

Bertrand SÃ©raphin

List of Publications by Year in descending order

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100601

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citing authors

#	ARTICLE	IF	CITATIONS
1	A conserved motif in human BTG1 and BTG2 proteins mediates interaction with the poly(A) binding protein PABPC1 to stimulate mRNA deadenylation. <i>RNA Biology</i> , 2021, 18, 2450-2465.	1.5	10
2	Pby1 is a direct partner of the Dcp2 decapping enzyme. <i>Nucleic Acids Research</i> , 2020, 48, 6353-6366.	6.5	4
3	Mammalian Hbs1L deficiency causes congenital anomalies and developmental delay associated with Pelota depletion and 80S monosome accumulation. <i>PLoS Genetics</i> , 2019, 15, e1007917.	1.5	15
4	Architecture of the yeast Elongator complex. <i>EMBO Reports</i> , 2017, 18, 264-279.	2.0	75
5	Structures and Activities of the Elongator Complex and Its Cofactors. <i>The Enzymes</i> , 2017, 41, 117-149.	0.7	14
6	A unique surface on Pat1 C-terminal domain directly interacts with Dcp2 decapping enzyme and Xrn1 5'â€”3' mRNA exonuclease in yeast. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E9493-E9501.	3.3	45
7	Structure of the active form of Dcp1â€”Dcp2 decapping enzyme bound to m7GDP and its Edc3 activator. <i>Nature Structural and Molecular Biology</i> , 2016, 23, 982-986.	3.6	48
8	Structural basis for tRNA modification by Elp3 from <i>Dehalococcoides mccartyi</i> . <i>Nature Structural and Molecular Biology</i> , 2016, 23, 794-802.	3.6	59
9	Acetylation-Dependent Control of Global Poly(A) RNA Degradation by CBP/p300 and HDAC1/2. <i>Molecular Cell</i> , 2016, 63, 927-938.	4.5	35
10	BTG2 bridges PABPC1 RNA-binding domains and CAF1 deadenylase to control cell proliferation. <i>Nature Communications</i> , 2016, 7, 10811.	5.8	69
11	Cbp2 interacts with THO/TREX through a novel type of RRM domain. <i>Nucleic Acids Research</i> , 2016, 44, 437-448.	6.5	26
12	Structure of the Elongator cofactor complex Kti11/Kti13 provides insight into the role of Kti13 in Elongatorâ€”dependent tRNA modification. <i>FEBS Journal</i> , 2015, 282, 819-833.	2.2	20
13	Loss of the scavenger mRNA decapping enzyme DCPS causes syndromic intellectual disability with neuromuscular defects. <i>Human Molecular Genetics</i> , 2015, 24, 3163-3171.	1.4	31
14	Elimination of cap structures generated by mRNA decay involves the new scavenger mRNA decapping enzyme Aph1/FHIT together with DcpS. <i>Nucleic Acids Research</i> , 2015, 43, 482-492.	6.5	43
15	A Novel Protein-Protein Interaction in the RES (REtention and Splicing) Complex. <i>Journal of Biological Chemistry</i> , 2014, 289, 28640-28650.	1.6	19
16	Dom34-Hbs1 mediated dissociation of inactive 80S ribosomes promotes restart of translation after stress. <i>EMBO Journal</i> , 2014, 33, n/a-n/a.	3.5	74
17	The C-Terminal Domain from <i>S. cerevisiae</i> Pat1 Displays Two Conserved Regions Involved in Decapping Factor Recruitment. <i>PLoS ONE</i> , 2014, 9, e96828.	1.1	14
18	Rapid screening of yeast mutants with reporters identifies new splicing phenotypes. <i>FEBS Journal</i> , 2013, 280, 2712-2726.	2.2	6

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19	Intracellular ribonucleases involved in transcript processing and decay: Precision tools for RNA. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2013, 1829, 491-513.	0.9	52
20	Identification of the Rps28 binding motif from yeast Edc3 involved in the autoregulatory feedback loop controlling RPS28B mRNA decay. <i>Nucleic Acids Research</i> , 2013, 41, 9514-9523.	6.5	19
21	C2ORF29/CNOT11 and CNOT10 form a new module of the CCR4-NOT complex. <i>RNA Biology</i> , 2013, 10, 267-276.	1.5	66
22	Rbg1â€™Tma46 dimer structure reveals new functional domains and their role in polysome recruitment. <i>Nucleic Acids Research</i> , 2012, 40, 11100-11114.	6.5	23
23	Elongator. <i>Transcription</i> , 2012, 3, 273-276.	1.7	28
24	Architecture of the Nuclease Module of the Yeast Ccr4-Not Complex: the Not1-Caf1-Ccr4 Interaction. <i>Molecular Cell</i> , 2012, 48, 207-218.	4.5	131
25	Extensive Degradation of RNA Precursors by the Exosome in Wild-Type Cells. <i>Molecular Cell</i> , 2012, 48, 409-421.	4.5	218
26	Surveillance pathways rescuing eukaryotic ribosomes lost in translation. <i>Nature Reviews Molecular Cell Biology</i> , 2012, 13, 727-735.	16.1	99
27	The Elongator subcomplex Elp456 is a hexameric RecA-like ATPase. <i>Nature Structural and Molecular Biology</i> , 2012, 19, 314-320.	3.6	85
28	Cotranscriptional spliceosome assembly and splicing are independent of the Prp40p WW domain. <i>Rna</i> , 2011, 17, 2119-2129.	1.6	28
29	The highly conserved eukaryotic DRG factors are required for efficient translation in a manner redundant with the putative RNA helicase Slh1. <i>Nucleic Acids Research</i> , 2011, 39, 2221-2233.	6.5	28
30	Dissection of Dom34â€™Hbs1 reveals independent functions in two RNA quality control pathways. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1446-1452.	3.6	60
31	Twins take the job. <i>EMBO Journal</i> , 2010, 29, 2260-2261.	3.5	2
32	Catalytic Properties of the Eukaryotic Exosome. <i>Advances in Experimental Medicine and Biology</i> , 2010, 702, 63-78.	0.8	28
33	Structure of the yeast Pml1 splicing factor and its integration into the RES complex. <i>Nucleic Acids Research</i> , 2009, 37, 129-143.	6.5	69
34	The BTG2 protein is a general activator of mRNA deadenylation. <i>EMBO Journal</i> , 2008, 27, 1039-1048.	3.5	100
35	Endonucleolytic RNA cleavage by a eukaryotic exosome. <i>Nature</i> , 2008, 456, 993-996.	13.7	284
36	Exosome-mediated quality control: Substrate recruitment and molecular activity. <i>Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms</i> , 2008, 1779, 558-565.	0.9	67

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37	The U1 snRNP-associated factor Luc7p affects 5' splice site selection in yeast and human. <i>Nucleic Acids Research</i> , 2007, 35, 5874-5885.	6.5	44
38	RNA channelling by the archaeal exosome. <i>EMBO Reports</i> , 2007, 8, 470-476.	2.0	108
39	A single subunit, Dis3, is essentially responsible for yeast exosome core activity. <i>Nature Structural and Molecular Biology</i> , 2007, 14, 15-22.	3.6	381
40	Subunit architecture of multimeric complexes isolated directly from cells. <i>EMBO Reports</i> , 2006, 7, 605-610.	2.0	168
41	In Vivo Targeting of the Yeast Pop2 Deadenylation Subunit to Reporter Transcripts Induces Their Rapid Degradation and Generates New Decay Intermediates. <i>Journal of Biological Chemistry</i> , 2006, 281, 25940-25947.	1.6	31
42	Conservation of the deadenylation activity of proteins of the Caf1 family in human. <i>Rna</i> , 2005, 11, 487-494.	1.6	84
43	Cryptic Pol II Transcripts Are Degraded by a Nuclear Quality Control Pathway Involving a New Poly(A) Polymerase. <i>Cell</i> , 2005, 121, 725-737.	13.5	764
44	Cytoplasmic foci are sites of mRNA decay in human cells. <i>Journal of Cell Biology</i> , 2004, 165, 31-40.	2.3	553
45	Proteomic analysis identifies a new complex required for nuclear pre-mRNA retention and splicing. <i>EMBO Journal</i> , 2004, 23, 4847-4856.	3.5	139
46	â€œCap-tabolismâ€™. <i>Trends in Biochemical Sciences</i> , 2004, 29, 436-444.	3.7	97
47	Xâ€ray structure and activity of the yeast Pop2 protein: a nuclease subunit of the mRNA deadenylation complex. <i>EMBO Reports</i> , 2003, 4, 1150-1155.	2.0	104
48	DcpS can act in the 5'-3' mRNA decay pathway in addition to the 3'-5' pathway. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2003, 100, 12081-12086.	3.3	75
49	Human Dcp2: a catalytically active mRNA decapping enzyme located in specific cytoplasmic structures. <i>EMBO Journal</i> , 2002, 21, 6915-6924.	3.5	398
50	The Tandem Affinity Purification (TAP) Method: A General Procedure of Protein Complex Purification. <i>Methods</i> , 2001, 24, 218-229.	1.9	1,550
51	REF, an evolutionarily conserved family of hnRNP-like proteins, interacts with TAP/Mex67p and participates in mRNA nuclear export. <i>Rna</i> , 2000, 6, 638-650.	1.6	331
52	The Apoptosis-Promoting Factor TIA-1 Is a Regulator of Alternative Pre-mRNA Splicing. <i>Molecular Cell</i> , 2000, 6, 1089-1098.	4.5	252
53	Transient interaction of BBP/ScSF1 and Mud2 with the splicing machinery affects the kinetics of spliceosome assembly. <i>Rna</i> , 1999, 5, 819-831.	1.6	79
54	Genomic-scale quantitative analysis of yeast pre-mRNA splicing: Implications for splice-site recognition. <i>Rna</i> , 1999, 5, 1135-1137.	1.6	62

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55	A generic protein purification method for protein complex characterization and proteome exploration. <i>Nature Biotechnology</i> , 1999, 17, 1030-1032.	9.4	2,543
56	The yeast U2Aâ€²/U2Bâ€³ complex is required for pre-spliceosome formation. <i>EMBO Journal</i> , 1998, 17, 6348-6358.	3.5	49
57	New constructs and strategies for efficient PCR-based gene manipulations in yeast. <i>Yeast</i> , 1998, 14, 1139-1146.	0.8	86
58	A role for U2/U6 helix Ib in 5â€² splice site selection. <i>Rna</i> , 1998, 4, 915-927.	1.6	25
59	Small nuclear RNAs in messenger RNA and ribosomal RNA processing.. <i>FASEB Journal</i> , 1993, 7, 47-53.	0.2	98
60	The HIT protein family: a new family of proteins present in prokaryotes, yeast and mammals. <i>DNA Sequence</i> , 1992, 3, 177-179.	0.7	82
61	Identification of functional U1 snRNA-pre-mRNA complexes committed to spliceosome assembly and splicing. <i>Cell</i> , 1989, 59, 349-358.	13.5	396