-resolution structure of the 90S preribosome before A1 pre-rRNA cleavage. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 954-964.	8.2	95
35	Structural Basis for Polyproline-Mediated Ribosome Stalling and Rescue by the Translation Elongation Factor EF-P. <i>Molecular Cell</i> , 2017, 68, 515-527.e6.	9.7	118
36	An antimicrobial peptide that inhibits translation by trapping release factors on the ribosome. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 752-757.	8.2	123

#	ARTICLE	IF	CITATIONS
37	Visualizing the Assembly Pathway of Nucleolar Pre-60S Ribosomes. <i>Cell</i> , 2017, 171, 1599-1610.e14.	28.9	162
38	The force-sensing peptide VemP employs extreme compaction and secondary structure formation to induce ribosomal stalling. <i>ELife</i> , 2017, 6, .	6.0	81
39	Cryo-EM structure of a late pre-40S ribosomal subunit from <i>Saccharomyces cerevisiae</i> . <i>ELife</i> , 2017, 6, .	6.0	77
40	Structural Dynamics of the YidC:Ribosome Complex during Membrane Protein Biogenesis. <i>Cell Reports</i> , 2016, 17, 2943-2954.	6.4	48
41	The cryo-EM structure of a ribosome-Ski2-Ski3-Ski8 helicase complex. <i>Science</i> , 2016, 354, 1431-1433.	12.6	108
42	The stringent factor RelA adopts an open conformation on the ribosome to stimulate ppGpp synthesis. <i>Nucleic Acids Research</i> , 2016, 44, 6471-6481.	14.5	129
43	Architecture of the 90S Pre-ribosome: A Structural View on the Birth of the Eukaryotic Ribosome. <i>Cell</i> , 2016, 166, 380-393.	28.9	184
44	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
45	Architecture of the Rix1-Rea1 checkpoint machinery during pre-60S-ribosome remodeling. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 37-44.	8.2	104
46	Parallel Structural Evolution of Mitochondrial Ribosomes and OXPHOS Complexes. <i>Genome Biology and Evolution</i> , 2015, 7, 1235-1251.	2.5	77
47	Structure of a human translation termination complex. <i>Nucleic Acids Research</i> , 2015, 43, 8615-8626.	14.5	99
48	Structure of the <i>Bacillus subtilis</i> 70S ribosome reveals the basis for species-specific stalling. <i>Nature Communications</i> , 2015, 6, 6941.	12.8	105
49	Molecular Basis for the Ribosome Functioning as an L-Tryptophan Sensor. <i>Cell Reports</i> , 2014, 9, 469-475.	6.4	73
50	Structures of the Sec61 complex engaged in nascent peptide translocation or membrane insertion. <i>Nature</i> , 2014, 506, 107-110.	27.8	186
51	Drug Sensing by the Ribosome Induces Translational Arrest via Active Site Perturbation. <i>Molecular Cell</i> , 2014, 56, 446-452.	9.7	104
52	Molecular basis for erythromycin-dependent ribosome stalling during translation of the ErmBL leader peptide. <i>Nature Communications</i> , 2014, 5, 3501.	12.8	115
53	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
54	60S ribosome biogenesis requires rotation of the 5S ribonucleoprotein particle. <i>Nature Communications</i> , 2014, 5, 3491.	12.8	117

#	ARTICLE	IF	CITATIONS
55	Visualization of a polytopic membrane protein during SecY-mediated membrane insertion. <i>Nature Communications</i> , 2014, 5, 4103.	12.8	60
56	A structural model of the active ribosome-bound membrane protein insertase YidC. <i>ELife</i> , 2014, 3, e03035.	6.0	69
57	Structures of the human and <i>Drosophila</i> 80S ribosome. <i>Nature</i> , 2013, 497, 80-85.	27.8	474
58	Structural basis of highly conserved ribosome recycling in eukaryotes and archaea. <i>Nature</i> , 2012, 482, 501-506.	27.8	210
59	Structure of the no-go mRNA decay complex Dom34-Hbs1 bound to a stalled 80S ribosome. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 715-720.	8.2	150
60	Cryo-EM structure and rRNA model of a translating eukaryotic 80S ribosome at 5.5-Å resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19748-19753.	7.1	196
61	Structural Basis for Translational Stalling by Human Cytomegalovirus and Fungal Arginine Attenuator Peptide. <i>Molecular Cell</i> , 2010, 40, 138-146.	9.7	106
62	Structure of Monomeric Yeast and Mammalian Sec61 Complexes Interacting with the Translating Ribosome. <i>Science</i> , 2009, 326, 1369-1373.	12.6	263