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Ms.	Cora	Beckmann	1	Transcriptional architecture and chromatin landscape of the core circadian clock in mammals.	Achim Kramer's group	<a href="mailto:achim.kramer@charite.de">achim.kramer@charite.de</a>
Mr.	David	Willnow	2	Circadian rhythms: mechanisms and therapeutic implications.	Achim Kramer's group	<a href="mailto:achim.kramer@charite.de">achim.kramer@charite.de</a>
Ms.	Anuprabha	Bhargava	3	Mistimed sleep disrupts circadian regulation of the human transcriptome.	Achim Kramer's group	<a href="mailto:achim.kramer@charite.de">achim.kramer@charite.de</a>
Mr.	Gonzalo	Ortiz-Álvarez	4	Dynamic circadian protein-protein interaction networks predict temporal organization of cellular functions.	Achim Kramer's group	<a href="mailto:achim.kramer@charite.de">achim.kramer@charite.de</a>
Ms.	Uta	Rösler	5	System-level feedbacks make the anaphase switch irreversible.	Fridolin Gross	<a href="mailto:fridolin.gross@hu-berlin.de">fridolin.gross@hu-berlin.de</a>
Ms.	Ekaterina	Eroshok	7	TH17 cell differentiation is regulated by the circadian clock.	Fridolin Gross	<a href="mailto:fridolin.gross@hu-berlin.de">fridolin.gross@hu-berlin.de</a>
Ms.	Melanie	Pieber	8	Global chromatin state analysis reveals lineage - specific enhancers during the initiation of human T helper 1 and T helper 2 cell polarization.	Fridolin Gross	<a href="mailto:fridolin.gross@hu-berlin.de">fridolin.gross@hu-berlin.de</a>
Ms.	Brinja	Leinweber	9	Modeling the cell cycle: why do certain circuits oscillate?	Grigory Bordyugov	<a href="mailto:Grigory.Bordyugov@hu-berlin.de">Grigory.Bordyugov@hu-berlin.de</a>
Mr.	Ulrich	Genske	10	Genomic and chromatin signals underlying transcription start-site selection.	Hanspeter Herzel	<a href="mailto:h.herzel@biologie.hu-berlin.de">h.herzel@biologie.hu-berlin.de</a>
Ms.	Christina	Ambrosi	12	Histone modification levels are predictive for gene expression.	Hanspeter Herzel	<a href="mailto:h.herzel@biologie.hu-berlin.de">h.herzel@biologie.hu-berlin.de</a>
Mr.	Slim	Khouja	13	Accelerating the tempo of the segmentation clock by reducing the number of introns in the Hes7 gene.	Hanspeter Herzel	<a href="mailto:h.herzel@biologie.hu-berlin.de">h.herzel@biologie.hu-berlin.de</a>
Mr.	Federico José	Barreda Tomás	14	Non-optimal codon usage is a mechanism to achieve circadian clock conditionality.	Christian Beck	<a href="mailto:christian.beck@biologie.hu-berlin.de">christian.beck@biologie.hu-berlin.de</a>
Ms.	Burcu	Vitrinel	15	Global quantification of mammalian gene expression control.	Matthias Selbach	<a href="mailto:matthias.selbach@mdc-berlin.de">matthias.selbach@mdc-berlin.de</a>
Ms.	Qingyao	Huang	16	Proteome half-life dynamics in living human cells.	Nils Bluethgen's group	<a href="mailto:nils.bluethgen@charite.de">nils.bluethgen@charite.de</a>
Mr.	Sungsoo	Lim	17	Ultrasensitivity in the Regulation of Cdc25C by Cdk1.	Nils Bluethgen's group	<a href="mailto:nils.bluethgen@charite.de">nils.bluethgen@charite.de</a>
Mr.	Ahmed	Elsanhouri	18	Mathematical modeling of PDGF-driven glioblastoma reveals optimized radiation dosing schedules.	Nils Bluethgen's group	<a href="mailto:nils.bluethgen@charite.de">nils.bluethgen@charite.de</a>
Mr.	Felix	Kallenberg	19	Network quantification of EGFR signaling unveils potential for targeted combination therapy.	Nils Bluethgen's group	<a href="mailto:nils.bluethgen@charite.de">nils.bluethgen@charite.de</a>
Mr.	Matthew	Kondoff	20	Regulatory element copy number differences shape primate expression profiles.	Pål Westermark's group	<a href="mailto:p.westermark@biologie.hu-berlin.de">p.westermark@biologie.hu-berlin.de</a>
Ms.	Julia Catherine	Berkmann	23	Defining the transcriptome and proteome in three functionally different human cell lines.	Pål Westermark's group	<a href="mailto:p.westermark@biologie.hu-berlin.de">p.westermark@biologie.hu-berlin.de</a>
Ms.	Priyavathi	Dhandapani	25	Circadian clock-dependent and -independent rhythmic proteomes implement distinct diurnal functions in mouse liver.	Pål Westermark's group	<a href="mailto:p.westermark@biologie.hu-berlin.de">p.westermark@biologie.hu-berlin.de</a>
Ms.	Jingwei	Zhang	26	Predicting cell-type-specific gene expression from regions of open chromatin.	Uwe Ohler	<a href="mailto:uwe.ohler@mdc-berlin.de">uwe.ohler@mdc-berlin.de</a>
Ms.	Lisa	Conrad	27	Genomic regions flanking E-box binding sites influence DNA binding specificity of bHLH transcription factors through DNA shape.	Christoph Schmal	<a href="mailto:cschmal@CeBiTec.Uni-Bielefeld.DE">cschmal@CeBiTec.Uni-Bielefeld.DE</a>