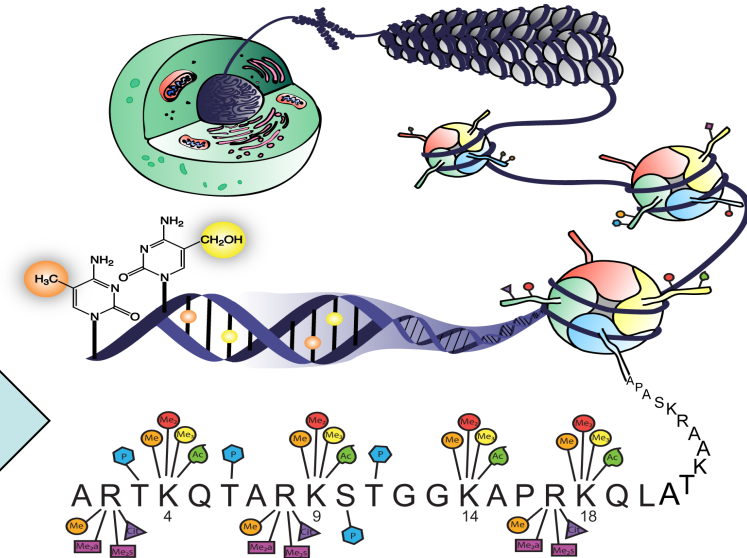


# Environment, Metabolism and the Epigenome



## Gut microbiota & the host epigenome

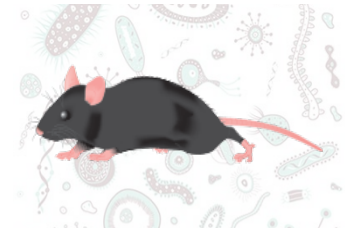
Collaboration with  
Federico Rey (UW)



germ-free

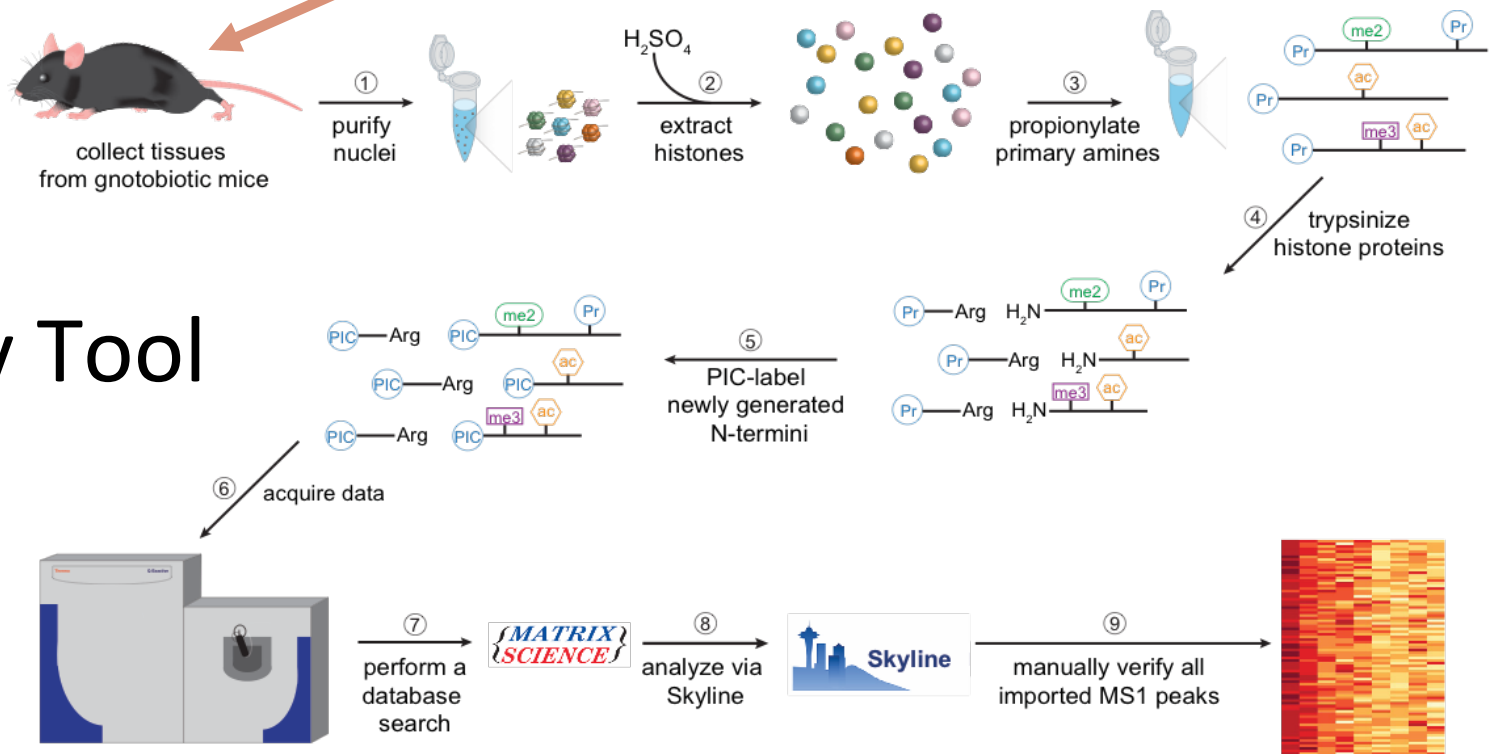


germ-free  
+ short chain  
fatty acids



conventionalized

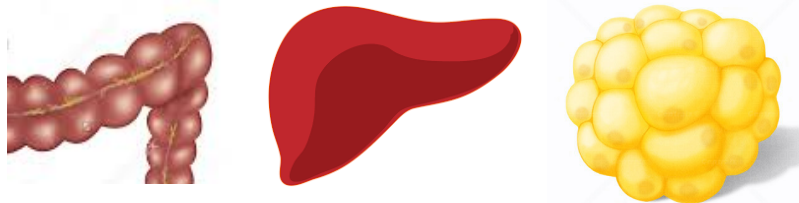
# 'histone-typing' work-flow



# Discovery Tool

# Gut microbiota regulate host histone PTM states

Krautkramer et al *Mol Cell* 2016  
 Posters: James Dowell & Spencer Haws

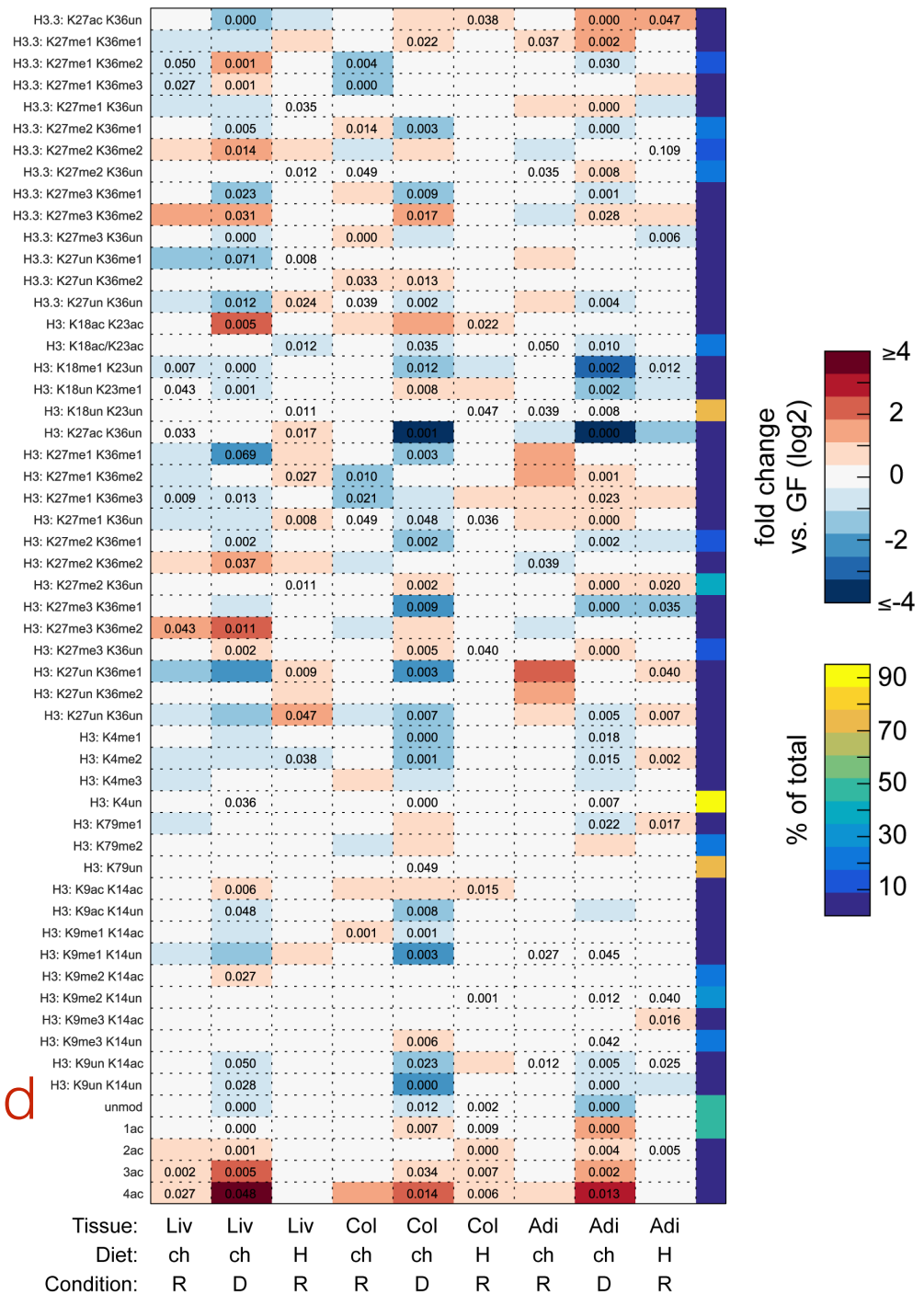


H3: K18ac+K23ac, ~4-fold

H4: tetra-acetylation, 12-fold

H3: K27me3+K36me2, ~4-fold

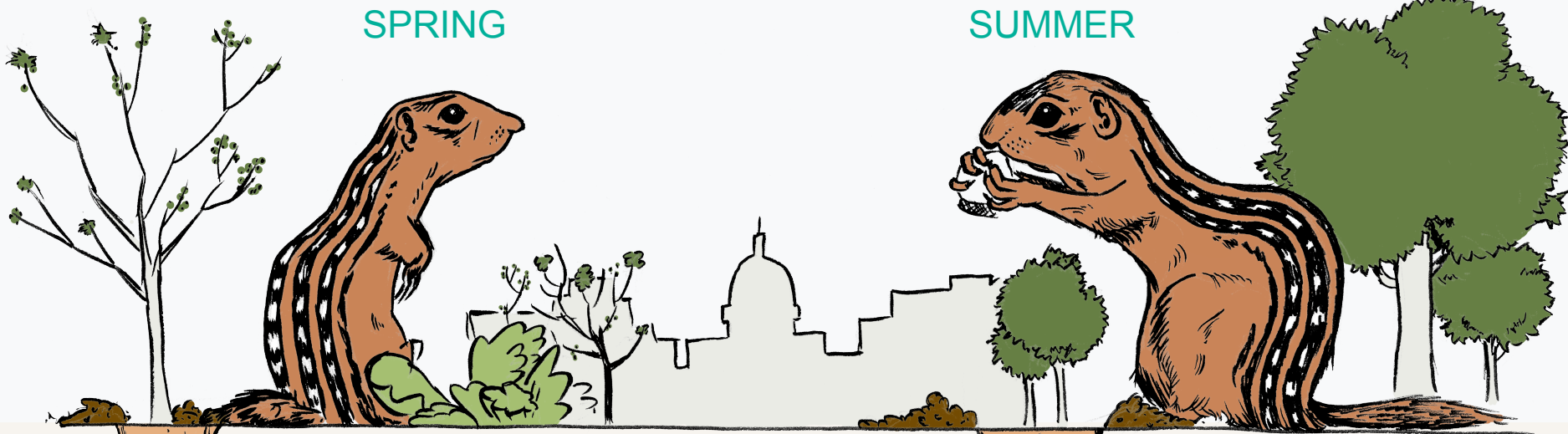
H3: K18me1+K23un, ~8-fold



# CIRCANNUAL CYCLE OF THE 13-LINED GROUND SQUIRREL

SPRING

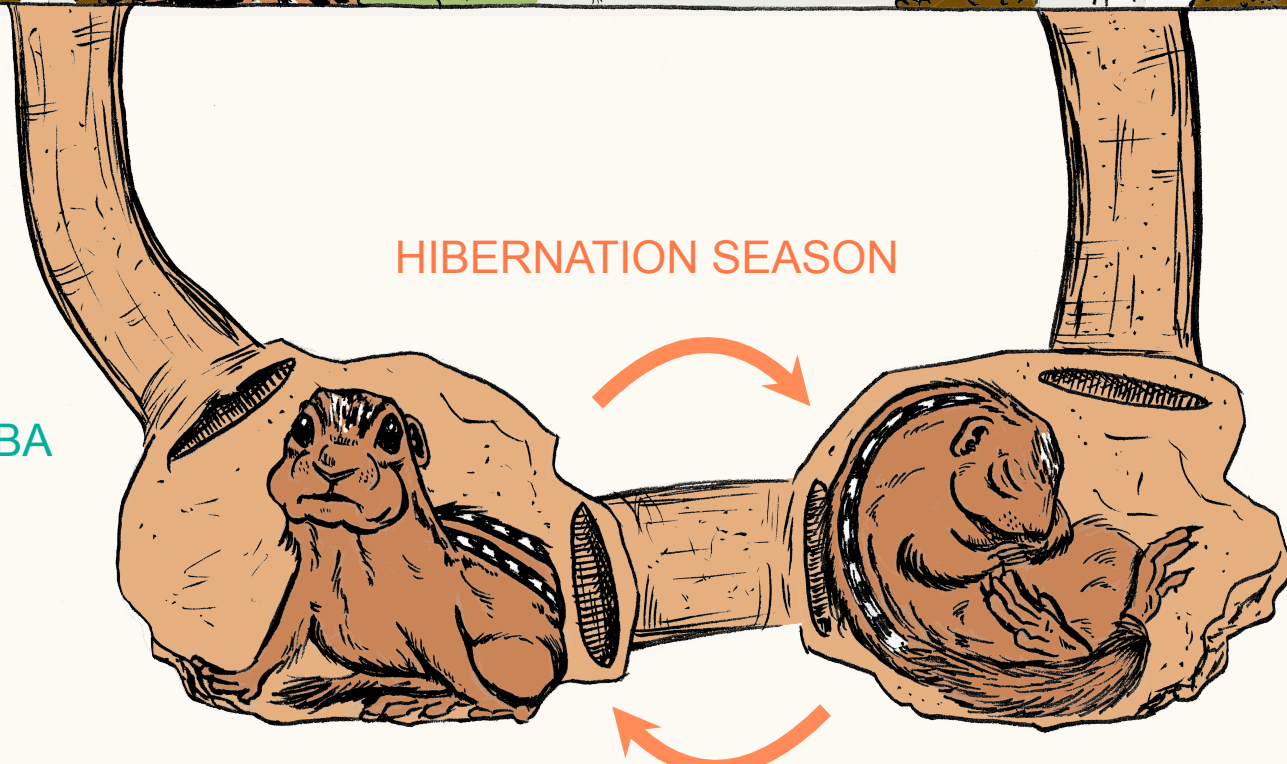
SUMMER



HIBERNATION SEASON

IBA

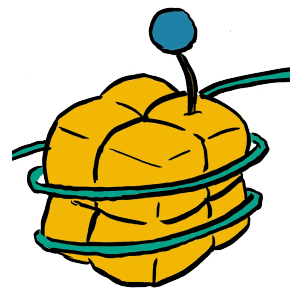
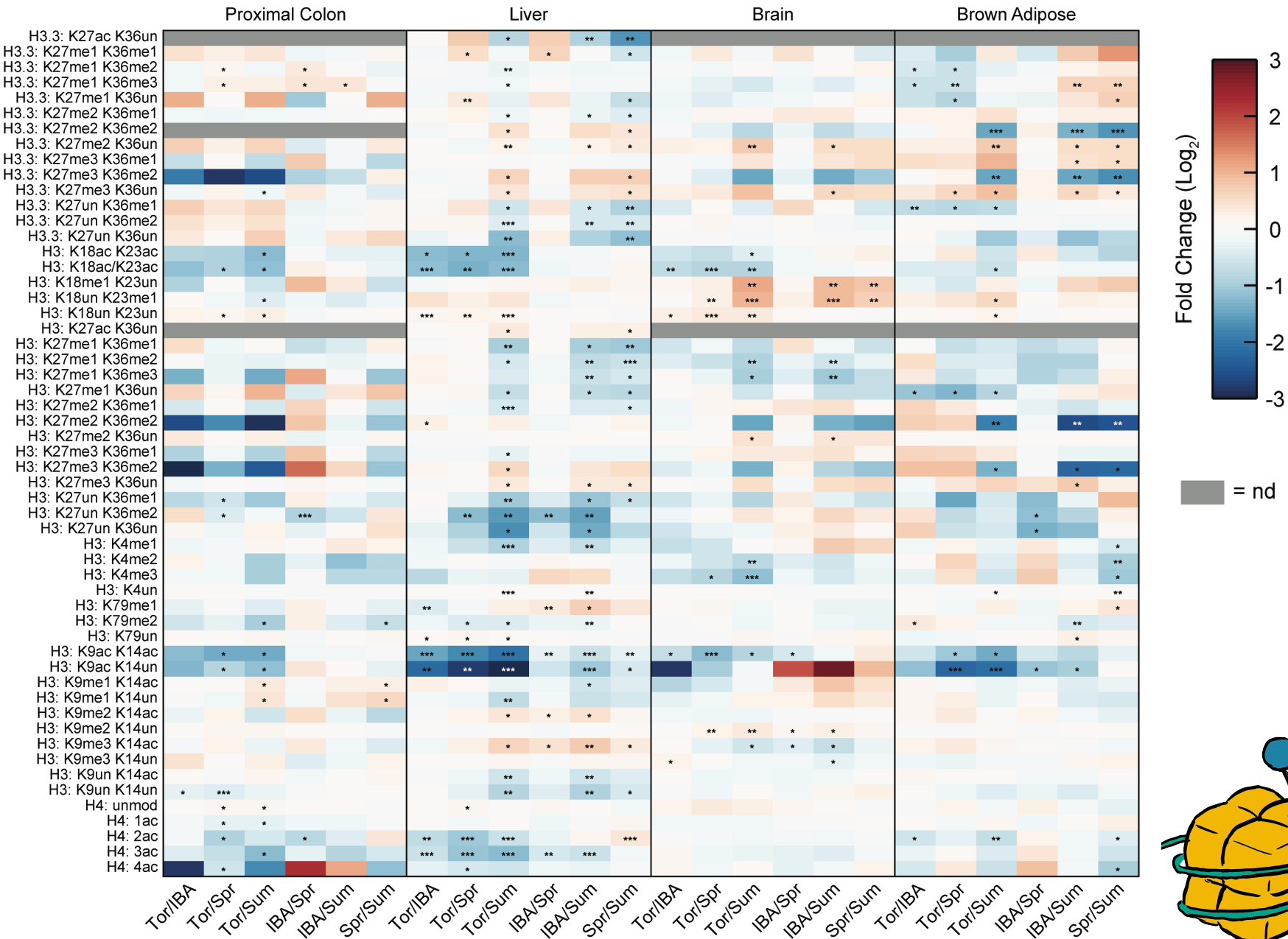
TORPOR



Rush Dhillon  
Hannah Carey  
Kim Krautkramer



# HISTONE PTM STATES VARY THROUGHOUT THE YEAR



## *Efforts at WID*

*Building a pipeline for multi-omics integration that includes epigenomics, histone typing, metabolomics and metagenomics*

*Showcase these efforts as GRAND Challenges within the Healthy People multi-disciplinary team at WID and throughout campus*