Danesh Moazed

List of Publications by Year
in descending order

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79	13,299	38742 50	66911 78
papers	citations	h-index	g-index

93	93	93	10340
all docs	docs citations	times ranked	citing authors

#	Article	IF	Citations
1	RNAi-Mediated Targeting of Heterochromatin by the RITS Complex. Science, 2004, 303, 672-676.	12.6	1,110
2	Heterochromatin and Epigenetic Control of Gene Expression. Science, 2003, 301, 798-802.	12.6	926
3	RNA-mediated epigenetic regulation of gene expression. Nature Reviews Genetics, 2015, 16, 71-84.	16.3	832
4	Small RNAs in transcriptional gene silencing and genome defence. Nature, 2009, 457, 413-420.	27.8	773
5	Exit from Mitosis Is Triggered by Tem1-Dependent Release of the Protein Phosphatase Cdc14 from Nucleolar RENT Complex. Cell, 1999, 97, 233-244.	28.9	684
6	Two RNAi Complexes, RITS and RDRC, Physically Interact and Localize to Noncoding Centromeric RNAs. Cell, 2004, 119, 789-802.	28.9	506
7	Identification of a Class of Small Molecule Inhibitors of the Sirtuin Family of NAD-dependent Deacetylases by Phenotypic Screening. Journal of Biological Chemistry, 2001, 276, 38837-38843.	3.4	482
8	An Enzymatic Activity in the Yeast Sir2 Protein that Is Essential for Gene Silencing. Cell, 1999, 99, 735-745.	28.9	384
9	RITS acts in cis to promote RNA interferenceâ€“mediated transcriptional and post-transcriptional silencing. Nature Genetics, 2004, 36, 1174-1180.	21.4	375
10	Net1, a Sir2-Associated Nucleolar Protein Required for rDNA Silencing and Nucleolar Integrity. Cell, 1999, 97, 245-256.	28.9	366
11	Tethering RITS to a Nascent Transcript Initiates RNAi- and Heterochromatin-Dependent Gene Silencing. Cell, 2006, 125, 873-886.	28.9	355
12	Steps in Assembly of Silent Chromatin in Yeast: Sir3-Independent Binding of a Sir2/Sir4 Complex to Silencers and Role for Sir2-Dependent Deacetylation. Molecular and Cellular Biology, 2002, 22, 4167-4180.	2.3	275
13	RNA-dependent RNA polymerase is an essential component of a self-enforcing loop coupling heterochromatin assembly to siRNA production. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 152-157.	7.1	263
14	Epigenetic inheritance uncoupled from sequence-specific recruitment. Science, 2015, 348, 1258699.	12.6	256
15	Common Themes in Mechanisms of Gene Silencing. Molecular Cell, 2001, 8, 489-498.	9.7	252
16	The nuclear envelope in genome organization, expression and stability. Nature Reviews Molecular Cell Biology, 2010, 11, 317-328.	37.0	248
17	A Deubiquitinating Enzyme Interacts with SIR4 and Regulates Silencing in S. cerevisiae. Cell, 1996, 86, 667-677.	28.9	244
18	Assembly of the SIR Complex and Its Regulation by O -Acetyl-ADP-Ribose, a Product of NAD-Dependent Histone Deacetylation. Cell, 2005, 121, 515-527.	28.9	242

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19	RNAi and Heterochromatin Assembly. Cold Spring Harbor Perspectives in Biology, 2015, 7, a019323.	5.5	236
20	RNAi-Dependent and -Independent RNAÂTurnover Mechanisms Contribute toÂHeterochromatic Gene Silencing. Cell, 2007, 129, 707-721.	28.9	226
21	Role for perinuclear chromosome tethering in maintenance of genome stability. Nature, 2008, 456, 667-670.	27.8	215
22	Transcription and RNAi in heterochromatic gene silencing. Nature Structural and Molecular Biology, 2007, 14, 1041-1048.	8.2	211
23	Mechanisms for the Inheritance of Chromatin States. Cell, 2011, 146, 510-518.	28.9	207
24	Association of the RENT complex with nontranscribed and coding regions of rDNA and a regional requirement for the replication fork block protein Fob1 in rDNA silencing. Genes and Development, 2003, 17, 2162-2176.	5.9	203
25	HP1 Proteins Form Distinct Complexes and Mediate Heterochromatic Gene Silencing by Nonoverlapping Mechanisms. Molecular Cell, 2008, 32, 778-790.	9.7	195
26	Sir2 Regulates Histone H3 Lysine 9 Methylation and Heterochromatin Assembly in Fission Yeast. Current Biology, 2003, 13, 1240-1246.	3.9	185
27	TRAMP-mediated RNA surveillance prevents spurious entry of RNAs into the Schizosaccharomyces pombe siRNA pathway. Nature Structural and Molecular Biology, 2008, 15, 1015-1023.	8.2	173
28	Enzymatic activities of Sir2 and chromatin silencing. Current Opinion in Cell Biology, 2001, 13, 232-238.	5.4	159
29	Dicer-Independent Primal RNAs Trigger RNAi and Heterochromatin Formation. Cell, 2010, 140, 504-516.	28.9	156
30	A Cullin E3 Ubiquitin Ligase Complex Associates with Rik1 and the Clr4 Histone H3-K9 Methyltransferase and is Required for RNAi-Mediated Heterochromatin Formation. RNA Biology, 2005, 2, 106-111.	3.1	149
31	Role of the Conserved Sir3-BAH Domain in Nucleosome Binding and Silent Chromatin Assembly. Molecular Cell, 2007, 28, 1015-1028.	9.7	145
32	Inhibition of homologous recombination by a cohesin-associated clamp complex recruited to the rDNA recombination enhancer. Genes and Development, 2006, 20, 2887-2901.	5.9	144
33	Coupling of Double-Stranded RNA Synthesis and siRNA Generation in Fission Yeast RNAi. Molecular Cell, 2007, 27, 449-461.	9.7	134
34	RNAi-directed assembly of heterochromatin in fission yeast. FEBS Letters, 2005, 579, 5872-5878.	2.8	124
35	DNA sequence-dependent epigenetic inheritance of gene silencing and histone H3K9 methylation. Science, 2017, 356, 88-91.	12.6	107
36	Two different Argonaute complexes are required for siRNA generation and heterochromatin assembly in fission yeast. Nature Structural and Molecular Biology, 2007, 14, 200-207.	8.2	105

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37	siRNA-Mediated Heterochromatin Establishment Requires HP1 and Is Associated with Antisense Transcription. Molecular Cell, 2008, 31, 178-189.	9.7	98
38	Unique roles for histone H3K9me states in RNAi and heritable silencing of transcription. Nature, 2017, 547, 463-467.	27.8	96
39	Epigenetic inheritance mediated by coupling of RNAi and histone H3K9 methylation. Nature, 2018, 558, 615-619.	27.8	91
40	Post-transcriptional regulation of meiotic genes by a nuclear RNA silencing complex. Rna, 2014, 20, 867-881.	3.5	90
41	A Nonhistone Protein-Protein Interaction Required for Assembly of the SIR Complex and Silent Chromatin. Molecular and Cellular Biology, 2005, 25, 4514-4528.	2.3	85
42	Reconstitution of Heterochromatin-Dependent Transcriptional Gene Silencing. Molecular Cell, 2009, 35, 769-781.	9.7	77
43	Native Chromatin Proteomics Reveals a Role for Specific Nucleoporins in Heterochromatin Organization and Maintenance. Molecular Cell, 2020, 77, 51-66.e8.	9.7	75
44	Budding Yeast Silencing Complexes and Regulation of Sir2 Activity by Protein-Protein Interactions. Molecular and Cellular Biology, 2004, 24, 6931-6946.	2.3	73
45	Recombinational Repair within Heterochromatin Requires ATP-Dependent Chromatin Remodeling. Cell, 2009, 138, 1109-1121.	28.9	73
46	The Methyltransferase Activity of Clr4Suv39h Triggers RNAi Independently of Histone H3K9 Methylation. Molecular Cell, 2010, 39, 360-372.	9.7	63
47	Structure of the Coiled-Coil Dimerization Motif of Sir4 and Its Interaction with Sir3. Structure, 2003, 11, 637-649.	3.3	60
48	Centromere Assembly and Propagation. Cell, 2007, 128, 647-650.	28.9	59
49	Automethylation-induced conformational switch in Clr4 (Suv39h) maintains epigenetic stability. Nature, 2018, 560, 504-508.	27.8	59
50	Heterochromatin protein Sir3 induces contacts between the amino terminus of histone H4 and nucleosomal DNA. Proceedings of the National Academy of Sciences of the United States of America, 2013, 110, 8495-8500.	7.1	57
51	Determinants of Heterochromatic siRNA Biogenesis and Function. Molecular Cell, 2014, 53, 262-276.	9.7	56
52	Sir3-Nucleosome Interactions in Spreading of Silent Chromatin in Saccharomyces cerevisiae. Molecular and Cellular Biology, 2008, 28, 6903-6918.	2.3	54
53	A Model for Step-Wise Assembly of Heterochromatin in Yeast. Novartis Foundation Symposium, 2008, , 48-62.	1.1	35
54	Small-RNA loading licenses Argonaute for assembly into a transcriptional silencing complex. Nature Structural and Molecular Biology, 2015, 22, 328-335.	8.2	34

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55	Affinity Pull-Down of Proteins Using Anti-FLAG M2 Agarose Beads. Methods in Enzymology, 2015, 559, 99-110.	1.0	32
56	An Alpha Motif at Tas3 C Terminus Mediates RITS cis Spreading and Promotes Heterochromatic Gene Silencing. Molecular Cell, 2009, 34, 155-167.	9.7	31
57	A conserved RNA degradation complex required for spreading and epigenetic inheritance of heterochromatin. ELife, 2020, 9, .	6.0	31
58	Heterochromatin assembly by interrupted Sir3 bridges across neighboring nucleosomes. ELife, 2016, 5, .	6.0	30
59	A microRNA negative feedback loop downregulates vesicle transport and inhibits fear memory. ELife, 2016, 5, .	6.0	29
60	Heterochromatic Gene Silencing by Activator Interference and a Transcription Elongation Barrier*. Journal of Biological Chemistry, 2013, 288, 28771-28782.	3.4	26
61	A model for step-wise assembly of heterochromatin in yeast. Novartis Foundation Symposium, 2004, 259, 48-56; discussion 56-62, 163-9.	1.1	26
62	Rejoiceâ€”RNAi for Yeast. Science, 2009, 326, 533-534.	12.6	24
63	Evolving Models of Heterochromatin: From Foci to Liquid Droplets. Molecular Cell, 2017, 67, 725-727.	9.7	23
64	Affinity Purification of Protein Complexes Using TAP Tags. Methods in Enzymology, 2015, 559, 37-52.	1.0	21
65	Coimmunoprecipitation of Proteins from Yeast. Methods in Enzymology, 2014, 541, 13-26.	1.0	19
66	A composite DNA element that functions as a maintainer required for epigenetic inheritance of heterochromatin. Molecular Cell, 2021, 81, 3979-3991.e4.	9.7	18
67	Rixosomal RNA degradation contributes to silencing of Polycomb target genes. Nature, 2022, 604, 167-174.	27.8	18
68	New Alleles of SIR2 Define Cell-Cycle-Specific Silencing Functions. Genetics, 2006, 173, 1939-1950.	2.9	16
69	Distinct Functions of Argonaute Slicer in siRNA Maturation and Heterochromatin Formation. Molecular Cell, 2016, 63, 191-205.	9.7	15
70	Silencing repetitive DNA. ELife, 2017, 6, .	6.0	15
71	Chromatin affinity-precipitation using a small metabolic molecule: its application to analysis of O-acetyl-ADP-ribose. Cellular and Molecular Life Sciences, 2012, 69, 641-650.	5.4	11
72	Clr4 specificity and catalytic activity beyond H3K9 methylation. Biochimie, 2017, 135, 83-88.	2.6	9

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73	Recognition of Acetylated Proteins. Structure, 2002, 10, 1290-1292.	3.3	5
74	A piRNA to Remember. Cell, 2012, 149, 512-514.	28.9	4
75	Evaluation of the Nucleolar Localization of the RENT Complex to Ribosomal DNA by Chromatin Immunoprecipitation Assays. Methods in Molecular Biology, 2017, 1505, 195-213.	0.9	3
76	CSR-1 Slices a Balance. Cell, 2016, 165, 267-269.	28.9	2
77	Chromatin: A Tail of Repression. Current Biology, 2013, 23, R456-R459.	3.9	1
78	Real-Time Quantitative PCR and Fluorescence In Situ Hybridization for Subcellular Localization of miRNAs in Neurons. Methods in Molecular Biology, 2022, 2417, 1-17.	0.9	1
79	Role of Nonâ€coding RNAs in Heterochromatin Formation. FASEB Journal, 2008, 22, 534.1.	0.5	0