

MMRRC - Supporting the use of RRIDs

Reproducibility is one of the cornerstones of effective, open and transparent biomedical published research. However, too often resources (e.g. model organisms, antibodies, and tools) are not reported with adequate detail to ensure others can replicate or expand upon the published results.

The [Research Resource Identification Initiative](#) (#RRI), through the work of Force 11, seeks to change these holes in reporting by the use of unique Resource Identifiers (RRIDs). This initiative is designed to encourage authors to provide identification of the types of resources used in their research by adding a globally unique accession number to the resources described in the Materials and Methods section on their manuscript. These identifiers, called RRIDs, will allow authors to cite the resources that they use in their manuscripts.

Here at the MMRRC, we are strong supporters of reproducibility and as such are supporting the RRID initiative. As such, we will be asking investigators to do one of two things to support the RRID initiative.

First, if your model has a standard RRID, please reference the RRIDs to identify the model used in the research. You can check on standard RRIDs found in the [RRID portal](#). If your model does not have an RRID associated with it, you can create a new RRID by visiting the [RRID portal](#) where you can search across different databases, such as The [Model Organism Registry](#).

Once you have your RRID, you simply include your RRID number in the text of your manuscript at their first mention. If you have a long list of accession numbers, we recommend that you include an additional section at the end of your manuscript.

Here the preferred method for reporting of Model Organisms

- a. For all organisms an NCBI taxonomy name and identifier should be used to indicate species (e.g. "Mus musculus, NCBI Taxonomy ID:10090"). This can be omitted when more specific reference to a strain is provided (see below)
- b. For 'wild-type' strains such as 'C57BL/6' mice), an unambiguous name or identifier from an authoritative source [1] should be provided as well as a source vendor, repository, or lab.
- c. For genetically modified strains, reference to an identifier in a MOD or other authoritative source is sufficient. In the absence of this, all known genotype information should be reported. This includes genetic background, breeding information relevant to propagating the variation, and precise alterations identified in or introduced into the genome (including the known sequence, genomic location, and zygosity of alterations). For random transgene insertions, it is not required that genomic location of insertion(s) is known, but precise sequence of inserted sequence should be unambiguously resolvable according to sequence identification criteria above. For targeted alterations, reporting the sequence and location of an alteration is required to the degree that it is known, according

to sequence identification criteria above. Note that this information can be provided directly in a publication, or through reference to an external source such as a MOD record or catalog offering where such information is provided.

Good example:

“B6.129(Cg)-Kcnn2tm1.1Jpad/J (Jax ID: 009592) (Background: C57BL/6 , SK2delta targeted knockout (Gene ID: 140492)), obtained from Jackson Labs)”

Bad example: “SK2delta knockout mouse”

How exactly do RRIDs work? The Resource Identification Initiative has three criteria for RRIDs:

1. Machine readable
2. Free to generate and access
3. Consistent across publishers and journals

What if my resource doesn't exist in the database? The Resource Identification Portal allows you to make new entries using the “Add a Resource” option on their homepage. This makes it very easy to generate a new RRID.

When did this initiative start? This project was an outcome of a meeting held at NIH on June 26th, 2013. A diverse range of journals and publishers are on board with the project and by the end of 2014, over 200 papers contained RRIDs. Publications currently reporting RRIDs can be found in [Google Scholar](#) or [PubMed](#).

Why should I support this initiative? The great value behind this initiative is that it allows for easy tracking of all papers that have used the same resource making it easy to access how the same resources works in other scenarios. In addition, once a RRID has been assigned, an investigator will be able to see how frequently it is used by others, and to gain proper recognition via RRID citations for their materials.

Here at the MMRRC, we believe in promoting reproducible science. Supporting the RRID initiative is just one more way we help investigators further their research efforts.