Akshay A Bhinge

List of Publications by Year in descending order

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Version: 2024-02-01

23 papers 22,840 citations

430874 18 h-index 642732 23 g-index

25 all docs

25 docs citations

25 times ranked

41954 citing authors

#	Article	IF	CITATIONS
1	Upregulation of \hat{l}^2 -catenin due to loss of miR-139 contributes to motor neuron death in amyotrophic lateral sclerosis. Stem Cell Reports, 2022, , .	4.8	9
2	Novel epigenetic clock for fetal brain development predicts prenatal age for cellular stem cell models and derived neurons. Molecular Brain, 2021, 14, 98.	2.6	19
3	Single-cell transcriptomics identifies master regulators of neurodegeneration in SOD1 ALS iPSC-derived motor neurons. Stem Cell Reports, 2021, 16, 3020-3035.	4.8	14
4	Cyclin-Dependent Kinase-Dependent Phosphorylation of Sox2 at Serine 39 Regulates Neurogenesis. Molecular and Cellular Biology, 2017, 37, .	2.3	18
5	Genetic Correction of SOD1 Mutant iPSCs Reveals ERK and JNK Activated AP1 as a Driver of Neurodegeneration in Amyotrophic Lateral Sclerosis. Stem Cell Reports, 2017, 8, 856-869.	4.8	108
6	Single-cell gene expression analysis reveals regulators of distinct cell subpopulations among developing human neurons. Genome Research, 2017, 27, 1783-1794.	5.5	39
7	MiR-375 is Essential for Human Spinal Motor Neuron Development and May Be Involved in Motor Neuron Degeneration. Stem Cells, 2016, 34, 124-134.	3.2	64
8	NeuO: a Fluorescent Chemical Probe for Live Neuron Labeling. Angewandte Chemie - International Edition, 2015, 54, 2442-2446.	13.8	73
9	Mi <scp>R</scp> â€135b is a direct <scp>PAX</scp> 6 target and specifies human neuroectoderm by inhibiting <scp>TGF</scp> â€Î²/ <scp>BMP</scp> signaling. EMBO Journal, 2014, 33, 1271-1283.	7.8	53
10	A Myc–microRNA network promotes exit from quiescence by suppressing the interferon response and cell-cycle arrest genes. Nucleic Acids Research, 2013, 41, 2239-2254.	14.5	49
11	A Genome-Wide Screen for Genetic Variants That Modify the Recruitment of REST to Its Target Genes. PLoS Genetics, 2012, 8, e1002624.	3.5	17
12	Cell-type specific and combinatorial usage of diverse transcription factors revealed by genome-wide binding studies in multiple human cells. Genome Research, 2012, 22, 9-24.	5.5	119
13	An integrated encyclopedia of DNA elements in the human genome. Nature, 2012, 489, 57-74.	27.8	15,516
14	A User's Guide to the Encyclopedia of DNA Elements (ENCODE). PLoS Biology, 2011, 9, e1001046.	5.6	1,257
15	Wide-ranging functions of E2F4 in transcriptional activation and repression revealed by genome-wide analysis. Nucleic Acids Research, 2011, 39, 3558-3573.	14.5	132
16	Epigenetics of human T cells during the G ₀ â†'G ₁ transition. Genome Research, 2009, 19, 1325-1337.	5.5	19
17	Dynamic Remodeling of Individual Nucleosomes Across a Eukaryotic Genome in Response to Transcriptional Perturbation. PLoS Biology, 2008, 6, e65.	5.6	353
18	Mapping the chromosomal targets of STAT1 by Sequence Tag Analysis of Genomic Enrichment (STAGE). Genome Research, 2007, 17, 910-916.	5 . 5	61

#	Article	IF	CITATIONS
19	Identification and analysis of functional elements in 1% of the human genome by the ENCODE pilot project. Nature, 2007, 447, 799-816.	27.8	4,709
20	Mapping DNA-protein interactions in large genomes by sequence tag analysis of genomic enrichment. Nature Methods, 2005, 2, 47-53.	19.0	108
21	Accurate Detection of Protein:Ligand Binding Sites Using Molecular Dynamics Simulations. Structure, 2004, 12, 1989-1999.	3.3	25
22	A Procedure for Detection and Quantitation of Cavity Volumes in Proteins. Journal of Biological Chemistry, 2002, 277, 31345-31353.	3.4	44
23	Lysine: Is it worth more?. Cytotechnology, 2001, 36, 3-32.	1.6	31