Jesper Qualmann Svejstrup

List of Publications by Year
in descending order

115 papers	10,454 citations	28274 55 h-index	33894 99 g-index
122 all docs	122 docs citations	122 times ranked	8981 citing authors

#	Article	IF	Citations
1	Heat shock induces premature transcript termination and reconfigures the human transcriptome. Molecular Cell, 2022, 82, 1573-1588.e10.	9.7	27
2	Developmental regulation of neuronal gene expression by Elongator complex protein 1 dosage. Journal of Genetics and Genomics, 2022, 49, 654-665.	3.9	6
3	UBAP2/UBAP2L regulate UV-induced ubiquitylation of RNA polymerase II and are the human orthologues of yeast Def1. DNA Repair, 2022, 115, 103343.	2.8	6
4	Causes and consequences of RNA polymerase II stalling during transcript elongation. Nature Reviews Molecular Cell Biology, 2021, 22, 3-21.	37.0	119
5	Elongation factor ELOF1 drives transcription-coupled repair and prevents genome instability. Nature Cell Biology, 2021, 23, 608-619.	10.3	41
6	Translation stress and collided ribosomes are co-activators of cGAS. Molecular Cell, 2021, 81, 2808-2822.e10.	9.7	52
7	Transcription-coupled repair and the transcriptional response to UV-Irradiation. DNA Repair, 2021, 107, 103208.	2.8	13
8	Using TTchem-seq for profiling nascent transcription and measuring transcript elongation. Nature Protocols, 2020, 15, 604-627.	12.0	46
9	Annotation matters: validating the discovery of cancer drivers. Molecular and Cellular Oncology, 2020, 7, 1806679.	0.7	1
10	CDK13 cooperates with CDK12 to control global RNA polymerase II processivity. Science Advances, 2020, 6, .	10.3	79
11	DDI2 Is a Ubiquitin-Directed Endoprotease Responsible for Cleavage of Transcription Factor NRF1. Molecular Cell, 2020, 79, 332-341.e7.	9.7	45
12	Regulation of the RNAPII Pool Is Integral to the DNA Damage Response. Cell, 2020, 180, 1245-1261.e21.	28.9	116
13	Evidence That STK19 Is Not an NRAS-dependent Melanoma Driver. Cell, 2020, 181, 1395-1405.e11.	28.9	13
14	The ASC-1 Complex Disassembles Collided Ribosomes. Molecular Cell, 2020, 79, 603-614.e8.	9.7	117
15	A Ubiquitin-Binding Domain that Binds a Structural Fold Distinct from that of Ubiquitin. Structure, 2019, 27, 1316-1325.e6.	3.3	23
16	Elongation Factor TFIIS Prevents Transcription Stress and R-Loop Accumulation to Maintain Genome Stability. Molecular Cell, 2019, 76, 57-69.e9.	9.7	79
17	Genome-wide reconstitution of chromatin transactions reveals that RSC preferentially disrupts H2AZ-containing nucleosomes. Genome Research, 2019, 29, 988-998.	5.5	21
18	SCAF4 and SCAF8, mRNA Anti-Terminator Proteins. Cell, 2019, 177, 1797-1813.e18.	28.9	85

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19	Analysis of RNA polymerase II ubiquitylation and proteasomal degradation. Methods, 2019, 159-160, 146-156.	3.8	17
20	Watch Out for Those Terrible Twos! Dinucleotide Accumulation Dysregulates Mitochondrial Transcription. Molecular Cell, 2019, 76, 696-698.	9.7	1
21	The Cellular Response to Transcription-Blocking DNA Damage. Trends in Biochemical Sciences, 2018, 43, 327-341.	7.5	107
22	UV Irradiation Induces a Non-coding RNA that Functionally Opposes the Protein Encoded by the Same Gene. Cell, 2017, 168, 843-855.e13.	28.9	157
23	Cockayne syndrome B protein regulates recruitment of the Elongin A ubiquitin ligase to sites of DNA damage. Journal of Biological Chemistry, 2017, 292, 6431-6437.	3.4	16
24	A ubiquitylation site in Cockayne syndrome B required for repair of oxidative DNA damage, but not for transcription-coupled nucleotide excision repair. Nucleic Acids Research, 2016, 44, 5246-5255.	14.5	30
25	Pharmacological Bypass of Cockayne Syndrome B Function in Neuronal Differentiation. Cell Reports, 2016, 14, 2554-2561.	6.4	18
26	Multiomic Analysis of the UV-Induced DNA Damage Response. Cell Reports, 2016, 15, 1597-1610.	6.4	162
27	Mutation of cancer driver<i>MLL2</i>results in transcription stress and genome instability. Genes and Development, 2016, 30, 408-420.	5.9	112
28	Retention of the Native Epigenome in Purified Mammalian Chromatin. PLoS ONE, 2015, 10, e0133246.	2.5	7
29	Dysregulation of gene expression as a cause of Cockayne syndrome neurological disease. Proceedings of the National Academy of Sciences of the United States of America, 2014, 111, 14454-14459.	7.1	78
30	RECQL5 Controls Transcript Elongation and Suppresses Genome Instability Associated with Transcription Stress. Cell, 2014, 157, 1037-1049.	28.9	162
31	Mechanistic Interpretation of Promoter-Proximal Peaks and RNAPII Density Maps. Cell, 2013, 154, 713-715.	28.9	109
32	Ubiquitylation and degradation of elongating RNA polymerase II: The last resort. Biochimica Et Biophysica Acta - Gene Regulatory Mechanisms, 2013, 1829, 151-157.	1.9	141
33	Proteasome-Mediated Processing of Def1, a Critical Step in the Cellular Response to Transcription Stress. Cell, 2013, 154, 983-995.	28.9	69
34	Synovial Sarcoma Mechanisms: A Series of Unfortunate Events. Cell, 2013, 153, 11-12.	28.9	12
35	Transcription: another mark in the tail. EMBO Journal, 2012, 31, 2753-2754.	7.8	8
36	DERP6 (ELP5) and C3ORF75 (ELP6) Regulate Tumorigenicity and Migration of Melanoma Cells as Subunits of Elongator. Journal of Biological Chemistry, 2012, 287, 32535-32545.	3.4	47

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37	Reprogramming chromatin. Critical Reviews in Biochemistry and Molecular Biology, 2012, 47, 464-482.	5.2	14
38	RNA Polymerase II Collision Interrupts Convergent Transcription. Molecular Cell, 2012, 48, 365-374.	9.7	149
39	DBIRD complex integrates alternative mRNA splicing with RNA polymerase II transcript elongation. Nature, 2012, 484, 386-389.	27.8	99
40	MultiDsk: A Ubiquitin-Specific Affinity Resin. PLoS ONE, 2012, 7, e46398.	2.5	27
41	Studying RNAâ€“Protein Interactions In Vivo By RNA Immunoprecipitation. Methods in Molecular Biology, 2011, 791, 253-264.	0.9	22
42	GTP-dependent Binding and Nuclear Transport of RNA Polymerase II by Npa3 Protein. Journal of Biological Chemistry, 2011, 286, 35553-35561.	3.4	45
43	Role of Elongator Subunit Elp3 in <i>Drosophila melanogaster</i> Larval Development and Immunity. Genetics, 2011, 187, 1067-1075.	2.9	51
44	The interface between transcription and mechanisms maintaining genome integrity. Trends in Biochemical Sciences, 2010, 35, 333-338.	7.5	62
45	Interacting partners of the Tfb2 subunit from yeast TFIIH. DNA Repair, 2010, 9, 33-39.	2.8	13
46	RECQL5 helicase: Connections to DNA recombination and RNA polymerase II transcription. DNA Repair, 2010, 9, 345-353.	2.8	25
47	In Vitro Reconstitution of PHO5 Promoter Chromatin Remodeling Points to a Role for Activator-Nucleosome Competition In Vivo. Molecular and Cellular Biology, 2010, 30, 4060-4076.	2.3	16
48	A Role for Checkpoint Kinase-Dependent Rad26 Phosphorylation in Transcription-Coupled DNA Repair in <i>Saccharomyces cerevisiae</i>. Molecular and Cellular Biology, 2010, 30, 436-446.	2.3	18
49	Transcript Elongation by RNA Polymerase II. Annual Review of Biochemistry, 2010, 79, 271-293.	11.1	160
50	Evidence that Transcript Cleavage Is Essential for RNA Polymerase II Transcription and Cell Viability. Molecular Cell, 2010, 38, 202-210.	9.7	116
51	A Ubiquitin-Binding Domain in Cockayne Syndrome B Required for Transcription-Coupled Nucleotide Excision Repair. Molecular Cell, 2010, 38, 637-648.	9.7	109
52	Triptolide is an inhibitor of RNA polymerase I and IIâ€“dependent transcription leading predominantly to down-regulation of short-lived mRNA. Molecular Cancer Therapeutics, 2009, 8, 2780-2790.	4.1	152
53	An Iron-Sulfur Cluster Domain in Elp3 Important for the Structural Integrity of Elongator. Journal of Biological Chemistry, 2009, 284, 141-149.	3.4	52
54	Distinct ubiquitin ligases act sequentially for RNA polymerase II polyubiquitylation. Proceedings of the National Academy of Sciences of the United States of America, 2009, 106, 20705-20710.	7.1	144

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55	Direct Inhibition of RNA Polymerase II Transcription by RECQL5. Journal of Biological Chemistry, 2009, 284, 23197-23203.	3.4	52
56	RNA Immunoprecipitation to Determine RNA-Protein Associations In Vivo. Cold Spring Harbor Protocols, 2009, 2009, pdb.prot5234.	0.3	54
57	Stability, Flexibility, and Dynamic Interactions of Colliding RNA Polymerase II Elongation Complexes. Molecular Cell, 2009, 35, 191-205.	9.7	83
58	An Rtt109-Independent Role for Vps75 in Transcription-Associated Nucleosome Dynamics. Molecular and Cellular Biology, 2009, 29, 4220-4234.	2.3	26
59	Reversal of RNA Polymerase II Ubiquitylation by the Ubiquitin Protease Ubp3. Molecular Cell, 2008, 30, 498-506.	9.7	56
60	A RECQ5â€"RNA polymerase II association identified by targeted proteomic analysis of human chromatin. Proceedings of the National Academy of Sciences of the United States of America, 2008, 105, 8580-8584.	7.1	123
61	Vps75, A New Yeast Member of the NAP Histone Chaperone Family. Journal of Biological Chemistry, 2007, 282, 12358-12362.	3.4	75
62	Hyperphosphorylation of the C-terminal Repeat Domain of RNA Polymerase II Facilitates Dissociation of Its Complex with Mediator. Journal of Biological Chemistry, 2007, 282, 14113-14120.	3.4	99
63	A role for noncoding transcription in activation of the yeast PHO5 gene. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 8011-8016.	7.1	150
64	Communication between Distant Sites in RNA Polymerase II through Ubiquitylation Factors and the Polymerase CTD. Cell, 2007, 129, 57-68.	28.9	65
65	Damage-Induced Ubiquitylation of Human RNA Polymerase II by the Ubiquitin Ligase Nedd4, but Not Cockayne Syndrome Proteins or BRCA1. Molecular Cell, 2007, 28, 386-397.	9.7	175
66	Elongator complex: how many roles does it play?. Current Opinion in Cell Biology, 2007, 19, 331-336.	5.4	142
67	Contending with transcriptional arrest during RNAPII transcript elongation. Trends in Biochemical Sciences, 2007, 32, 165-171.	7.5	94
68	RNA Immunoprecipitation for Determining RNAâ€Protein Associations In Vivo. Current Protocols in Molecular Biology, 2006, 75, Unit 27.4.	2.9	84
69	Transcription Impairment and Cell Migration Defects in Elongator-Depleted Cells: Implication for Familial Dysautonomia. Molecular Cell, 2006, 22, 521-531.	9.7	191
70	RNA Polymerase II: A â€œNobelâ€•Enzyme Demystified. Molecular Cell, 2006, 24, 637-642.	9.7	3
71	An Assay for Studying Ubiquitylation of RNA Polymerase II and Other Proteins in Crude Yeast Extracts. Methods in Enzymology, 2006, 408, 264-273.	1.0	1
72	Physical and Functional Interaction between Elongator and the Chromatin-associated Kti12 Protein. Journal of Biological Chemistry, 2005, 280, 19454-19460.	3.4	31

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73	Interaction of Fcp1 Phosphatase with Elongating RNA Polymerase II Holoenzyme, Enzymatic Mechanism of Action, and Genetic Interaction with Elongator. Journal of Biological Chemistry, 2005, 280, 4299-4306.	3.4	36
74	Multiple Mechanisms Confining RNA Polymerase II Ubiquitylation to Polymerases Undergoing Transcriptional Arrest. Cell, 2005, 121, 913-923.	28.9	198
75	Molecular Architecture, Structure-Function Relationship, and Importance of the Elp3 Subunit for the RNA Binding of Holo-Elongator. Journal of Biological Chemistry, 2004, 279, 32087-32092.	3.4	34
76	DNA Damage-induced Def1-RNA Polymerase II Interaction and Def1 Requirement for Polymerase Ubiquitylation in Vitro. Journal of Biological Chemistry, 2004, 279, 29875-29878.	3.4	46
77	Evidence for distinct mechanisms facilitating transcript elongation through chromatin in vivo. EMBO Journal, 2004, 23, 4243-4252.	7.8	160
78	The RNA polymerase II transcription cycle: cycling through chromatin. Biochimica Et Biophysica Acta Gene Regulatory Mechanisms, 2004, 1677, 64-73.	2.4	78
79	Elongator Interactions with Nascent mRNA Revealed by RNA Immunoprecipitation. Molecular Cell, 2004, 14, 457-464.	9.7	125
80	Hereditary dysautonomias: current knowledge and collaborations for the future. Clinical Autonomic Research, 2003, 13, 180-195.	2.5	2
81	Purification of Elongating RNA Polymerase II and Other Factors from Yeast Chromatin. Methods in Enzymology, 2003, 371, 491-498.	1.0	7
82	Keeping RNA and DNA Apart during Transcription. Molecular Cell, 2003, 12, 538-539.	9.7	11
83	Rescue of arrested RNA polymerase II complexes. Journal of Cell Science, 2003, 116, 447-451.	2.0	114
84	TRANSCRIPTION: Histones Face the FACT. Science, 2003, 301, 1053-1055.	12.6	34
85	Spreading of Sir3 protein in cells with severe histone H3 hypoacetylation. Proceedings of the National Academy of Sciences of the United States of America, 2003, 100, 7551-7556.	7.1	38
86	Purification and Characterization of the Human Elongator Complex. Journal of Biological Chemistry, 2002, 277, 3047-3052.	3.4	230
87	Elongator is a histone H3 and H4 acetyltransferase important for normal histone acetylation levelsin vivo. Proceedings of the National Academy of Sciences of the United States of America, 2002, 99, 3517-3522.	7.1	503
88	The NC2 alpha and beta subunits play different roles in vivo. Genes and Development, 2002, 16, 3265-3276.	5.9	27
89	Isolation and mass spectrometry of transcription factor complexes. Methods, 2002, 26, 260-269.	3.8	81
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91	Transcriptional Inhibition of Genes with Severe Histone H3 Hypoacetylation in the Coding Region. Molecular Cell, 2002, 10, 925-933.	9.7	109
92	Incision of a 1,3-intrastrand d(GpTpG)-cisplatin adduct by nucleotide excision repair proteins from yeast. DNA Repair, 2002, 1, 731-741.	2.8	15
93	Chromatin elongation factors. Current Opinion in Genetics and Development, 2002, 12, 156-161.	3.3	40
94	A Rad26â€“Def1 complex coordinates repair and RNA pol II proteolysis in response to DNA damage. Nature, 2002, 415, 929-933.	27.8	205
95	Mechanisms of transcription-coupled DNA repair. Nature Reviews Molecular Cell Biology, 2002, 3, 21-29.	37.0	349
96	Involvement of yeast carboxy-terminal domain kinase I (CTDK-I) in transcription elongation in vivo. Gene, 2001, 267, 31-36.	2.2	50
97	Transcription-coupled DNA repair without the transcription-coupling repair factor. Trends in Biochemical Sciences, 2001, 26, 151.	7.5	2
98	RNA Polymerase II Elongator Holoenzyme Is Composed of Two Discrete Subcomplexes. Journal of Biological Chemistry, 2001, 276, 32743-32749.	3.4	153
99	The Elp2 Subunit of Elongator and Elongating RNA Polymerase II Holoenzyme Is a WD40 Repeat Protein. Journal of Biological Chemistry, 2000, 275, 12896-12899.	3.4	58
100	Elongator, a Multisubunit Component of a Novel RNA Polymerase II Holoenzyme for Transcriptional Elongation. Molecular Cell, 1999, 3, 109-118.	9.7	713
101	A Novel Histone Acetyltransferase Is an Integral Subunit of Elongating RNA Polymerase II Holoenzyme. Molecular Cell, 1999, 4, 123-128.	9.7	432
102	Genes For Tfb2, Tfb3, and Tfb4 Subunits of Yeast Transcription/Repair Factor IIH. Journal of Biological Chemistry, 1997, 272, 19319-19327.	3.4	72
103	Purification and Characterization of Human Topoisomerase I Mutants. FEBS Journal, 1996, 236, 389-394.	0.2	29
104	Subunits of Yeast RNA Polymerase II Transcription Factor TFIIH Encoded by the CCL1 Gene. Journal of Biological Chemistry, 1996, 271, 643-645.	3.4	37
105	Different forms of TFIIH for transcription and DNA repair: Holo-TFIIH and a nucleotide excision repairosome. Cell, 1995, 80, 21-28.	28.9	271
106	Nucleotide excision repair in the yeast Saccharomyces cerevisiae: its relationship to specialized mitotic recombination and RNA polymerase II basal transcription. , 1995, , 59-64.		1
107	Transcription factor b (TFIIH) is required during nucleotide-excision repair in yeast. Nature, 1994, 368, 74-76.	27.8	176
108	Relationship of CDK-activating kinase and RNA polymerase II CTD kinase TFIIH/TFIIK. Cell, 1994, 79, 1103-1109.	28.9	419

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109	Recent Insights on DNA Repair: The Mechanism of Damaged Nucleotide Excision in Eukaryotes and Its Relationship to Other Cellular Processes. Annals of the New York Academy of Sciences, 1994, 726, 281-291.	3.8	7
110	The DNA Binding, Cleavage, and Religation Reactions of Eukaryotic Topoisomerases I and II. Advances in Pharmacology, 1994, 29A, 83-101.	2.0	29
111	Dual roles of a multiprotein complex from S. cerevisiae in transcription and DNA repair. Cell, 1993, 75, 1379-1387.	28.9	337
112	Characterization of an altered DNA catalysis of a camptothecin-resistant eukaryotic topoisomerase I. Nucleic Acids Research, 1993, 21, 593-600.	14.5	41
113	Camptothecin inhibits both the cleavage and religation reactions of eukaryotic DNA topoisomerase I. Journal of Molecular Biology, 1992, 228, 1025-1030.	4.2	81
114	New technique for uncoupling the cleavage and religation reactions of Eukaryotic Topoisomerase I.. Journal of Molecular Biology, 1991, 222, 669-678.	4.2	150
115	Elongation Factor TFIIS Prevents Transcription Stress and R-Loop Accumulation to Maintain Genome Stability. SSRN Electronic Journal, 0, , .	0.4	0