

# UCSC GENOME BROWSER AND BIOMART

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# UCSC Genome Browser

- The University of California, Santa Cruz (UCSC) Genome Browser (<http://genome.ucsc.edu>) contains a variety of tools
- The **Genome Browser** allows for interactive visualization of genomic data, which is visualized across tracks
  - NCBI RefSeq information
  - OMIM alleles
  - Clinical variants and SNPs, etc
- The **Table Browser** allows you to download sequence or feature data from all (selected) genes
  - Can download promoter regions, introns, exons, etc

# UCSC Genome Browser examples

- Using the Genome Browser, let's look at the gene BRCA2
  - From the OMIM allele track, a one base-pair insertion in what exon was found in a patient with prostate cancer?
- Using the Table Browser
  - Get selected fields from the table containing the NCBI RefSEQ known genes
  - Get the CDS exon and intron sequences for BRCA2
  - Get the 5' UTR exon sequences for all human genes

# BioMart

- BioMart (<http://www.ensembl.org/biomart/martview/>) is a database system providing access to genomic feature and sequence data for specific genes or proteins
- Ensemble is a genome browser and a joint project of the European Bioinformatics Institute (EBI) of the European Molecular Biology Laboratory (EMBL), and the Wellcome Trust Sanger Institute
- Using BioMart
  - Select a Dataset, such as Ensemble Genes → Human genes
  - Select your Filters (this is the query step, where you can enter the genes of interest, for example)
  - Select the Attributes (the desired output)
  - Click on Results

# BioMart ortholog example

- I have recently received data from a mouse experiment
- High expression of the following genes (MGI symbols) were associated with resistance to radiation treatment in mice with bladder cancer:
  - Arl4a
  - Birc6
  - Zfp110
- The next step is to evaluate these genes in human bladder cancer patients – what are the orthologs of these genes?