



Modeling breast cancer in mice; testing bioinformatic driven predictions and therapies



Mouse models have long been used to study breast cancer, revealing key insights into the role of various signal transduction pathways. Using a bioinformatics approach to generate testable hypotheses, we have integrated our studies of gene expression and whole genome sequencing with mouse models. Predictions for genes regulating metastasis, tumor suppression and optimal therapy have been tested and will be discussed.

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Host: Dr. Sean Egan

Date: Thursday February 15th, 2018 Time: 3:30PM Place: CCBR Red Seminar Room; 160 College St