

Kosuke Hashimoto

List of Publications by Year in descending order

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Version: 2024-02-01

36
papers

2,689
citations

361413

20
h-index

395702

33
g-index

42
all docs

42
docs citations

42
times ranked

5217
citing authors

#	ARTICLE	IF	CITATIONS
1	DUX4 is a multifunctional factor priming human embryonic genome activation. <i>IScience</i> , 2022, 25, 104137.	4.1	20
2	Discovery of widespread transcription initiation at microsatellites predictable by sequence-based deep neural network. <i>Nature Communications</i> , 2021, 12, 3297.	12.8	11
3	Embryonic LTR retrotransposons supply promoter modules to somatic tissues. <i>Genome Research</i> , 2021, 31, 1983-1993.	5.5	7
4	Use of Cap Analysis Gene Expression to detect human papillomavirus promoter activity patterns at different disease stages. <i>Scientific Reports</i> , 2020, 10, 17991.	3.3	1
5	RADICL-seq identifies general and cell type-specific principles of genome-wide RNA-chromatin interactions. <i>Nature Communications</i> , 2020, 11, 1018.	12.8	98
6	Single-cell transcriptomics reveals expansion of cytotoxic CD4 T cells in supercentenarians. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2019, 116, 24242-24251.	7.1	215
7	Prevention of hepatocellular carcinoma by targeting MYCN-positive liver cancer stem cells with acyclic retinoid. <i>Proceedings of the National Academy of Sciences of the United States of America</i> , 2018, 115, 4969-4974.	7.1	78
8	An integrated expression atlas of miRNAs and their promoters in human and mouse. <i>Nature Biotechnology</i> , 2017, 35, 872-878.	17.5	456
9	Single-Nucleotide Resolution Mapping of Hepatitis B Virus Promoters in Infected Human Livers and Hepatocellular Carcinoma. <i>Journal of Virology</i> , 2016, 90, 10811-10822.	3.4	27
10	Deficiency of multidrug resistance 2 contributes to cell transformation through oxidative stress. <i>Carcinogenesis</i> , 2016, 37, 39-48.	2.8	15
11	Nuclear transcriptome profiling of induced pluripotent stem cells and embryonic stem cells identify non-coding loci resistant to reprogramming. <i>Cell Cycle</i> , 2015, 14, 1148-1155.	2.6	14
12	Characterization of Novel Transcripts of Human Papillomavirus Type 16 Using Cap Analysis Gene Expression Technology. <i>Journal of Virology</i> , 2015, 89, 2448-2452.	3.4	6
13	STAP cells are derived from ES cells. <i>Nature</i> , 2015, 525, E4-E5.	27.8	8
14	CAGE profiling of ncRNAs in hepatocellular carcinoma reveals widespread activation of retroviral LTR promoters in virus-induced tumors. <i>Genome Research</i> , 2015, 25, 1812-1824.	5.5	49
15	Deep transcriptome profiling of mammalian stem cells supports a regulatory role for retrotransposons in pluripotency maintenance. <i>Nature Genetics</i> , 2014, 46, 558-566.	21.4	271
16	Evolutionary, Physicochemical, and Functional Mechanisms of Protein Homooligomerization. <i>Progress in Molecular Biology and Translational Science</i> , 2013, 117, 3-24.	1.7	34
17	Cancer Missense Mutations Alter Binding Properties of Proteins and Their Interaction Networks. <i>PLoS ONE</i> , 2013, 8, e66273.	2.5	102
18	Mutations that reduce its specific DNA binding inhibit high NaCl-induced nuclear localization of the osmoprotective transcription factor NFAT5. <i>American Journal of Physiology - Cell Physiology</i> , 2012, 303, C1061-C1069.	4.6	10

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19	Large-scale mapping of human protein interactome using structural complexes. EMBO Reports, 2012, 13, 266-271.	4.5	43
20	Oncogenic potential is related to activating effect of cancer single and double somatic mutations in receptor tyrosine kinases. Human Mutation, 2012, 33, 1566-1575.	2.5	26
21	Phosphorylation in Protein-Protein Binding: Effect on Stability and Function. Structure, 2011, 19, 1807-1815.	3.3	246
22	Caught in self-interaction: evolutionary and functional mechanisms of protein homooligomerization. Physical Biology, 2011, 8, 035007.	1.8	94
23	Mechanisms of protein oligomerization, the critical role of insertions and deletions in maintaining different oligomeric states. Proceedings of the National Academy of Sciences of the United States of America, 2010, 107, 20352-20357.	7.1	160
24	Functional States of Homooligomers: Insights from the Evolution of Glycosyltransferases. Journal of Molecular Biology, 2010, 399, 196-206.	4.2	39
25	KEGG GLYCAN for Integrated Analysis of Pathways, Genes, and Glycan Structures. , 2010, , 197-210.		0
26	Comprehensive analysis of glycosyltransferases in eukaryotic genomes for structural and functional characterization of glycans. Carbohydrate Research, 2009, 344, 881-887.	2.3	37
27	Mining significant tree patterns in carbohydrate sugar chains. Bioinformatics, 2008, 24, i167-i173.	4.1	33
28	A new efficient probabilistic model for mining labeled ordered trees applied to glycobiology. ACM Transactions on Knowledge Discovery From Data, 2008, 2, 1-30.	3.5	10
29	The repertoire of desaturases and elongases reveals fatty acid variations in 56 eukaryotic genomes. Journal of Lipid Research, 2008, 49, 183-191.	4.2	150
30	KEGG GLYCAN for Integrated Analysis of Pathways, Genes, and Structures. , 2008, , 441-444.		3
31	AN IMPROVED SCORING SCHEME FOR PREDICTING GLYCAN STRUCTURES FROM GENE EXPRESSION DATA. , 2007, , .		18
32	KEGG as a glycome informatics resource. Glycobiology, 2006, 16, 63R-70R.	2.5	279
33	The repertoire of desaturases for unsaturated fatty acid synthesis in 397 genomes. Genome Informatics, 2006, 17, 173-83.	0.4	9
34	Prediction of glycan structures from gene expression data based on glycosyltransferase reactions. Bioinformatics, 2005, 21, 3976-3982.	4.1	78
35	A global representation of the carbohydrate structures: a tool for the analysis of glycan. Genome Informatics, 2005, 16, 214-22.	0.4	7
36	Extraction of species-specific glycan substructures. Genome Informatics, 2004, 15, 69-81.	0.4	5