

Elena Conti

List of Publications by Year in descending order

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47
papers

3,839
citations

147801
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223800
46
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83
all docs

83
docs citations

83
times ranked

3490
citing authors

#	ARTICLE	IF	CITATIONS
1	A single subunit, Dis3, is essentially responsible for yeast exosome core activity. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 15-22.	8.2	381
2	Structural and Biochemical Insights to the Role of the CCR4-NOT Complex and DDX6 ATPase in MicroRNA Repression. <i>Molecular Cell</i> , 2014, 54, 751-765.	9.7	276
3	Molecular Mechanisms for the RNA-Dependent ATPase Activity of Upf1 and Its Regulation by Upf2. <i>Molecular Cell</i> , 2011, 41, 693-703.	9.7	243
4	The Yeast Exosome Functions as a Macromolecular Cage to Channel RNA Substrates for Degradation. <i>Cell</i> , 2009, 139, 547-559.	28.9	225
5	Crystal structure of an RNA-bound 11-subunit eukaryotic exosome complex. <i>Nature</i> , 2013, 495, 70-75.	27.8	213
6	The archaeal exosome core is a hexameric ring structure with three catalytic subunits. <i>Nature Structural and Molecular Biology</i> , 2005, 12, 575-581.	8.2	198
7	Structure of the Active Subunit of the Yeast Exosome Core, Rrp44: Diverse Modes of Substrate Recruitment in the RNase II Nuclease Family. <i>Molecular Cell</i> , 2008, 29, 717-728.	9.7	175
8	Structural analysis reveals the characteristic features of Mtr4, a DExH helicase involved in nuclear RNA processing and surveillance. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 12139-12144.	7.1	129
9	Structural Model of a CRISPR RNA-Silencing Complex Reveals the RNA-Target Cleavage Activity in Cmr4. <i>Molecular Cell</i> , 2014, 56, 43-54.	9.7	129
10	RNA degradation paths in a 12-subunit nuclear exosome complex. <i>Nature</i> , 2015, 524, 54-58.	27.8	120
11	The cryo-EM structure of a ribosome-Ski2-Ski3-Ski8 helicase complex. <i>Science</i> , 2016, 354, 1431-1433.	12.6	108
12	Structural Basis of 3' End RNA Recognition and Exoribonucleolytic Cleavage by an Exosome RNase PH Core. <i>Molecular Cell</i> , 2005, 20, 473-481.	9.7	104
13	The exosome-binding factors Rrp6 and Rrp47 form a composite surface for recruiting the Mtr4 helicase. <i>EMBO Journal</i> , 2014, 33, 2829-2846.	7.8	102
14	Structure of a Human 4E-T/DDX6/CNOT1 Complex Reveals the Different Interplay of DDX6-Binding Proteins with the CCR4-NOT Complex. <i>Cell Reports</i> , 2015, 13, 703-711.	6.4	95
15	The conformational plasticity of eukaryotic RNA-dependent ATPases. <i>FEBS Journal</i> , 2015, 282, 850-863.	4.7	94
16	Phospho-dependent and phospho-independent interactions of the helicase UPF1 with the NMD factors SMG5-SMG7 and SMG6. <i>Nucleic Acids Research</i> , 2014, 42, 9447-9460.	14.5	92
17	Structure of the nuclear exosome captured on a maturing preribosome. <i>Science</i> , 2018, 360, 219-222.	12.6	92
18	The RNA exosome and proteasome: common principles of degradation control. <i>Nature Reviews Molecular Cell Biology</i> , 2013, 14, 654-660.	37.0	74

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19	Structure of a Cytoplasmic 11-Subunit RNA Exosome Complex. <i>Molecular Cell</i> , 2016, 63, 125-134.	9.7	72
20	The Molecular Architecture of the TRAMP Complex Reveals the Organization and Interplay of Its Two Catalytic Activities. <i>Molecular Cell</i> , 2014, 55, 856-867.	9.7	69
21	RNA channelling by the eukaryotic exosome. <i>EMBO Reports</i> , 2010, 11, 936-942.	4.5	68
22	Structure of the RNA Helicase MLE Reveals the Molecular Mechanisms for Uridine Specificity and RNA-ATP Coupling. <i>Molecular Cell</i> , 2015, 60, 487-499.	9.7	67
23	Reconstitution of the complete pathway of ITS2 processing at the pre-ribosome. <i>Nature Communications</i> , 2017, 8, 1787.	12.8	66
24	Mpp6 Incorporation in the Nuclear Exosome Contributes to RNA Channeling through the Mtr4 Helicase. <i>Cell Reports</i> , 2017, 20, 2279-2286.	6.4	49
25	Distinct and evolutionary conserved structural features of the human nuclear exosome complex. <i>ELife</i> , 2018, 7, .	6.0	47
26	The structure of the Pan2â€“Pan3 core complex reveals cross-talk between deadenylase and pseudokinase. <i>Nature Structural and Molecular Biology</i> , 2014, 21, 591-598.	8.2	45
27	Sen1 has unique structural features grafted on the architecture of the Upf1â€“like helicase family. <i>EMBO Journal</i> , 2017, 36, 1590-1604.	7.8	45
28	Structural insights into the interaction of the nuclear exosome helicase Mtr4 with the preribosomal protein Nop53. <i>Rna</i> , 2017, 23, 1780-1787.	3.5	42
29	The MTR4 helicase recruits nuclear adaptors of the human RNA exosome using distinct arch-interacting motifs. <i>Nature Communications</i> , 2019, 10, 3393.	12.8	41
30	Structure of the RBM7â€“ZCCHC8 core of the NEXT complex reveals connections to splicing factors. <i>Nature Communications</i> , 2016, 7, 13573.	12.8	38
31	Structure and RNA-binding properties of the Type III-A CRISPR-associated protein Csm3. <i>RNA Biology</i> , 2013, 10, 1670-1678.	3.1	35
32	Architecture of the Ubiquitylation Module of the Yeast Ccr4-Not Complex. <i>Structure</i> , 2015, 23, 921-928.	3.3	33
33	InsP6 binding to PIKK kinases revealed by the cryo-EM structure of an SMG1â€“SMG8â€“SMG9 complex. <i>Nature Structural and Molecular Biology</i> , 2019, 26, 1089-1093.	8.2	30
34	<i>Saccharomyces cerevisiae</i> Ski7 Is a GTP-Binding Protein Adopting the Characteristic Conformation of Active Translational GTPases. <i>Structure</i> , 2015, 23, 1336-1343.	3.3	26
35	Reconstitution of 3â€“ end processing of mammalian pre-mRNA reveals a central role of RBBP6. <i>Genes and Development</i> , 2022, 36, 195-209.	5.9	26
36	Analysis of proteinâ€“RNA interactions in CRISPR proteins and effector complexes by UV-induced cross-linking and mass spectrometry. <i>Methods</i> , 2015, 89, 138-148.	3.8	25

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37	Structure of substrate-bound SMG1-8-9 kinase complex reveals molecular basis for phosphorylation specificity. <i>ELife</i> , 2020, 9, .	6.0	25
38	Structural basis for the activation of the <i>C. elegans</i> noncanonical cytoplasmic poly(A)-polymerase GLD-2 by GLD-3. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2015, 112, 8614-8619.	7.1	23
39	The human SKI complex regulates channeling of ribosome-bound RNA to the exosome via an intrinsic gatekeeping mechanism. <i>Molecular Cell</i> , 2022, 82, 756-769.e8.	9.7	23
40	Structural insights into the nucleic acid remodeling mechanisms of the yeast THO-Sub2 complex. <i>ELife</i> , 2020, 9, .	6.0	21
41	Cryo-EM reconstructions of inhibitor-bound SMG1 kinase reveal an autoinhibitory state dependent on SMG8. <i>ELife</i> , 2021, 10, .	6.0	18
42	To Process or to Decay: A Mechanistic View of the Nuclear RNA Exosome. <i>Cold Spring Harbor Symposia on Quantitative Biology</i> , 2019, 84, 155-163.	1.1	16
43	Structure and regulation of the nuclear exosome targeting complex guides RNA substrates to the exosome. <i>Molecular Cell</i> , 2022, 82, 2505-2518.e7.	9.7	15
44	Molecular Mechanism of Processive 3' to 5' RNA Translocation in the Active Subunit of the RNA Exosome Complex. <i>Journal of the American Chemical Society</i> , 2016, 138, 4069-4078.	13.7	11
45	Structure of a SMG8-SMG9 complex identifies a G-domain heterodimer in the NMD effector proteins. <i>Rna</i> , 2017, 23, 1028-1034.	3.5	10
46	Purification and Reconstitution of the <i>S. cerevisiae</i> TRAMP and Ski Complexes for Biochemical and Structural Studies. <i>Methods in Molecular Biology</i> , 2020, 2062, 491-513.	0.9	1
47	Molecular mechanisms of mRNA degradation. <i>FASEB Journal</i> , 2008, 22, 247.3.	0.5	0