



Cornell University College of Veterinary Medicine

[Home](#) > [News](#) >

Full-service research facility offers RNA sequencing across campus

🐾 Monday, March 31, 2014 - 12:00am

Cornell scientists exploring the road from genes to proteins can access a new research service that helps map some of its more mysterious turns. The university has established a new RNA Sequencing Core (RSC) for any Cornell researchers interested in studying RNA, ubiquitous builder molecules that help translate DNA's blueprints into the proteins they code for.

Like workers on a construction team, most RNAs code for proteins, but some shorter pieces called small RNAs act as managers instead, influencing which proteins are built and thus which genes are expressed. The new facility will offer two separate sequencing services, one for each kind of RNA. As the University's first full-service facility, the RSC will use a new cheaper RNA sequencing technology able to discover new genes and will offer research assistance as a one-stop shop.



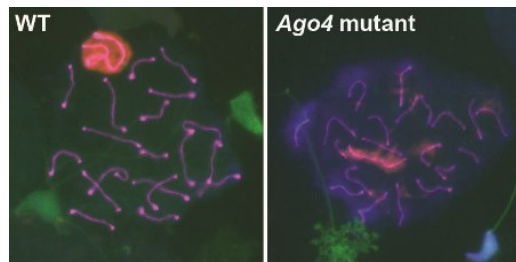
"We're offering a new concept for a core facility at Cornell, giving a comprehensive package of research services spanning experimental design to data collection to analysis," said Dr. Jen Grenier, who will serve as director of the RSC. "Other facilities on campus offer more of an a la carte model, helping with a piece of the whole experimental pipeline while the client lab has to put the pieces together. However, our facility is using a very new technology that requires technological expertise few labs have. Our goal is to bring this technology to any researcher who might be interested."

The RSC will use a next-generation sequencing technology called Illumina to sequence RNA and measure gene expression. Unlike microarrays, the older standard technology for these tasks, Illumina can sequence many RNA molecules at once at a very low cost per molecule. Illumina can also discover new genes, unlike microarrays, which can only measure the expression of genes already known.

Dr. Grenier will be available as a new technology expert to work directly with scientists at all stages of research. With 14 years of experience in technology development, she has developed platforms for high-throughput RNA quantification at the Broad Institute of Harvard and MIT in Cambridge, Mass. and managed Illumina sequencing projects in the Department of Molecular Biology and Genetics at Cornell University. In her new role as RSC director, she is joining the Department of Biomedical Sciences at the College of Veterinary Medicine, which will house the facility and several support staff.

Users can drop off RNA samples with Grenier, who will prepare it for analysis, conduct sequencing, generate a bioinformatics report to quantify gene expression, and help interpret the results.

Localization of microRNAs (red) to the XY body in prophase I spermatocytes from wildtype (WT) and Ago4 mutant males. Paula E. Cohen and Andrew Modzelewski



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“Often our researchers are interested in the difference between two samples,” said Grenier. “Say one sample is normal and one is diseased—a report would indicate what genes are expressed differently between the two, including quantitative measurements of gene expression. Analyzing RNA is a great way to conduct research because it’s easy to purify and handle. With a single sample you can measure the level of expression of all genes at once. It gives a powerful wide-angle snapshot of what’s happening in a cell.”

Sponsored by Cornell’s new NIH-sponsored Center for Reproductive Genomics and in part by the Department of Biomedical Sciences at Cornell’s College of Veterinary Medicine, the RSC offers RNA sequencing for any interested Cornell researchers, with subsidies available for researchers at the College of Veterinary Medicine. Contact Jen Grenier (jkg47@cornell.edu) for more information.