

# WWTP field study



This dataset exemplifies transcriptomic responses after exposure to contaminant mixtures in complex environmental samples. Fathead minnow were exposed to water upstream, downstream, and at the point source of the Hutchinson waste water treatment plant (Hutchinson, MN).

## Dataset overview

Organism: Fathead minnow (*Pimephales promelas*)

Tissue: Liver

Exposure conditions: Environmental samples

NCBI Accession #: GSE49098

Citation: [dx.doi.org/10.1021/es404027n](https://dx.doi.org/10.1021/es404027n)

## Details on experimental design

Fathead minnows were held in aerated containers at the field site that were continually supplied with a flow of water from the US, DS, and point-source locations (exposure duration = 4 days). Each container held 4 males and 4 females. After 4 days, RNA samples were collected from male livers and assessed with Agilent microarrays (GPL9248). Each microarray profile represents liver RNA samples from an individual fish. See the citation listed above for further details.