

Roland Beckmann

List of Publications by Year in descending order

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120
papers

13,058
citations

17440

63
h-index

28297

105
g-index

141
all docs

141
docs citations

141
times ranked

10771
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	A new system for naming ribosomal proteins. <i>Current Opinion in Structural Biology</i> , 2014, 24, 165-169.	5.7	481
3	Structures of the human and <i>Drosophila</i> 80S ribosome. <i>Nature</i> , 2013, 497, 80-85.	27.8	474
4	Structure of the 80S Ribosome from <i>Saccharomyces cerevisiae</i> tRNA-Ribosome and Subunit-Subunit Interactions. <i>Cell</i> , 2001, 107, 373-386.	28.9	462
5	Structure of the signal recognition particle interacting with the elongation-arrested ribosome. <i>Nature</i> , 2004, 427, 808-814.	27.8	382
6	Domain movements of elongation factor eEF2 and the eukaryotic 80S ribosome facilitate tRNA translocation. <i>EMBO Journal</i> , 2004, 23, 1008-1019.	7.8	373
7	Architecture of the Protein-Conducting Channel Associated with the Translating 80S Ribosome. <i>Cell</i> , 2001, 107, 361-372.	28.9	368
8	Cryo-EM structure of the ribosome- <i>SecYE</i> complex in the membrane environment. <i>Nature Structural and Molecular Biology</i> , 2011, 18, 614-621.	8.2	264
9	Structural Insight into Nascent Polypeptide Chain-Mediated Translational Stalling. <i>Science</i> , 2009, 326, 1412-1415.	12.6	263
10	Structure of Monomeric Yeast and Mammalian <i>Sec61</i> Complexes Interacting with the Translating Ribosome. <i>Science</i> , 2009, 326, 1369-1373.	12.6	263
11	Ubiquitination of stalled ribosome triggers ribosome-associated quality control. <i>Nature Communications</i> , 2017, 8, 159.	12.8	249
12	Cotranslational Protein Folding inside the Ribosome Exit Tunnel. <i>Cell Reports</i> , 2015, 12, 1533-1540.	6.4	234
13	Collided ribosomes form a unique structural interface to induce Hel2-driven quality control pathways. <i>EMBO Journal</i> , 2019, 38, .	7.8	232
14	Structural basis of highly conserved ribosome recycling in eukaryotes and archaea. <i>Nature</i> , 2012, 482, 501-506.	27.8	210
15	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
16	±-Helical nascent polypeptide chains visualized within distinct regions of the ribosomal exit tunnel. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 313-317.	8.2	187
17	Structures of the <i>Sec61</i> complex engaged in nascent peptide translocation or membrane insertion. <i>Nature</i> , 2014, 506, 107-110.	27.8	186
18	Following the signal sequence from ribosomal tunnel exit to signal recognition particle. <i>Nature</i> , 2006, 444, 507-511.	27.8	184

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19	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
20	The Ccr4-Not complex monitors the translating ribosome for codon optimality. <i>Science</i> , 2020, 368, .	12.6	180
21	The ribosomal tunnel as a functional environment for nascent polypeptide folding and translational stalling. <i>Current Opinion in Structural Biology</i> , 2011, 21, 274-282.	5.7	179
22	Structural basis for coupling protein transport and N-glycosylation at the mammalian endoplasmic reticulum. <i>Science</i> , 2018, 360, 215-219.	12.6	177
23	Structure of the native Sec61 protein-conducting channel. <i>Nature Communications</i> , 2015, 6, 8403.	12.8	169
24	Visualizing the Assembly Pathway of Nucleolar Pre-60S Ribosomes. <i>Cell</i> , 2017, 171, 1599-1610.e14.	28.9	162
25	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
26	Translation regulation via nascent polypeptide-mediated ribosome stalling. <i>Current Opinion in Structural Biology</i> , 2016, 37, 123-133.	5.7	137
27	Signal Recognition Particle Receptor Exposes the Ribosomal Translocon Binding Site. <i>Science</i> , 2006, 312, 745-747.	12.6	133
28	SecM-Stalled Ribosomes Adopt an Altered Geometry at the Peptidyl Transferase Center. <i>PLoS Biology</i> , 2011, 9, e1000581.	5.6	132
29	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
30	Structure of the mammalian oligosaccharyl-transferase complex in the native ER protein translocon. <i>Nature Communications</i> , 2014, 5, 3072.	12.8	127
31	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
32	Localization of eukaryote-specific ribosomal proteins in a 5.5-Å cryo-EM map of the 80S eukaryotic ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 19754-19759.	7.1	122
33	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
34	Visualizing late states of human 40S ribosomal subunit maturation. <i>Nature</i> , 2018, 558, 249-253.	27.8	118
35	60S ribosome biogenesis requires rotation of the 5S ribonucleoprotein particle. <i>Nature Communications</i> , 2014, 5, 3491.	12.8	117
36	Molecular basis for erythromycin-dependent ribosome stalling during translation of the ErmBL leader peptide. <i>Nature Communications</i> , 2014, 5, 3501.	12.8	115

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37	Molecular mechanism of translational stalling by inhibitory codon combinations and poly(A) tracts. <i>EMBO Journal</i> , 2020, 39, e103365.	7.8	113
38	The cryo-EM structure of a ribosome-Ski2-Ski3-Ski8 helicase complex. <i>Science</i> , 2016, 354, 1431-1433.	12.6	108
39	Mechanism of eIF6-mediated Inhibition of Ribosomal Subunit Joining. <i>Journal of Biological Chemistry</i> , 2010, 285, 14848-14851.	3.4	107
40	Structural Basis for Translational Stalling by Human Cytomegalovirus and Fungal Arginine Attenuator Peptide. <i>Molecular Cell</i> , 2010, 40, 138-146.	9.7	106
41	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
42	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
43	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
44	Drug Sensing by the Ribosome Induces Translational Arrest via Active Site Perturbation. <i>Molecular Cell</i> , 2014, 56, 446-452.	9.7	104
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	Structure of the pre-60S ribosomal subunit with nuclear export factor Arx1 bound at the exit tunnel. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 1234-1241.	8.2	103
47	A combined cryo-EM and molecular dynamics approach reveals the mechanism of ErmBL-mediated translation arrest. <i>Nature Communications</i> , 2016, 7, 12026.	12.8	103
48	Structure of a human translation termination complex. <i>Nucleic Acids Research</i> , 2015, 43, 8615-8626.	14.5	99
49	Cotranslational folding of spectrin domains via partially structured states. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 221-225.	8.2	97
50	RQT complex dissociates ribosomes collided on endogenous RQC substrate SDD1. <i>Nature Structural and Molecular Biology</i> , 2020, 27, 323-332.	8.2	97
51	SRP meets the ribosome. <i>Nature Structural and Molecular Biology</i> , 2004, 11, 1049-1053.	8.2	96
52	EDF1 coordinates cellular responses to ribosome collisions. <i>ELife</i> , 2020, 9, .	6.0	96
53	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
54	Spectrum and functional validation of PSMB5 mutations in multiple myeloma. <i>Leukemia</i> , 2019, 33, 447-456.	7.2	93

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55	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
56	Folding pathway of an Ig domain is conserved on and off the ribosome. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E11284-E11293.	7.1	86
57	Mechanisms of SecM-Mediated Stalling in the Ribosome. <i>Biophysical Journal</i> , 2012, 103, 331-341.	0.5	82
58	The force-sensing peptide VemP employs extreme compaction and secondary structure formation to induce ribosomal stalling. <i>ELife</i> , 2017, 6, .	6.0	81
59	Structural characterization of a eukaryotic chaperone-ribosome-associated complex. <i>Nature Structural and Molecular Biology</i> , 2013, 20, 23-28.	8.2	79
60	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
61	Structure of Gcn1 bound to stalled and colliding 80S ribosomes. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2021, 118, .	7.1	79
62	Parallel Structural Evolution of Mitochondrial Ribosomes and OXPHOS Complexes. <i>Genome Biology and Evolution</i> , 2015, 7, 1235-1251.	2.5	77
63	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
64	Cryo-EM structure of a late pre-40S ribosomal subunit from <i>Saccharomyces cerevisiae</i> . <i>ELife</i> , 2017, 6, .	6.0	77
65	ATP hydrolysis by the viral RNA sensor RIG-I prevents unintentional recognition of self-RNA. <i>ELife</i> , 2015, 4, .	6.0	75
66	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
67	BAX/BAK-Induced Apoptosis Results in Caspase-8-Dependent IL-1 β Maturation in Macrophages. <i>Cell Reports</i> , 2018, 25, 2354-2368.e5.	6.4	74
68	Molecular Basis for the Ribosome Functioning as an L-Tryptophan Sensor. <i>Cell Reports</i> , 2014, 9, 469-475.	6.4	73
69	Crystal structures of ribosome anti-association factor IF6. <i>Nature Structural Biology</i> , 2000, 7, 1156-1164.	9.7	70
70	Small protein domains fold inside the ribosome exit tunnel. <i>FEBS Letters</i> , 2016, 590, 655-660.	2.8	69
71	A structural model of the active ribosome-bound membrane protein insertase YidC. <i>ELife</i> , 2014, 3, e03035.	6.0	69
72	Structure and function of Vms1 and Arb1 in RQC and mitochondrial proteome homeostasis. <i>Nature</i> , 2019, 570, 538-542.	27.8	63

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73	Structure of the 80S ribosomeâ€“Xrn1 nuclease complex. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 275-280.	8.2	62
74	Visualization of a polytopic membrane protein during SecY-mediated membrane insertion. <i>Nature Communications</i> , 2014, 5, 4103.	12.8	60
75	Promiscuous behaviour of archaeal ribosomal proteins: Implications for eukaryotic ribosome evolution. <i>Nucleic Acids Research</i> , 2013, 41, 1284-1293.	14.5	59
76	90 <i>S</i> pre-ribosome transformation into the primordial 40 <i>S</i> subunit. <i>Science</i> , 2020, 369, 1470-1476.	12.6	59
77	Cryo-EM structure of the tetracycline resistance protein TetM in complex with a translating ribosome at 3.9-Å... resolution. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 5401-5406.	7.1	58
78	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. <i>PLoS Biology</i> , 2020, 18, e3000780.	5.6	56
79	Structural basis for the final steps of human 40S ribosome maturation. <i>Nature</i> , 2020, 587, 683-687.	27.8	52
80	Structural and mutational analysis of the ribosome-arresting human XBP1u. <i>ELife</i> , 2019, 8, .	6.0	51
81	Ribosome collisions induce mRNA cleavage and ribosome rescue in bacteria. <i>Nature</i> , 2022, 603, 503-508.	27.8	50
82	Structural Dynamics of the YidC:Ribosome Complex during Membrane Protein Biogenesis. <i>Cell Reports</i> , 2016, 17, 2943-2954.	6.4	48
83	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
84	Construction of the Central Protuberance and L1 Stalk during 60S Subunit Biogenesis. <i>Molecular Cell</i> , 2020, 79, 615-628.e5.	9.7	48
85	Sucrose sensing through nascent peptideâ€“mediated ribosome stalling at the stop codon of <i>Arabidopsis ZIP11</i> <i>uORF2</i> . <i>FEBS Letters</i> , 2017, 591, 1266-1277.	2.8	46
86	A network of assembly factors is involved in remodeling rRNA elements during preribosome maturation. <i>Journal of Cell Biology</i> , 2014, 207, 481-498.	5.2	44
87	The C-terminal regions of YidC from <i>Rhodospirillum rubrum</i> and <i>Oceanicola alexandrii</i> bind to ribosomes and partially substitute for SRP receptor function in <i>Escherichia coli</i> . <i>Molecular Microbiology</i> , 2014, 91, 408-421.	2.5	43
88	Tetracenomycin X inhibits translation by binding within the ribosomal exit tunnel. <i>Nature Chemical Biology</i> , 2020, 16, 1071-1077.	8.0	43
89	Structural basis for ArfAâ€“RF2-mediated translation termination on mRNAs lacking stop codons. <i>Nature</i> , 2017, 541, 546-549.	27.8	39
90	Partially inserted nascent chain unzips the lateral gate of the Sec translocon. <i>EMBO Reports</i> , 2019, 20, e48191.	4.5	39

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91	Signal sequence-independent SRP-SR complex formation at the membrane suggests an alternative targeting pathway within the SRP cycle. <i>Molecular Biology of the Cell</i> , 2011, 22, 2309-2323.	2.1	38
92	Interdependent action of KH domain proteins Krr1 and Dim2 drive the 40S platform assembly. <i>Nature Communications</i> , 2017, 8, 2213.	12.8	38
93	Structural view on recycling of archaeal and eukaryotic ribosomes after canonical termination and ribosome rescue. <i>Current Opinion in Structural Biology</i> , 2012, 22, 786-796.	5.7	37
94	Ribosome-stalk biogenesis is coupled with recruitment of nuclear-export factor to the nascent 60S subunit. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 1074-1082.	8.2	36
95	Structure of the Maturing 90S Pre-ribosome in Association with the RNA Exosome. <i>Molecular Cell</i> , 2021, 81, 293-303.e4.	9.7	36
96	Preribosomes escaping from the nucleus are caught during translation by cytoplasmic quality control. <i>Nature Structural and Molecular Biology</i> , 2017, 24, 1107-1115.	8.2	35
97	A structural inventory of native ribosomal ABCE1-43S pre-initiation complexes. <i>EMBO Journal</i> , 2021, 40, e105179.	7.8	35
98	Architecture of the active post-translational Sec translocon. <i>EMBO Journal</i> , 2021, 40, e105643.	7.8	33
99	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
100	ALKBH5-induced demethylation of mono- and dimethylated adenosine. <i>Chemical Communications</i> , 2018, 54, 8591-8593.	4.1	31
101	Role of the Cytosolic Loop C2 and the C Terminus of YidC in Ribosome Binding and Insertion Activity. <i>Journal of Biological Chemistry</i> , 2015, 290, 17250-17261.	3.4	29
102	Translational arrest by a prokaryotic signal recognition particle is mediated by RNA interactions. <i>Nature Structural and Molecular Biology</i> , 2015, 22, 767-773.	8.2	29
103	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
104	A distinct assembly pathway of the human 39S late pre-mitoribosome. <i>Nature Communications</i> , 2021, 12, 4544.	12.8	27
105	Automatic post-picking using MAPPOS improves particle image detection from cryo-EM micrographs. <i>Journal of Structural Biology</i> , 2013, 182, 59-66.	2.8	26
106	The SARS-unique domain (SUD) of SARS-CoV and SARS-CoV-2 interacts with human Paip1 to enhance viral RNA translation. <i>EMBO Journal</i> , 2021, 40, e102277.	7.8	26
107	Reconstitution of the human SRP system and quantitative and systematic analysis of its ribosome interactions. <i>Nucleic Acids Research</i> , 2019, 47, 3184-3196.	14.5	25
108	Molecular analysis of the ribosome recycling factor <sc>ABCE</sc> 1 bound to the 30S post-splitting complex. <i>EMBO Journal</i> , 2020, 39, e103788.	7.8	24

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109	Suppressor mutations in Rpf2â€“Rrs1 or Rpl5 bypass the Cgr1 function for pre-ribosomal 5S RNP-rotation. Nature Communications, 2018, 9, 4094.	12.8	22
110	Emergence of the primordial pre-60S from the 90S pre-ribosome. Cell Reports, 2022, 39, 110640.	6.4	17
111	Inhibition of SRP-dependent protein secretion by the bacterial alarmone (p)ppGpp. Nature Communications, 2022, 13, 1069.	12.8	16
112	SAP domain forms a flexible part of DNA aperture in Ku70/80. FEBS Journal, 2021, 288, 4382-4393.	4.7	13
113	Structural basis of <scp> </scp>-tryptophan-dependent inhibition of release factor 2 by the TnaC arrest peptide. Nucleic Acids Research, 2021, 49, 9539-9547.	14.5	12
114	Mitoribosome oddities. Science, 2015, 348, 288-289.	12.6	8
115	Reconstitution of Isotopically Labeled Ribosomal Protein L29 in the 50S Large Ribosomal Subunit for Solution-State and Solid-State NMR. Methods in Molecular Biology, 2018, 1764, 87-100.	0.9	6
116	Structures of Nascent Polypeptide Chain-Dependent-Stalled Ribosome Complexes. , 2014, , 45-59.		1
117	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. , 2020, 18, e3000780.		0
118	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. , 2020, 18, e3000780.		0
119	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. , 2020, 18, e3000780.		0
120	Structure and function of yeast Lso2 and human CCDC124 bound to hibernating ribosomes. , 2020, 18, e3000780.		0