Fabien Bonneau

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26 15 1,173 20 h-index g-index citations papers 26 4.15 1,443 15.7 avg, IF L-index ext. citations ext. papers

#	Paper	IF	Citations
20	Structural and biochemical insights to the role of the CCR4-NOT complex and DDX6 ATPase in microRNA repression. <i>Molecular Cell</i> , 2014 , 54, 751-65	17.6	201
19	The yeast exosome functions as a macromolecular cage to channel RNA substrates for degradation. <i>Cell</i> , 2009 , 139, 547-59	56.2	201
18	Molecular mechanisms for the RNA-dependent ATPase activity of Upf1 and its regulation by Upf2. <i>Molecular Cell</i> , 2011 , 41, 693-703	17.6	183
17	Structural model of a CRISPR RNA-silencing complex reveals the RNA-target cleavage activity in Cmr4. <i>Molecular Cell</i> , 2014 , 56, 43-54	17.6	112
16	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, 12139-44	11.5	106
15	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, 9447-60	20.1	68
14	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	17.6	53
13	Structure of the RNA Helicase MLE Reveals the Molecular Mechanisms for Uridine Specificity and RNA-ATP Coupling. <i>Molecular Cell</i> , 2015 , 60, 487-99	17.6	47
12	The structure of the Pan2-Pan3 core complex reveals cross-talk between deadenylase and pseudokinase. <i>Nature Structural and Molecular Biology</i> , 2014 , 21, 591-8	17.6	40
11	Mpp6 Incorporation in the Nuclear Exosome Contributes to RNA Channeling through the Mtr4 Helicase. <i>Cell Reports</i> , 2017 , 20, 2279-2286	10.6	29
10	Distinct and evolutionary conserved structural features of the human nuclear exosome complex. <i>ELife</i> , 2018 , 7,	8.9	22
9	Structural basis for the activation of the C. elegans 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, 8614-9	11.5	21
8	Sen1 has unique structural features grafted on the architecture of the Upf1-like helicase family. <i>EMBO Journal</i> , 2017 , 36, 1590-1604	13	20
7	InsP binding to PIKK kinases revealed by the cryo-EM structure of an SMG1-SMG8-SMG9 complex. <i>Nature Structural and Molecular Biology</i> , 2019 , 26, 1089-1093	17.6	20
6	A conserved structural element in the RNA helicase UPF1 regulates its catalytic activity in an isoform-specific manner. <i>Nucleic Acids Research</i> , 2018 , 46, 2648-2659	20.1	15
5	Structure of substrate-bound SMG1-8-9 kinase complex reveals molecular basis for phosphorylation specificity. <i>ELife</i> , 2020 , 9,	8.9	11
4	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	3.9	9

LIST OF PUBLICATIONS

3	Structural insights into the nucleic acid remodeling mechanisms of the yeast THO-Sub2 complex. <i>ELife</i> , 2020 , 9,	8.9	6
2	Cryo-EM reconstructions of inhibitor-bound SMG1 kinase reveal an autoinhibitory state dependent on SMG8. <i>ELife</i> , 2021 , 10,	8.9	5
1	The human SKI complex regulates channeling of ribosome-bound RNA to the exosome via an intrinsic gatekeeping mechanism <i>Molecular Cell</i> , 2022 ,	17.6	3