Some Guidelines

* We have uploaded a starter set of articles from Pubmed Central (PMC) onto fair.bioassayexpress.com
* For each article, annotate only *one* assay. Each article will have only *one* template (NextGen Sequencing, MIARE, MIQE, MIFlowCyt, or MISFISHIE) associated with it.
  + Use the **Origin** button to access the full text and supplementary material of any article.
  + For **NextGen Sequencing**, you will also want to view the linked SRA, BioProject, or BioSample pages associated with a paper (accessible from PMC)
* If a metadata field is not provided in the article, use on the absence tree terms. Most useful:
  + **unknown -** There should be a term assigned, but the value was not specified in the article
  + **ambiguous** - The article is ambiguous, there are multiple indeterminate possibilities. Also use for papers that reference another article’s methods without providing real specification of their own (ie: experiment performed as in Doe, J. Nature 2018
  + **not applicable -** Term does not apply to this assay.
* If a metadata field is provided in the article, add it to the template:
  + Begin typing or check the **Tree** button to see if the term already exists
  + For terms that do not exist in the ontology tree:
    - **Request Term** to add a provisional term. This will be accessible by other Hackathon members
    - **Free Text** - used in cases where a common term would not be applicable (ie: age, hypothesis, etc).
* Our overall goal is to: **Assess how successful the minimum information guidelines have been at enforcing metadata capture.** 
  + The more papers we can investigate, the better.
  + Our goal is not to completely annotate every paper, but rather find out how many of the suggested terms are being reported.
  + In some cases, providing a more generic term like *“complete details provided”* might be a better use of time than entering all terms.
* You may use any paper in PubMed Central published within the last 5 years (all of our minimum reporting templates have been around for at least that long)
* You will run out of papers to annotate that are currently imported into the fair.bioassayexpress.com database. To find new papers use the following links and use the PMC number as the ID.
  + **MIQE:** [**http://bit.ly/fairMIQE**](http://bit.ly/fairMIQE)
  + **MIFlowCyt:** [**http://bit.ly/fairMIFlowCyt**](http://bit.ly/fairMIFlowCyt)
  + **MIARE:** [**http://bit.ly/fairMIARE**](http://bit.ly/fairMIARE)
  + **MISFISHIE:** [**http://bit.ly/fairMISFISHIE**](http://bit.ly/fairMISFISHIE)
  + **NextGen Sequencing:** [**http://bit.ly/fairNGS**](http://bit.ly/fairNGS)