

by Mark Gerstein 3 minutes ago

## Favorite Tweets from Late Nov. '17 Meetings - ERCC9, RSG '17+ misc (#ERCC9,i0exrna17,#RSGDream17, i0rsg17)

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**Anthony Gitter**

@anthonygitter

[@FertigLab](#) Changes in expression come before changes in methylation, contrary to their initial expectations. [#rsgdream17](#)



5 HOURS AGO

Dynamic patterns with CoGAPS Non-negative matrix factorization (NMF)

CoGAPS Bayesian NMF uses an "atomic prior"

Data = Amplitude × Pattern

Atomic prior for A matrix

$$\alpha_1 \sim \Gamma(\alpha_1^0, \lambda)$$

$$\alpha_i \sim \text{Poisson}(\alpha)$$

$$A_{8,3} \sim \Gamma(1, \lambda)$$

$$A_{9,3} \sim \Gamma(1, \lambda)$$

$$A_{10,3} \sim \Gamma(2, \lambda)$$

$$A_{11,3} \sim \Gamma(1, \lambda)$$

Use prior distribution in MCMC to enforce sparsity and non-negativity of solutions, implemented in the R/Bioconductor package CoGAPS.

Fertig et al (2010) *Bioinformatics*; Stein-O'Brien et al (2016) *Bioinformatics*

E. J. Fertig (@FertigLab) Integrated time course analysis RSG 2017 9 / 16

Talk on integrated time-series multi-omics from @FertigLab makes me want to read CoGAPS paper ASAP #RsgDream17 @iscb pic.twitter.com/0NBiOoGFMI

RICHARD BONNEAU @RICHBONNEAUNYU · 5 HOURS AGO



**Mark Gerstein**  
@markgerstein

.@FertigLab cites PatternMarkers & GWCoGAPS for novel data-driven biomarkers via whole transcriptome NMF [academic.OUP.com/bioinformatics...](http://academic.OUP.com/bioinformatics...) Sparsely decomposes gene expression into patterns #rsgdream17



5 HOURS AGO

**Anthony Gitter**

@anthonygitter

.@FertigLab presents dynamics of therapeutic response in cancer. Focusing on EGFR inhibitors  
[#rsgdream17](#)



6 HOURS AGO

**gagneurlab**

@gagneurlab

Ziga Avsec presents his poster "Modeling positional effects of regulatory sequences with spline transformations increases prediction accuracy of DNN" at [#RSGDream17](#) - paper now online  
[doi.org/10.1093/bioinf...](https://doi.org/10.1093/bioinf...)



6 HOURS AGO

**Manolis Kellis**

@manoliskellis

Outstanding keynote by Christina Leslie on epigenomic signatures distinguishing 'reprogrammable' vs. 'non-reprogrammable' immune cells, and cell surface markers that can be used to distinguish them to guide cancer immunotherapy [#RSGDream17](#)  
[twitter.com/markgerstein/s...](https://twitter.com/markgerstein/s...)



6 HOURS AGO



It is hard to bridge cutting edge data-science and cutting edge immunotherapy/the clinical side of things: Christina Leslie of MSKCC shows us how it's done! #RsgDream17  
[pic.twitter.com/H68KkbuLhx](https://pic.twitter.com/H68KkbuLhx)

 RICHARD BONNEAU @RICHBONNEAUNYU · 6 HOURS AGO



**Mark Gerstein**  
 @markgerstein

@anshulkundaje @RalucaGordan I might have transcribed it wrongly but my impression was @RalucaGordan indicated that binding events in open chromatin regions appear "stronger" than otherwise #rsgdream17

 6 HOURS AGO



**Mark Gerstein**

@markgerstein

Leslie cites "Chromatin states define tumour-specific T cell dysfunction and reprogramming" [Nature.com/articles/natur...](https://www.nature.com/articles/natur...) Has changing ATAC-seq peaks & gene expression betw. tumor & normal #rsgdream17



6 HOURS AGO

**Katalin Susztak**

@KSusztak

@manoliskellis @markgerstein You forgot F2F :)



7 HOURS AGO

**Mark Gerstein**

@markgerstein

Parida's talk has lots of useful #DataScience buzzwords: 3Vs for data (= velocity, volume, variety) + WfG (@IBMWatson for Genomics) as a transparent, comprehensive, navigable, & scaleable system + the hologenome for microbiome #rsgdream17



8 HOURS AGO

**rahul metri**

@MetriRahul

@IBMWatson Genomics for Cancer cure. Excellent insights by Laxmi Parida at #RSGDream17



8 HOURS AGO



**Rani Powers**  
@ranipowers

Ooh. Interest piqued: Laxmi Parida talking about IBMResearch's findings working with the [@Genographic](#) Project genomics data ... [#RSGDREAM17](#)

9 HOURS AGO



**Manolis Kellis**  
@manoliskellis

[@markgerstein](#) After P2P and B2B, this is M2M :-)

9 HOURS AGO



**Manolis Kellis**  
@manoliskellis

Amazing talk on ribothrypsis by Manolis Maragkakis uncovers new mechanisms of ribo-stalling and mRNA degradation [mourelatos.med.upenn.edu/index.php/team...](http://mourelatos.med.upenn.edu/index.php/team...) [#RSGDream17](#)

9 HOURS AGO



**Mark Gerstein**  
@markgerstein

.[@RalucaGordan](#) reviews many key biases in chipseq - eg DS breaks depend on nt seq., PCR amplification, stronger signal related to open chromatin & high expression, different results w/ diff. antibodies (particularly variable in ENCODE comparisons for ATF2) [#rsgdream17](#)

9 HOURS AGO



**Johnny Israeli**  
@johnny\_israeli

Raluca Gordon: Chip-seq  $\neq$  in vivo binding. Combine multiple assays! [#RSGDream17](#)

9 HOURS AGO



**Rani Powers**  
@ranipowers

Bayesian nets, linear deconvolution, adaptive multitask lasso & deep learning all before 12pm.  
Feeling at home at #RSGDREAM17 🤔

9 HOURS AGO



**Rani Powers**  
@ranipowers

Nice keynote by @dana\_peer at #RSGDREAM17 Single cell RNAseq expts w/ high dropout use a little MAGIC, good application of manifold learning

9 HOURS AGO



**DREAMchallenges**  
@DR\_E\_A\_M

Chip-seq biases @RalucaGordan as comparing to cut&run from [elifesciences.org/articles/21856](http://elifesciences.org/articles/21856)  
#rsgdream17

9 HOURS AGO



**Anthony Gitter**  
@anthonygitter

#rsgdream17 made it to the fourth talk before a deep learning appearance (LINCS signature learning). I would have guessed fewer.

10 HOURS AGO

**Mark Gerstein**

@markgerstein

Castro in @RichBonneauNYU lab: Use TF activities to model gene expression via inferred networks. Using Adaptive Lasso (w/ a variety of sparse & block penalties) #rsgdream17

10 HOURS AGO

**DREAMchallenges**

@DR\_E\_A\_M

Single va Multitask learning and Network Inference from @RichBonneauNYU #RsgDream17

10 HOURS AGO

**Johnny Israeli**

@johnny\_israeli

A MAGICal keynote. Now Ryan Peckner on deconvolution of next gen mass spec data  
#RSGDream17

11 HOURS AGO

**Johnny Israeli**

@johnny\_israeli

Dana Pe'er: a potential downside of MAGIC is reduction of true stochasticity in the data  
#RSGDream17

11 HOURS AGO

**Mark Gerstein**

@markgerstein

From Peer, some key aspects of MAGIC: recovers gene-gene relationships, archetypical cell states & shape (manifold) data. Allows one see entire EMT from a single time point #rsgdream17

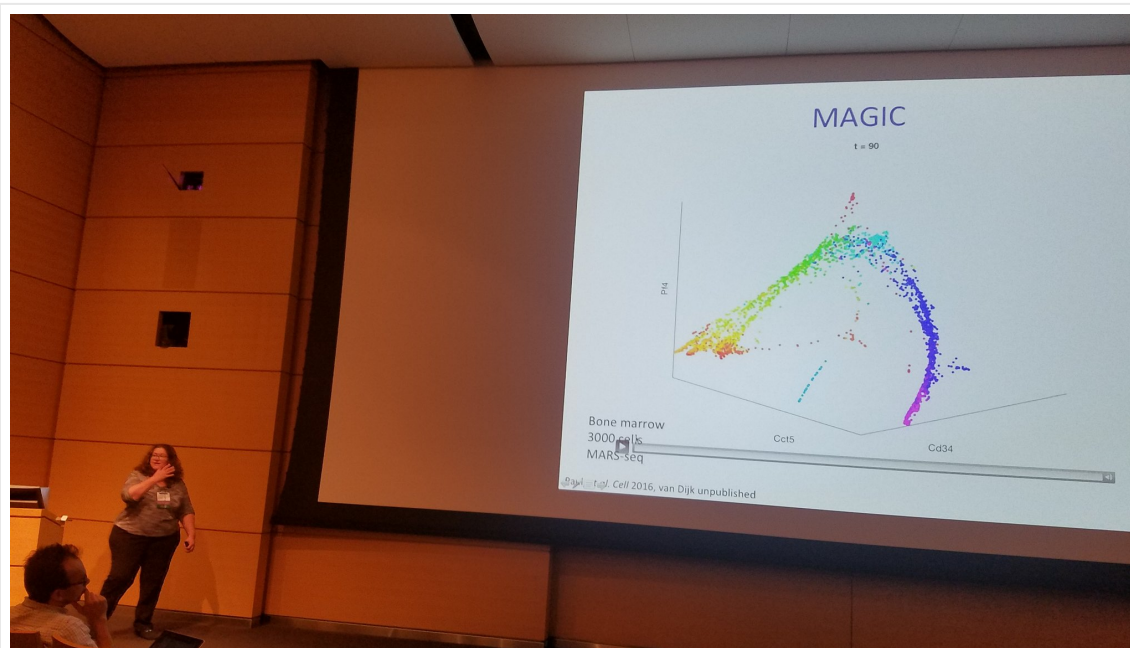
11 HOURS AGO



**Manolis Kellis**  
@manoliskellis

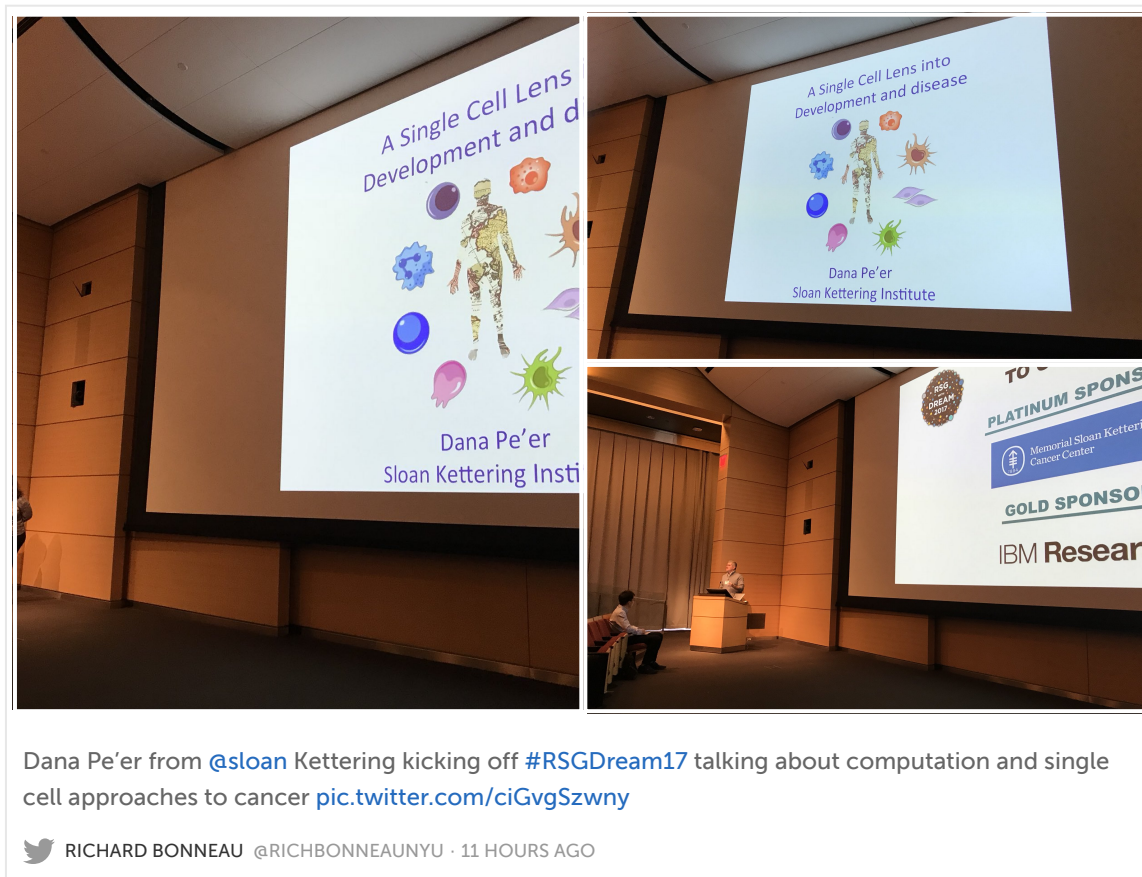
And here's the MAGIC pre-print [biorxiv.org/content/biorxi...](https://www.biorxiv.org/content/biorxiv/10.1101/214111) (Markov Affinity-based Graph Imputation of Cells) #RSGDream17

 11 HOURS AGO



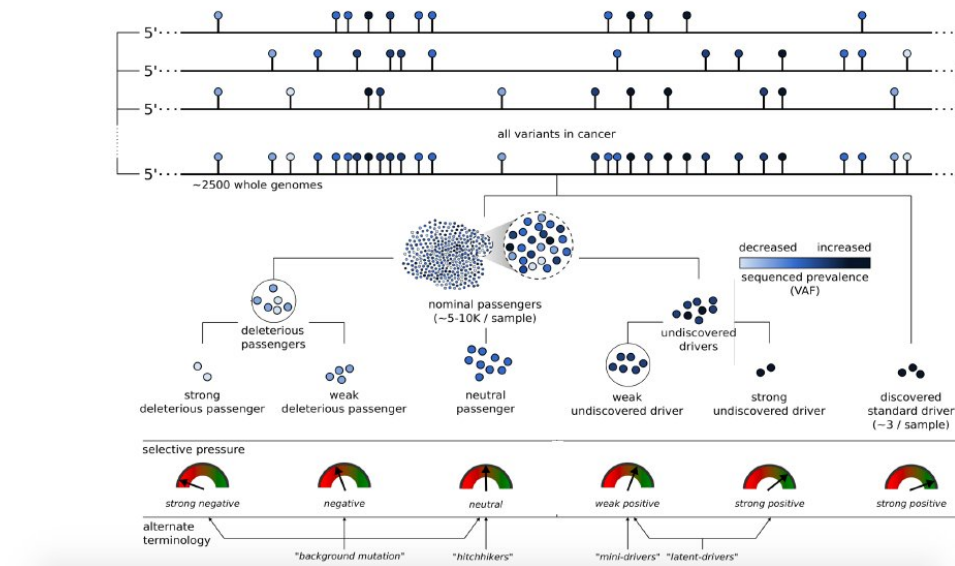
Dana Pe'er talking about MAGIC #RSGdream17 [pic.twitter.com/w9qBopBm9o](https://pic.twitter.com/w9qBopBm9o)

 MANOLIS KELLIS @MANOLISKELLIS · 11 HOURS AGO





## Conceptual extension of the canonical model of drivers & passengers



Conceptual extension of the canonical model of drivers and passengers in cancer by [@markgerstein](#) from [lectures.gersteinlab.org/summary/Mutati...](https://lectures.gersteinlab.org/summary/Mutati...) (nicely summarizing a bunch of papers I've read recently) [pic.twitter.com/TvulpVjv7Y](https://pic.twitter.com/TvulpVjv7Y)

ENDRE SEBESTYÉN [@ENDRE\\_SEBESTYEN](#) · 10 DAYS AGO



**UCONN Bioinformatics**  
[@UConn\\_Bioinfo](#)

Great talks at ISG 5yr Anniversary! Characterizing genomes w/ new methods, software, sequencing tools [@markgerstein](#) [@graveley](#) [@ENCODE\\_NIH](#)

11 DAYS AGO



**Mark Gerstein**  
@markgerstein

Posting talk tomorrow at 5-year celebration ceremony @UConn Institute for Systems Genomics [lectures.gersteinlab.org/summary/Genomi...](http://lectures.gersteinlab.org/summary/Genomi...) #Genomics & DataScience

 12 DAYS AGO


**Institute for Systems Genomics**  
**5 YEAR CELEBRATION SYMPOSIUM**

**Wednesday, November 8, 2017**

Student Union Theatre  
University of Connecticut  
2110 Hillside Road  
Storrs, Connecticut

8:00AM-4:00PM

UConn Institute for Systems Genomics FIVE year celebration symposium November 8  
[isg.uconn.edu/wp-content/upl...](http://isg.uconn.edu/wp-content/upl...) [pic.twitter.com/rPZplfq4pV](https://pic.twitter.com/rPZplfq4pV)

 UCONN STEM CELL CORE @UCONNSCORE · 13 DAYS AGO



**Caitlin Stewart**

@Cait\_Stewart

Janos Zemleni: Exosomes in cow milk and encapsulated RNA can survive pasteurization and are taken up by human (& 🐻) intestinal cells! #ERCC9



13 DAYS AGO



**Mark Gerstein**

@markgerstein

Rozowsky: the pipeline ([github.gersteinlab.org/exceRpt](https://github.com/markgerstein/exceRpt)) hows differences in exo-/endo- genous profiles across body fluids #ERCC9



13 DAYS AGO



**pointless**

@farminginva

Looking forward to trying out exceRpt pipeline when back home... #ERCC9



13 DAYS AGO



Joel Rozowsky @Yale: exceRpt extracellular RNA-Seq processing pipeline #ERCC9  
[pic.twitter.com/ETSvErXkdA](https://pic.twitter.com/ETSvErXkdA)

 EXRNA @EXRNA · 13 DAYS AGO



**Mark Gerstein**  
@markgerstein

Milosavljevic: Does the exRNA atlas lend itself to deconvolution? A: Carrier-specific exRNA profiles can be detected across body fluids #ERCC9

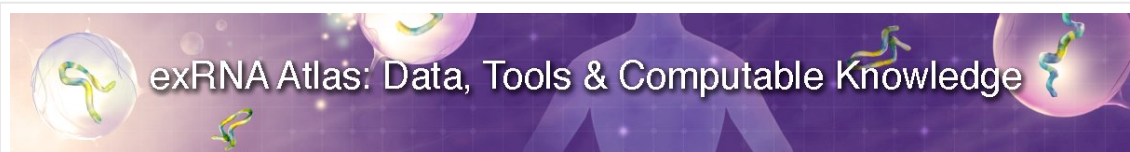
 13 DAYS AGO



**Mark Gerstein**  
@markgerstein

Milosavljevic: ~100 miRNAs present in reasonably high abundance in each body fluid (except for urine) #ERCC9

 13 DAYS AGO



Aleks Milosavljevic [@bcmhouston](#): Biological insights from exRNA Atlas through cross-study analysis [exrna-atlas.org](#) [#ERCC9](#) [pic.twitter.com/OVzawfPAwK](#)

 EXRNA [@EXRNA](#) · 13 DAYS AGO



**M. Selim Unlu**  
[@MSelimUnlu](#)

attending [#ERCC9](#). Looking forward to learning and sharing our capabilities on RNA and exosome detection at single particle level

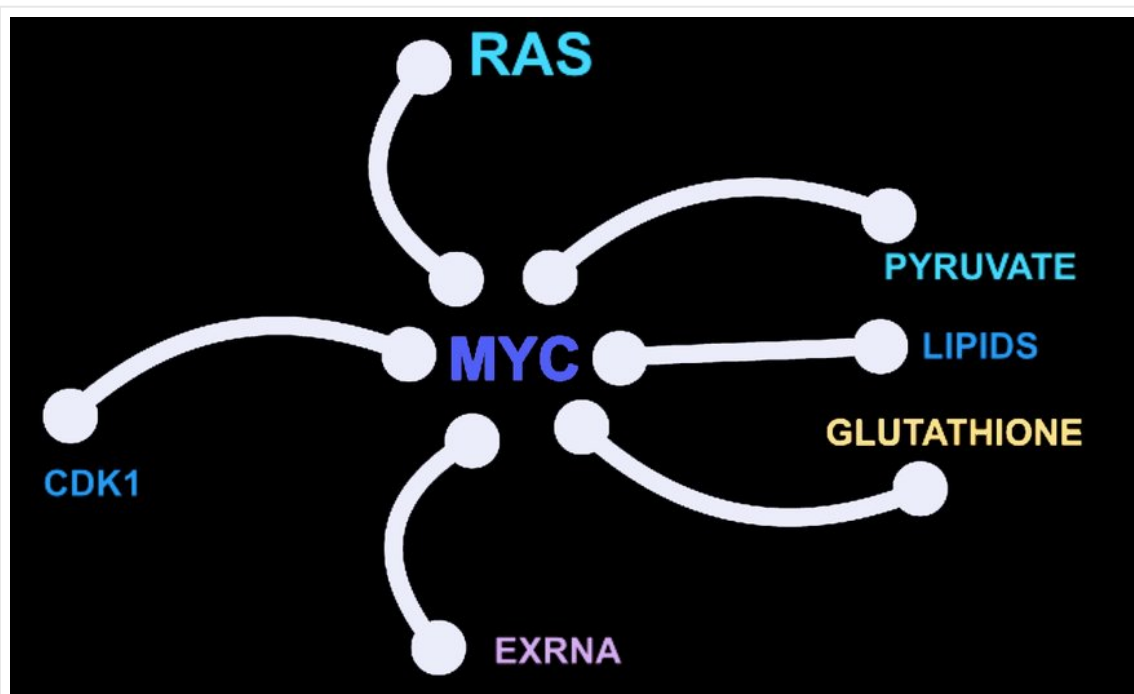
 13 DAYS AGO



**Caitlin Stewart**  
[@Cait\\_Stewart](#)

Seda Kilinc Avsarglu: Overexpressed oncogenes are released from tumour cells in extracellular vesicles. [#ERCC9](#)

 13 DAYS AGO



Seda Kilinc Avsaroglu @UCSF: Oncogene-regulated production and release of EVs and exRNAs  
[oncogenes.net](http://oncogenes.net) #ERCC9 [pic.twitter.com/sUI6QC4VMt](https://pic.twitter.com/sUI6QC4VMt)

 EXRNA @EXRNA · 13 DAYS AGO



**Mark Gerstein**  
 @markgerstein

Dixon: shows that the RBP HuR enhances uptake of RNAs into EVs & is up-regulated in colon cancer #ERCC9

 13 DAYS AGO





exRNA  
@exRNA

Daniel Dixon @KUMedCenter RNA binding protein HuR regulates EV secretion in colorectal cancer #ERCC9

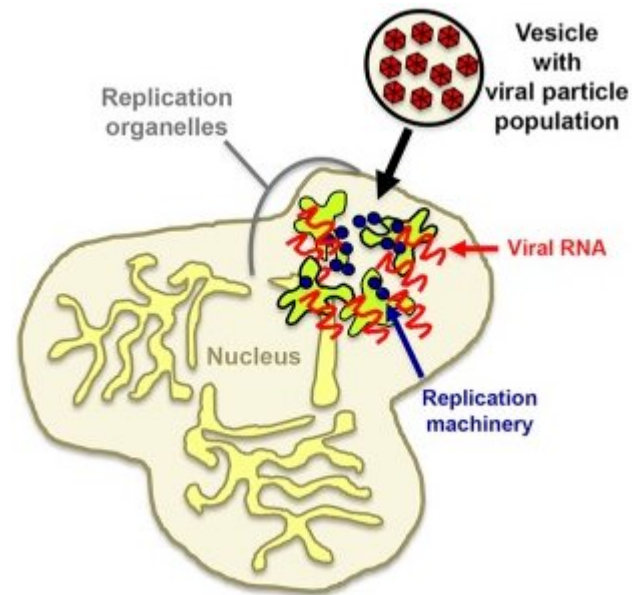
13 DAYS AGO



exRNA  
@exRNA

Sukhbir Kaur @NIH\_NCI: EVs sorted based on surface tags (CD63,CD47,MHC Class 1) have distinct ncRNA / miRNA profiles #ERCC9

13 DAYS AGO



Marianita Santiana @nih\_nhlbi: Transmission of viruses between organisms via vesicles  
[ncbi.nlm.nih.gov/pubmed/26423944](https://pubmed.ncbi.nlm.nih.gov/26423944) #ERCC9 [pic.twitter.com/2M0md3Rk6R](https://pic.twitter.com/2M0md3Rk6R)

EXRNA @EXRNA · 13 DAYS AGO



**ERCC9**  
**November 6 - 7, 2017**  
**Hilton Washington, DC ·**  
**Rockville Hotel & Executive Meeting Center**

Come join the conversation! [#ERCC9](https://twitter.com/ERCC9) [exrna.org/ercc9/](http://exrna.org/ercc9/) [pic.twitter.com/VMduFmljgT](https://pic.twitter.com/VMduFmljgT)

 EXRNA @EXRNA · 14 DAYS AGO