Aseem Z Ansari

List of Publications by Year
in descending order

53 papers	3,283 citations	201385 27 h-index	214527 47 g-index
56 all docs	56 docs citations	56 times ranked	3755 citing authors

#	Article	IF	Citations
1	Blocking the Enablers: Selective Inhibition of CDK9 Reins in an Unchecked Master Regulator. Cell Chemical Biology, 2021, 28, 113-115.	2.5	0
2	Fusion proteins form onco-condensates. Nature Structural and Molecular Biology, 2021, 28, 543-545.	3.6	6
3	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
4	De novo design of programmable inducible promoters. Nucleic Acids Research, 2019, 47, 10452-10463.	6.5	37
5	A chemoprobe tracks its target. Journal of Biological Chemistry, 2019, 294, 8323-8324.	1.6	1
6	Noncanonical CTD kinases regulate RNA polymerase II in a gene-class-specific manner. Nature Chemical Biology, 2019, 15, 123-131.	3.9	26
7	Manipulating Cellular Trafficking Positively Affects Synâ€TEF Function in Human Tissue. FASEB Journal, 2019, 33, lb178.	0.2	0
8	Reprogramming cell fate with artificial transcription factors. FEBS Letters, 2018, 592, 888-900.	1.3	13
9	Flexibility and structure of flanking DNA impact transcription factor affinity for its core motif. Nucleic Acids Research, 2018, 46, 11883-11897.	6.5	62
10	Specificity landscapes unmask submaximal binding site preferences of transcription factors. Proceedings of the National Academy of Sciences of the United States of America, 2018, 115, E10586-E10595.	3.3	16
11	Different phosphoisoforms of RNA polymerase II engage the Rtt103 termination factor in a structurally analogous manner. Proceedings of the National Academy of Sciences of the United States of America, 2017, 114, E3944-E3953.	3.3	24
12	Synthetic transcription elongation factors license transcription across repressive chromatin. Science, 2017, 358, 1617-1622.	6.0	110
13	Combinatorial bZIP dimers display complex DNA-binding specificity landscapes. ELife, 2017, 6, .	2.8	109
14	Reprogramming cell fate with a genome-scale library of artificial transcription factors. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E8257-E8266.	3.3	23
15	Engineered Covalent Inactivation of TFIIH-Kinase Reveals an Elongation Checkpoint and Results in Widespread mRNA Stabilization. Molecular Cell, 2016, 63, 433-444.	4.5	69
16	Sliding on DNA: From Peptides to Small Molecules. Angewandte Chemie, 2016, 128, 15334-15338.	1.6	0
17	Synthetic genome readers target clustered binding sites across diverse chromatin states. Proceedings of the National Academy of Sciences of the United States of America, 2016, 113, E7418-E7427.	3.3	20
18	Sliding on DNA: From Peptides to Small Molecules. Angewandte Chemie - International Edition, 2016, 55, 15110-15114.	7.2	5

#	Article	IF	Citations
19	Genome-wide Mapping of Drug-DNA Interactions in Cells with COSMIC (Crosslinking of Small) Tj ETQq1 1 0.784314 rgBT /Overlock 1	0.2	1
20	Mapping Polyamideâ€"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
21	Pathway connectivity and signaling coordination in the yeast stressâ€activated signaling network. Molecular Systems Biology, 2014, 10, 759.	3.2	83
22	Mapping Polyamideâ€"DNA Interactions in Human Cells Reveals a New Design Strategy for Effective Targeting of Genomic Sites. Angewandte Chemie - International Edition, 2014, 53, 10124-10128.	7.2	36
23	Controlling gene networks and cell fate with precision-targeted DNA-binding proteins and small-molecule-based genome readers. Biochemical Journal, 2014, 462, 397-413.	1.7	16
24	Ssu72 Phosphatase-dependent Erasure of Phospho-Ser7 Marks on the RNA Polymerase II C-terminal Domain Is Essential for Viability and Transcription Termination. Journal of Biological Chemistry, 2012, 287, 8541-8551.	1.6	90
25	Emerging Views on the CTD Code. Genetics Research International, 2012, 2012, 1-19.	2.0	45
26	Cooperativity in RNA-Protein Interactions: Global Analysis of RNA Binding Specificity. Cell Reports, 2012, 1, 570-581.	2.9	106
27	Interactions of Sen1, Nrd1, and Nab3 with Multiple Phosphorylated Forms of the Rpb1 C-Terminal Domain in Saccharomyces cerevisiae. Eukaryotic Cell, 2012, 11, 417-429.	3.4	46
28	A Partner Evokes Latent Differences between Hox Proteins. Cell, 2011, 147, 1220-1221.	13.5	9
29	Sequence-Specificity and Energy Landscapes of DNA-Binding Molecules. Methods in Enzymology, 2011, 497, 3-30.	0.4	22
30	Chemical-genomic dissection of the CTD code. Nature Structural and Molecular Biology, 2010, 17, 1154-1161.	3.6	130
31	Specificity landscapes of DNA binding molecules elucidate biological function. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 4544-4549.	3.3	97
32	Chemicalâ€genomic dissection of the CTD code. FASEB Journal, 2010, 24, 831.1.	0.2	0
33	Riboactivators: Transcription activation by noncoding RNA. Critical Reviews in Biochemistry and Molecular Biology, 2009, 44, 50-61.	2.3	7
34	CSIâ€"FID: High throughput label-free detection of DNA binding molecules. Bioorganic and Medicinal Chemistry Letters, 2009, 19, 3779-3782.	1.0	24
35	TFIIH Kinase Places Bivalent Marks on the Carboxy-Terminal Domain of RNA Polymerase II. Molecular Cell, 2009, 34, 387-393.	4.5	235
36	A Library of Yeast Transcription Factor Motifs Reveals a Widespread Function for Rsc3 in Targeting Nucleosome Exclusion at Promoters. Molecular Cell, 2008, 32, 878-887.	4.5	415

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37	Expanding the specificity of DNA targeting by harnessing cooperative assembly. Biochimie, 2008, 90, 1015-1025.	1.3	24
38	Targeted Chemical Wedges Reveal the Role of Allosteric DNA Modulation in Proteinâ˘DNA Assembly. ACS Chemical Biology, 2008, 3, 220-229.	1.6	47
39	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
40	Engineering small molecules that nucleate assembly of protein complexes. FASEB Journal, 2008, 22, 411.2.	0.2	0
41	Chemical inhibition of the TFIIH-associated kinase Cdk7/Kin28 does not impair global mRNA synthesis. Proceedings of the National Academy of Sciences of the United States of America, 2007, 104, 5812-5817.	3.3	96
42	Quantitative Microarray Profiling of DNA-Binding Molecules. Journal of the American Chemical Society, 2007, 129, 12310-12319.	6.6	70
43	A TAD Further: Exogenous Control of Gene Activation. ACS Chemical Biology, 2007, 2, 62-75.	1.6	65
44	Chemical crosshairs on the central dogma. , 2007, 3, 2-7.		8
45	Defining the sequence-recognition profile of DNA-binding molecules. Proceedings of the National Academy of Sciences of the United States of America, 2006, 103, 867-872.	3.3	221
46	Genome-Wide Distribution of Yeast RNA Polymerase II and Its Control by Sen1 Helicase. Molecular Cell, 2006, 24, 735-746.	4.5	293
47	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
48	Two Cyclin-Dependent Kinases Promote RNA Polymerase II Transcription and Formation of the Scaffold Complex. Molecular and Cellular Biology, 2004, 24, 1721-1735.	1.1	160
49	Toward Artificial Developmental Regulators. Journal of the American Chemical Society, 2003, 125, 13322-13323.	6.6	46
50	RNA sequences that work as transcriptional activating regions. Nucleic Acids Research, 2003, 31, 1565-1570.	6.5	39
51	Design of Artificial Transcriptional Activators with Rigid Poly-l-proline Linkers. Journal of the American Chemical Society, 2002, 124, 13067-13071.	6.6	105
52	Modular design of artificial transcription factors. Current Opinion in Chemical Biology, 2002, 6, 765-772.	2.8	96
53	Towards a minimal motif for artificial transcriptional activators. Chemistry and Biology, 2001, 8, 583-592.	6.2	85