Phillip A Sharp

List of Publications by Year in Descending Order

97 papers	37,038 citations	74 h-index	106 g-index
106 ext. papers	42,586 ext. citations	28.7 avg, IF	7.44 L-index

#	Paper	IF	Citations
97	RNA in formation and regulation of transcriptional condensates. *Rna*, **2021**,	5.8	5
96	RNA-Mediated Feedback Control of Transcriptional Condensates. *Cell*, **2021**, 184, 207-225.e24	56.2	99
95	Partitioning of cancer therapeutics in nuclear condensates. *Science*, **2020**, 368, 1386-1392	33.3	120
94	MicroRNAs organize intrinsic variation into stem cell states. *Proceedings of the National Academy of Sciences of the United States of America*, **2020**, 117, 6942-6950	11.5	10
93	Imprinted Maternally Expressed microRNAs Antagonize Paternally Driven Gene Programs in Neurons. *Molecular Cell*, **2020**, 78, 85-95.e8	17.6	14
92	Gain-of-function mutation of microRNA-140 in human skeletal dysplasia. *Nature Medicine*, **2019**, 25, 583-590	30.5	38
91	Pol□I phosphorylation regulates a switch between transcriptional and splicing condensates. *Nature*, **2019**, 572, 543-548	50.4	255
90	Enhancer Features that Drive Formation of Transcriptional Condensates. *Molecular Cell*, **2019**, 75, 549-561.e7	17.6	155
89	Sequestration of microRNA-mediated target repression by the Ago2-associated RNA-binding protein FAM120A. *Rna*, **2019**, 25, 1291-1297	5.8	12
88	Mapping a functional cancer genome atlas of tumor suppressors in mouse liver using AAV-CRISPR-mediated direct in vivo screening. *Science Advances*, **2018**, 4, eaao5508	14.3	37
87	Deconvolution of seed and RNA-binding protein crosstalk in RNAi-based functional genomics. *Nature Genetics*, **2018**, 50, 657-661	36.3	14
86	Transcriptional Pause Sites Delineate Stable Nucleosome-Associated Premature Polyadenylation Suppressed by U1 snRNP. *Molecular Cell*, **2018**, 69, 648-663.e7	17.6	65
85	CDK12 regulates DNA repair genes by suppressing intronic polyadenylation. *Nature*, **2018**, 564, 141-145	50.4	100
84	Evolution of weak cooperative interactions for biological specificity. *Proceedings of the National Academy of Sciences of the United States of America*, **2018**, 115, E11053-E11060	11.5	21
83	Coactivator condensation at super-enhancers links phase separation and gene control. *Science*, **2018**, 361,	33.3	951
82	Alternative RNA splicing in the endothelium mediated in part by Rbfox2 regulates the arterial response to low flow. *ELife*, **2018**, 7,	8.9	14
81	Super-Enhancer-Mediated RNA Processing Revealed by Integrative MicroRNA Network Analysis. *Cell*, **2017**, 168, 1000-1014.e15	56.2	167

80	Dicer loss and recovery induce an oncogenic switch driven by transcriptional activation of the oncofetal Imp1-3 family. *Genes and Development*, **2017**, 31, 674-687	12.6	11
79	A Phase Separation Model for Transcriptional Control. *Cell*, **2017**, 169, 13-23	56.2	856
78	Coordinated Splicing of Regulatory Detained Introns within Oncogenic Transcripts Creates an Exploitable Vulnerability in Malignant Glioma. *Cancer Cell*, **2017**, 32, 411-426.e11	24.3	99
77	Synthetic RNA-Based Immunomodulatory Gene Circuits for Cancer Immunotherapy. *Cell*, **2017**, 171, 1138-1150.e15	56.2	81
76	AAV-mediated direct in vivo CRISPR screen identifies functional suppressors in glioblastoma. *Nature Neuroscience*, **2017**, 20, 1329-1341	25.5	119
75	Cell-Type-Specific Alternative Splicing Governs Cell Fate in the Developing Cerebral Cortex. *Cell*, **2016**, 166, 1147-1162.e15	56.2	159
74	GENE EXPRESSION. Single-cell variability guided by microRNAs. *Science*, **2016**, 352, 1390-1	33.3	14
73	Elucidating MicroRNA Regulatory Networks Using Transcriptional, Post-transcriptional, and Histone Modification Measurements. *Cell Reports*, **2016**, 14, 310-9	10.6	71
72	Genome-wide CRISPR screen in a mouse model of tumor growth and metastasis. *Cell*, **2015**, 160, 1246-60	56.2	544
71	In vivo genome editing using Staphylococcus aureus Cas9. *Nature*, **2015**, 520, 186-91	50.4	1700
70	Transcription factor trapping by RNA in gene regulatory elements. *Science*, **2015**, 350, 978-81	33.3	267
69	Detained introns are a novel, widespread class of post-transcriptionally spliced introns. *Genes and Development*, **2015**, 29, 63-80	12.6	228
68	Rbfox2 controls autoregulation in RNA-binding protein networks. *Genes and Development*, **2014**, 28, 637-51	12.6	82
67	Genome-wide binding of the CRISPR endonuclease Cas9 in mammalian cells. *Nature Biotechnology*, **2014**, 32, 670-6	44.5	666
66	Global microRNA depletion suppresses tumor angiogenesis. *Genes and Development*, **2014**, 28, 1054-67	12.6	52
65	Endogenous miRNA and target concentrations determine susceptibility to potential ceRNA competition. *Molecular Cell*, **2014**, 56, 347-359	17.6	271
64	Target specificity of the CRISPR-Cas9 system. *Quantitative Biology*, **2014**, 2, 59-70	3.9	184
63	Building robust transcriptomes with master splicing factors. *Cell*, **2014**, 159, 487-98	56.2	104

62	CRISPR-mediated direct mutation of cancer genes in the mouse liver. *Nature*, **2014**, 514, 380-4	50.4	521
61	CRISPR-Cas9 knockin mice for genome editing and cancer modeling. *Cell*, **2014**, 159, 440-55	56.2	1089
60	RNA Bind-n-Seq: quantitative assessment of the sequence and structural binding specificity of RNA binding proteins. *Molecular Cell*, **2014**, 54, 887-900	17.6	251
59	LincRNA-p21 activates p21 in cis to promote Polycomb target gene expression and to enforce the G1/S checkpoint. *Molecular Cell*, **2014**, 54, 777-90	17.6	319
58	Genome editing with Cas9 in adult mice corrects a disease mutation and phenotype. *Nature Biotechnology*, **2014**, 32, 551-3	44.5	694
57	Argonaute-bound small RNAs from promoter-proximal RNA polymerase II. *Cell*, **2014**, 156, 920-34	56.2	83
56	Divergent transcription: a driving force for new gene origination?. *Cell*, **2013**, 155, 990-6	56.2	118
55	Divergent transcription of long noncoding RNA/mRNA gene pairs in embryonic stem cells. *Proceedings of the National Academy of Sciences of the United States of America*, **2013**, 110, 2876-81	11.5	345
54	The role of miRNAs in regulating gene expression networks. *Journal of Molecular Biology*, **2013**, 425, 3582-600	6.5	277
53	Promoter directionality is controlled by U1 snRNP and polyadenylation signals. *Nature*, **2013**, 499, 360-3	50.4	294
52	Let-7 represses Nr6a1 and a mid-gestation developmental program in adult fibroblasts. *Genes and Development*, **2013**, 27, 941-54	12.6	34
51	In vivo structure-function analysis of human Dicer reveals directional processing of precursor miRNAs. *Rna*, **2012**, 18, 1116-22	5.8	88
50	Roles for microRNAs in conferring robustness to biological processes. *Cell*, **2012**, 149, 515-24	56.2	1162
49	MicroRNAs can generate thresholds in target gene expression. *Nature Genetics*, **2011**, 43, 854-9	36.3	484
48	MiR-17/20/93/106 promote hematopoietic cell expansion by targeting sequestosome 1-regulated pathways in mice. *Blood*, **2011**, 118, 916-25	2.2	125
47	Genome-wide identification of Ago2 binding sites from mouse embryonic stem cells with and without mature microRNAs. *Nature Structural and Molecular Biology*, **2011**, 18, 237-44	17.6	202
46	Research agenda. Promoting convergence in biomedical science. *Science*, **2011**, 333, 527	33.3	87
45	Antisense RNA polymerase II divergent transcripts are P-TEFb dependent and substrates for the RNA exosome. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 10460-5	11.5	141

44	Genome-wide impact of a recently expanded microRNA cluster in mouse. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 15804-9	11.5	42
43	Mir-290-295 deficiency in mice results in partially penetrant embryonic lethality and germ cell defects. *Proceedings of the National Academy of Sciences of the United States of America*, **2011**, 108, 14163-8	11.5	120
42	A latent pro-survival function for the mir-290-295 cluster in mouse embryonic stem cells. *PLoS Genetics*, **2011**, 7, e1002054	6	83
41	Histone H3K27ac separates active from poised enhancers and predicts developmental state. *Proceedings of the National Academy of Sciences of the United States of America*, **2010**, 107, 21931-6	11.5	2453
40	c-Myc regulates transcriptional pause release. *Cell*, **2010**, 141, 432-45	56.2	930
39	MicroRNA sponges: progress and possibilities. *Rna*, **2010**, 16, 2043-50	5.8	512
38	Emerging roles for natural microRNA sponges. *Current Biology*, **2010**, 20, R858-61	6.3	379
37	The centrality of RNA. *Cell*, **2009**, 136, 577-80	56.2	322
36	Divergent transcription: a new feature of active promoters. *Cell Cycle*, **2009**, 8, 2557-64	4.7	140
35	Divergent transcription from active promoters. *Science*, **2008**, 322, 1849-51	33.3	695
34	Targeted deletion reveals essential and overlapping functions of the miR-17 through 92 family of miRNA clusters. *Cell*, **2008**, 132, 875-86	56.2	1332
33	Connecting microRNA genes to the core transcriptional regulatory circuitry of embryonic stem cells. *Cell*, **2008**, 134, 521-33	56.2	1228
32	MicroRNA sponges: competitive inhibitors of small RNAs in mammalian cells. *Nature Methods*, **2007**, 4, 721-6	21.6	1619
31	RNA sequence analysis defines Dicer1 role in mouse embryonic stem cells. *Proceedings of the National Academy of Sciences of the United States of America*, **2007**, 104, 18097-102	11.5	261
30	Characterization of a highly variable eutherian microRNA gene. *Rna*, **2005**, 11, 1245-57	5.8	117
29	Single nucleotide polymorphism-based validation of exonic splicing enhancers. *PLoS Biology*, **2004**, 2, E268	9.7	158
28	Specificity of microRNA target selection in translational repression. *Genes and Development*, **2004**, 18, 504-11	12.6	1249
27	siRNAs can function as miRNAs. *Genes and Development*, **2003**, 17, 438-42	12.6	935

26	Embryonic stem cell-specific MicroRNAs. *Developmental Cell*, **2003**, 5, 351-8	10.2	938
25	Lentivirus-delivered stable gene silencing by RNAi in primary cells. *Rna*, **2003**, 9, 493-501	5.8	920
24	A ribozyme selected from variants of U6 snRNA promotes 2',5'-branch formation. *Rna*, **2001**, 7, 29-43	5.8	16
23	The SRm160/300 splicing coactivator subunits. *Rna*, **2000**, 6, 111-20	5.8	76
22	A novel 50-kilodalton fragment of host cell factor 1 (C1) in G(0) cells. *Molecular and Cellular Biology*, **2000**, 20, 3568-75	4.8	7
21	RNAi: double-stranded RNA directs the ATP-dependent cleavage of mRNA at 21 to 23 nucleotide intervals. *Cell*, **2000**, 101, 25-33	56.2	2137
20	View of life sciences in the 21st century. *Journal of Dermatological Science*, **2000**, 24 Suppl 1, S1-14	4.3	
19	PUF60: a novel U2AF65-related splicing activity. *Rna*, **1999**, 5, 1548-60	5.8	101
18	Evolutionary fates and origins of U12-type introns. *Molecular Cell*, **1998**, 2, 773-85	17.6	213
17	Split Genes and RNA Splicing (Nobel Lecture). *Angewandte Chemie International Edition in English*, **1994**, 33, 1229-1240		12
16	DNA topology and a minimal set of basal factors for transcription by RNA polymerase II. *Cell*, **1993**, 73, 533-40	56.2	343
15	Evidence for two active sites in the spliceosome provided by stereochemistry of pre-mRNA splicing. *Nature*, **1993**, 365, 364-8	50.4	213
14	Five intermediate complexes in transcription initiation by RNA polymerase II. *Cell*, **1989**, 56, 549-61	56.2	987
13	Regulation by HIV Rev depends upon recognition of splice sites. *Cell*, **1989**, 59, 789-95	56.2	498
12	A nuclear factor that binds to a conserved sequence motif in transcriptional control elements of immunoglobulin genes. *Nature*, **1986**, 319, 154-8	50.4	1167
11	A lymphoid-specific protein binding to the octamer motif of immunoglobulin genes. *Nature*, **1986**, 323, 640-3	50.4	728
10	Characterization of the branch site in lariat RNAs produced by splicing of mRNA precursors. *Nature*, **1985**, 313, 552-7	50.4	213
9	Cofactor requirements of splicing of purified messenger RNA precursors. *Nature*, **1984**, 308, 375-7	50.4	84

8	Regulation of heat shock protein 70 gene expression by c-myc. *Nature*, **1984**, 312, 280-2	50.4	260
7	Conversion of RNA to DNA in mammals: Alu-like elements and pseudogenes. *Nature*, **1983**, 301, 471-2	50.4	202
6	Inhibition of adenovirus early region IV transcription in vitro by a purified viral DNA binding protein. *Nature*, **1983**, 302, 545-7	50.4	71
5	The sequences of an expressed rat alpha-tubulin gene and a pseudogene with an inserted repetitive element. *Nature*, **1982**, 300, 330-5	50.4	278
4	A gene chimaera of SV40 and mouse beta-globin is transcribed and properly spliced. *Nature*, **1981**, 289, 378-82	50.4	89
3	Spliced segments at the 5Ũterminus of adenovirus 2 late mRNA. *Proceedings of the National Academy of Sciences of the United States of America*, **1977**, 74, 3171-5	11.5	942
2	Enhancer features that drive formation of transcriptional condensates		1
1	CDK13 Mutations Drive Melanoma via Accumulation of Prematurely Terminated Transcripts		1