

ANNOTATOR'S WORKSHEET

For incorporation of cis-regulatory modules into the cis-Browser
These steps should be followed

Given a literature reference with primary information or a review:

1. List the gene name, any synonyms given by the author, and the NCBI gene ID or other identifying number
2. List all classes of function of regulated gene (Regulatory, signaling, housekeeping, differentiation, cell cycle, extracellular, cytoskeletal, and/or nuclear)
3. Download the NCBI gene model & sequence and establish the coordinates of the module your report considers
4. List species in which the module is conserved, if any
5. Find a map of the cis-regulatory inputs into that module
6. List separately each input that the map shows (1, 2, 3, etc)
7. Name each input in terms of the transcription factor—whatever author says
8. List species in which each individual target site sequence is conserved, if any
9. Determine from author's description the function of each input—canonical names
10. Determine from the reference the species and
 - a) **if embryo:** the author's description of stage & lineage/territory/part (e.g. E-cell lineage, endoderm, gut, etc)
 - b) **if adult:** what body part, cell type
 - c) **if culture:** what cell line