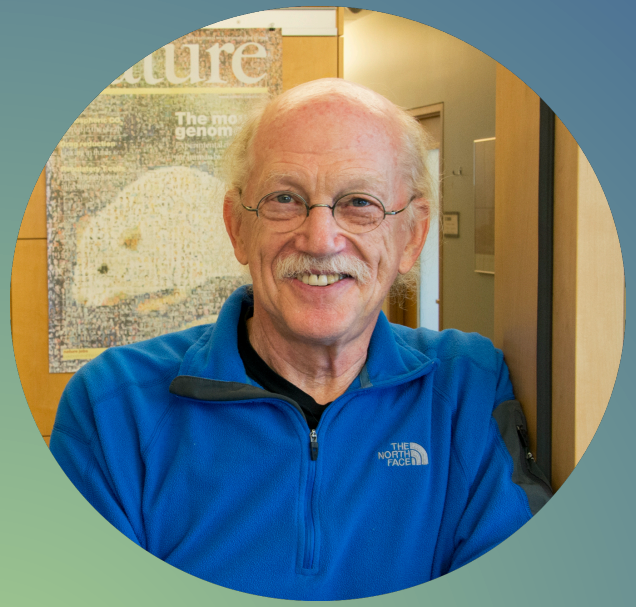
"Transcriptome profiling with lineage and single cell resolution in Caenorhabditis"

Abstract: Single cell RNA-seq of the developing C. elegans embryo revealed the expression changes from gastrulation to terminal cell differentiation (Packer et al., Science, 2019) of more than 110 terminal cell types. We have since extended the analysis to additional life stages, with the overall goal of delineating the transcriptome profile of the complete life cycle. In addition we have begun a comparative analysis, using C. briggsae, which has a nearly identical embryonic cell lineage, despite its extensive evolutionary divergence.



Robert H. Waterston is a Professor and former William Gates III chair of Genome Sciences at the University of Washington. He partnered with John Sulston in pioneering whole genome analysis, first with the construction of the physical map of the C. elegans genome and later with sequencing the worm, human and other genomes. He also joined with Sulston to advocate for the rapid, unconstrained release of the sequence. He was educated at Princeton University (BSE) and the University of Chicago (MD/PhD) and interned at Children's Hospital in Boston. After his postdoctoral fellowship at the MRC Laboratory of Molecular Biology with Sydney Brenner, where he first met Sulston, he joined the faculty at Washington University St. Louis. He moved to the University of Washington in 2002 as the founding chair of the Department of Genome Sciences. His lab now studies the genes of C. elegans and their expression in individual cells. He is a member of the National Academies of Science and Medicine and shared the Gairdner Award with Sulston and others.