Array Express:

Annotare submission guide:

<https://www.ebi.ac.uk/fg/annotare/help/index.html>

* Annotare step by step

Experiment:

* (title\*, description\*)
* Experiment type\* (in isa\_assay experiment type and technology type), experimental designs
* (date of public release\*)
* (name\*, email\*, role\*, affiliation\*, address\*)
* Information should already be included in first sheet of isa files

Sample attributes and protocols: 🡪 Template: ArrayExpress - Plant sample

For plants:

* Organism\*
* Cultivar or ecotype\*
* Age\*
* Developmental stage\*
* Genotype\*
* Organism part\* (not listed as mandatory in guide but in annotare itself when selected plant HTS experiment)
* Material type\* (not listed as mandatory in guide but in annotare itself when selected plant HTS experiment)
* Plus free choice attributes
* Sample collection protocol\*, nucleic acid extraction protocol\*, nucleic acid library construction protocol\*, nucleic acid sequencing protocol\* (optional: growth, treatment, normalization data transformation, conversion protocol)

Technology specific annotations:

Sequencing library information: 🡪 Template: ArrayExpress – Sequencing library

* Library layout\*
* Library source\*
* Library strategy\*
* Library selection\*
* (for paired end sequencing experiments: nominal length\*, nominal SDev\*, Orientation\*)
* (for strand-specific sequencing experiments: library strand\*)

Raw and processed data files

Single cell experiments: ……………

Two colour experiments: …………..

\*=mandatory