

Aseem Z Ansari

List of Publications by Year in descending order

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53
papers

3,283
citations

201385

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docs citations

56
times ranked

3755
citing authors

#	ARTICLE	IF	CITATIONS
1	A Library of Yeast Transcription Factor Motifs Reveals a Widespread Function for Rsc3 in Targeting Nucleosome Exclusion at Promoters. <i>Molecular Cell</i> , 2008, 32, 878-887.	4.5	415
2	Genome-Wide Distribution of Yeast RNA Polymerase II and Its Control by Sen1 Helicase. <i>Molecular Cell</i> , 2006, 24, 735-746.	4.5	293
3	TFIIH Kinase Places Bivalent Marks on the Carboxy-Terminal Domain of RNA Polymerase II. <i>Molecular Cell</i> , 2009, 34, 387-393.	4.5	235
4	Defining the sequence-recognition profile of DNA-binding molecules. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2006, 103, 867-872.	3.3	221
5	Two Cyclin-Dependent Kinases Promote RNA Polymerase II Transcription and Formation of the Scaffold Complex. <i>Molecular and Cellular Biology</i> , 2004, 24, 1721-1735.	1.1	160
6	Chemical-genomic dissection of the CTD code. <i>Nature Structural and Molecular Biology</i> , 2010, 17, 1154-1161.	3.6	130
7	Synthetic transcription elongation factors license transcription across repressive chromatin. <i>Science</i> , 2017, 358, 1617-1622.	6.0	110
8	Combinatorial bZIP dimers display complex DNA-binding specificity landscapes. <i>ELife</i> , 2017, 6, .	2.8	109
9	Cooperativity in RNA-Protein Interactions: Global Analysis of RNA Binding Specificity. <i>Cell Reports</i> , 2012, 1, 570-581.	2.9	106
10	Design of Artificial Transcriptional Activators with Rigid Poly-l-proline Linkers. <i>Journal of the American Chemical Society</i> , 2002, 124, 13067-13071.	6.6	105
11	Specificity landscapes of DNA binding molecules elucidate biological function. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2010, 107, 4544-4549.	3.3	97
12	Modular design of artificial transcription factors. <i>Current Opinion in Chemical Biology</i> , 2002, 6, 765-772.	2.8	96
13	Chemical inhibition of the TFIIH-associated kinase Cdk7/Kin28 does not impair global mRNA synthesis. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2007, 104, 5812-5817.	3.3	96
14	Ssu72 Phosphatase-dependent Erasure of Phospho-Ser7 Marks on the RNA Polymerase II C-terminal Domain Is Essential for Viability and Transcription Termination. <i>Journal of Biological Chemistry</i> , 2012, 287, 8541-8551.	1.6	90
15	Towards a minimal motif for artificial transcriptional activators. <i>Chemistry and Biology</i> , 2001, 8, 583-592.	6.2	85
16	Pathway connectivity and signaling coordination in the yeast stress-activated signaling network. <i>Molecular Systems Biology</i> , 2014, 10, 759.	3.2	83
17	Quantitative Microarray Profiling of DNA-Binding Molecules. <i>Journal of the American Chemical Society</i> , 2007, 129, 12310-12319.	6.6	70
18	Engineered Covalent Inactivation of TFIIH-Kinase Reveals an Elongation Checkpoint and Results in Widespread mRNA Stabilization. <i>Molecular Cell</i> , 2016, 63, 433-444.	4.5	69

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19	A TAD Further: Exogenous Control of Gene Activation. <i>ACS Chemical Biology</i> , 2007, 2, 62-75.	1.6	65
20	Flexibility and structure of flanking DNA impact transcription factor affinity for its core motif. <i>Nucleic Acids Research</i> , 2018, 46, 11883-11897.	6.5	62
21	Targeted Chemical Wedges Reveal the Role of Allosteric DNA Modulation in Protein-DNA Assembly. <i>ACS Chemical Biology</i> , 2008, 3, 220-229.	1.6	47
22	Toward Artificial Developmental Regulators. <i>Journal of the American Chemical Society</i> , 2003, 125, 13322-13323.	6.6	46
23	Interactions of Sen1, Nrd1, and Nab3 with Multiple Phosphorylated Forms of the Rpb1 C-Terminal Domain in <i>Saccharomyces cerevisiae</i> . <i>Eukaryotic Cell</i> , 2012, 11, 417-429.	3.4	46
24	Emerging Views on the CTD Code. <i>Genetics Research International</i> , 2012, 2012, 1-19.	2.0	45
25	RNA sequences that work as transcriptional activating regions. <i>Nucleic Acids Research</i> , 2003, 31, 1565-1570.	6.5	39
26	De novo design of programmable inducible promoters. <i>Nucleic Acids Research</i> , 2019, 47, 10452-10463.	6.5	37
27	Mapping Polyamide-DNA Interactions in Human Cells Reveals a New Design Strategy for Effective Targeting of Genomic Sites. <i>Angewandte Chemie - International Edition</i> , 2014, 53, 10124-10128.	7.2	36
28	Noncanonical CTD kinases regulate RNA polymerase II in a gene-class-specific manner. <i>Nature Chemical Biology</i> , 2019, 15, 123-131.	3.9	26
29	Expanding the specificity of DNA targeting by harnessing cooperative assembly. <i>Biochimie</i> , 2008, 90, 1015-1025.	1.3	24
30	CSI-FID: High throughput label-free detection of DNA binding molecules. <i>Bioorganic and Medicinal Chemistry Letters</i> , 2009, 19, 3779-3782.	1.0	24
31	Different phosphoisoforms of RNA polymerase II engage the Rtt103 termination factor in a structurally analogous manner. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2017, 114, E3944-E3953.	3.3	24
32	Reprogramming cell fate with a genome-scale library of artificial transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E8257-E8266.	3.3	23
33	Sequence-Specificity and Energy Landscapes of DNA-Binding Molecules. <i>Methods in Enzymology</i> , 2011, 497, 3-30.	0.4	22
34	Synthetic genome readers target clustered binding sites across diverse chromatin states. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2016, 113, E7418-E7427.	3.3	20
35	Controlling gene networks and cell fate with precision-targeted DNA-binding proteins and small-molecule-based genome readers. <i>Biochemical Journal</i> , 2014, 462, 397-413.	1.7	16
36	Specificity landscapes unmask submaximal binding site preferences of transcription factors. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, E10586-E10595.	3.3	16

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37	Transcriptional activating regions target attached substrates to a cyclin-dependent kinase. Proceedings of the National Academy of Sciences of the United States of America, 2005, 102, 2346-2349.	3.3	14
38	CSI-Tree: a regression tree approach for modeling binding properties of DNA-binding molecules based on cognate site identification (CSI) data. Nucleic Acids Research, 2008, 36, 3171-3184.	6.5	14
39	Reprogramming cell fate with artificial transcription factors. FEBS Letters, 2018, 592, 888-900.	1.3	13
40	Mapping Polyamide-DNA Interactions in Human Cells Reveals a New Design Strategy for Effective Targeting of Genomic Sites. Angewandte Chemie, 2014, 126, 10288-10292.	1.6	10
41	A Partner Evokes Latent Differences between Hox Proteins. Cell, 2011, 147, 1220-1221.	13.5	9
42	Chemical crosshairs on the central dogma. , 2007, 3, 2-7.		8
43	Riboactivators: Transcription activation by noncoding RNA. Critical Reviews in Biochemistry and Molecular Biology, 2009, 44, 50-61.	2.3	7
44	Fusion proteins form onco-condensates. Nature Structural and Molecular Biology, 2021, 28, 543-545.	3.6	6
45	Sliding on DNA: From Peptides to Small Molecules. Angewandte Chemie - International Edition, 2016, 55, 15110-15114.	7.2	5
46	Single position substitution of hairpin pyrrole-imidazole polyamides imparts distinct DNA-binding profiles across the human genome. PLoS ONE, 2020, 15, e0243905.	1.1	5
47	Genome-wide Mapping of Drug-DNA Interactions in Cells with COSMIC (Crosslinking of Small) Tj ETQq1 1 0.784314 rgBT /Overlock 101	0.2	1
48	A chemoprobe tracks its target. Journal of Biological Chemistry, 2019, 294, 8323-8324.	1.6	1
49	Sliding on DNA: From Peptides to Small Molecules. Angewandte Chemie, 2016, 128, 15334-15338.	1.6	0
50	Blocking the Enablers: Selective Inhibition of CDK9 Reins in an Unchecked Master Regulator. Cell Chemical Biology, 2021, 28, 113-115.	2.5	0
51	Engineering small molecules that nucleate assembly of protein complexes. FASEB Journal, 2008, 22, 411.2.	0.2	0
52	Chemical-genomic dissection of the CTD code. FASEB Journal, 2010, 24, 831.1.	0.2	0
53	Manipulating Cellular Trafficking Positively Affects Syn-TEF Function in Human Tissue. FASEB Journal, 2019, 33, lb178.	0.2	0