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# ALSF Resource Sharing Form

* Copy and insert completed form into the Resource Sharing section of the application.
* Complete relevant categories for unique research outputs expected from this grant.
* Delete the instruction text in italics when completing this form.
* See second page for example Resource Sharing Plan.

*\*Early Career investigators applying for Young Investigator, ‘A’ Award or Early Career RUNX1 grants are encouraged to describe past experience; however, it is understood this may be limited. The review will focus on how you would share outputs from this project.*

## FORM (1-page maximum)

**Data Sharing:**

* *Highlight how you have shared data publicly – i.e., not upon request – and how those data have been reused. Illustrate with reuse metrics such as citation counts, downloads, or other such data if available.*
* *Discuss how you plan to share the outputs from this proposal and how the data will be archived (via the recognized repository for the type of data or, for data without such a repository, via Zenodo, FigShare, or similar archival services). How will data be licensed (i.e., CC0 or* [*another license*](http://opendefinition.org/licenses/)*). You must discuss how and when data that you generate during the course of this project will be shared. If access will be controlled via a data access committee or other such structure, describe the conditions under which data will be shared and specify how relevant metrics (number of requests made, number of requests approved, time to respond to requests) will be stored and reported to us and the scientific community.*

**Protocol Sharing:**

* *Highlight how you have shared protocols openly – i.e., not upon request – and how those protocols have been used by others. For example, you may have posted them to* [*protocols.io*](http://www.protocols.io/) *or a similar service.*
* *Discuss how and when you plan to share the outputs from this proposal. Not all projects will result in protocols. If yours does not, this section can be deleted.*

**Material and Reagent Sharing:**

* *Highlight how you have shared materials and reagents and how those reagents have been reused.*
* *Discuss how and when you plan to share the reagents and materials developed in your group as part of the proposal (e.g. deposit plasmids in Addgene, deposit cell lines in the appropriate cell bank). Not all projects will produce new materials and reagents. If yours does not, this section can be deleted.*

**Source Code Sharing:**

* *Highlight how you have shared source code, software, and computational workflows openly – i.e., not upon request – and how the source code has been used by others. For example, you may have uploaded them to* [*GitHub*](http://github.com/) *or a similar service.*
* *Discuss how and when you plan to share the outputs from this proposal. How will software be licensed (i.e., MIT or* [*another license*](https://choosealicense.com/)*)? Are there plans to produce a polished software package? If so, how will that be distributed? Not all projects will result in source code. If yours does not, this section can be deleted.*

**Other Outputs:**

* *Highlight how you have shared other outputs and how those outputs have been used by others.*
* *Discuss how and when you will share other expected outputs from this work.*

**Clinical Trials Reporting:** *If you propose a clinical trial discuss how you will maintain up to date records on the relevant repositories (e.g., clinicaltrials.gov). Discuss the trials you have run in the past and the extent to which those records have been maintained. Please provide links.*

# Resource Sharing Example:

**Data Sharing:** In previous projects, we performed gene expression analysis of treated and untreated cell lines. We uploaded our data to NCBI’s GEO repository at the time the data were collected, and we made these data openly available with the publication of our manuscript [1]. In GEO these have been assigned the identifiers GSE1245, GSE1246, and GSE1247. We annotated these data with treatment date, processing batch, cell line, and treatment type. These data were downloaded and reanalyzed by Doe et al. [2] and Smith et al. [3] to identify additional targets. These data were integrated into a larger analysis of multiple datasets by Patel et al. [4]. In this project we will perform RNA-seq analysis of XYZ cell lines. We will upload sequencing data to SRA and link the raw data to summary information in NCBI’s GEO repository. We will annotate experimental metadata using terms from the Experiment Factor Ontology (EFO) where relevant terms are available. We will make these data publicly available to the community at the time of publication.