Institute Retreat 2024

Wednesday, September 18, 2024

Poster Session I (Wed): Poster Session A (5:00 PM - 7:00 PM)

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[6] More Details on Epigenetic Characteristics of Enhancers and Promoters	ZHANG, Yufei	01
[7] The evolutionary meaning of the splicing and transcription cross-talk	LISA, Martina	02
[8] Causes and consequences of TAD rewiring at the Xist locus at the onset of X-chromosome inactivation	MARTITZ, Alexandra	03
[11] Dissecting the epigenetic memory of Xist by constructing and perturbing a synthetic locus in embryonic stem cells	KANATA, Eleni	04
[12] Molecular coupling of Xist regulation to the formative pluripotency network	SCHWÄMMLE, Till	05
[14] How a handful of enhancer positions disrupt limb development in mouse	MADGWICK, Alicia	06
[15] High-throughput mapping of functional interactions between cis-regulatory elements and transcription factors at the X-inactivation centre	LIMBERG, Elodie	07
[101] Differential oligomerization modulates PHF13's role in chromatin organization	FRANCONI, Celeste ROSSI, Francesca	08
[17] Deciphering the Mechanisms of Female-Specific X-Chromosome Inactivation	FENG, Vivi	09
[19] Exploring Functional Redundancy and Compensation in BET Proteins	EISCHER, Nicole	10
[20] A kinetic model of gene expression in brain development	OLIANI, Eleonora	11
[21] Identifying determinants of inter-allelic heterogeneity at the Xist locus at the onset of X-chromosome inactivation	PELAEZ CONDE, Ingrid	12
[22] Long-read transcriptome sequencing - novel opportunities for analysis of alternative splicing in disease and development	BI, Yalan	13
[23] Deciphering transcriptome patterns in porcine mesenchymal stem cells promoting phenotypic maintenance and differentiation by key driver genes	KHAVEH, Nadia	14
[25] Autonomous transposon tunes their sequences to ensure somatic suppression	ILIK, Ibrahim	15
[28] Brain vasculature as a key regulator of brain gene expression kinetics and evolution	LLAOCID, Cecília	16
[64] How do Gene Regulatory Landscapes Integrate the Activity of Multiple Regulatory Elements ?	RODRIGUES CAVALHEIRO, Gabriel	17
[32] Beyond Backtracking: TFIIS as a Multifaceted Regulator of Transcription	VILLAFANO, Geno	18
[34] Investigating a protein sensor for transposon RNA and giant coding exons	SCHMIDT, Laura Katharina	19
[35] The prickly question of hedgehog spine evolution	BARTZOKA, Natalia	20
[37] Decoding the molecular makeup of biomolecular condensates via NuFANCI	ZHANG, Yaotian	21
[40] metilene3: differentially methylated tree inference from unsupervised identification of differentially methylated regions	ZHU, Zhihan	22
[42] Comprehensive Network Analysis for Genomic Discoveries	FATIMA, Abeera	23
[43] Single-cell activation screen identifies hepatic maturation regulators with zonal resolution	MAGALHÃES, Alexandre P.	24

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[44] Investigating the pathogenicity of mutations in human lncRNA: An evolutionary approach	KOILE, Daniel	25
[45] Environmental stress induced epigenetic memory in embryonic stem cells	STÖTZEL, Maximilian	26
[46] Sequence dependency of a micropeptide 'killswitch' solidifying nuclear condensates	SOMMER, Gregor	27
[47] Testing the TF suboptimization hypothesis in-vivo	AWAWDY, Mohammad	28
[48] Investigating the Altered Proteoepigenomic Landscape of Renal Cell Carcinoma	YOUSEFI, Niloufar	29
[50] Molecular analysis of relapse in TCF3-PBX1 pediatric acute lymphoblastic leukemia with multi-omics data	NOJSZEWSKA, Natalia	30
[30] Predict cancer cell of origin from single-cell expression data	ABDULLAEV, Eldar	31
[52] Uncovering the dynamics and consequences of RNA isoform changes during neuronal differentiation	SHAO, Zhihao	32
[51] The COVID-19 Pandemic: Lessons Learned? Towards a New Understanding of Immune Memory Imprinting and Plasticity	GIESECKE-THIEL, Claudia	33
[74] Seeing is believing – We help you seeing	MIELKE, Thorsten	34
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