Annotare submission tool

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This practical will introduce you to all functionalities of the submission tool Annotare (https://www.ebi.ac.uk/fg/annotare/login/) at EMBL-EBI. More information can be found on the EBI webinar "ArrayExpress: why and how to submit your data" (https://www.ebi.ac.uk/training/online/course/arrayexpress-why-and-how-submit-your-data).

Exercise 1

Submitting microarray data to ArrayExpress using Annotare

Scenario

You are working on a research project focus on the molecular characterization of human clear cell renal cell carcinoma (ccRCC) and its progression. As part of your project you have performed transcriptome profiling of primary human cell cultures derived from clear cell renal carcinoma tumors and matched renal cortex opposite to the tumor, collected after nephrectomy. You have some interesting results from your project that you want to publish and you are thinking about submitting your microarray data to ArrayExpress using Annotare.

Tasks – Extracting all metadata needed for submission

We are going to use the publication "Major Action of Endogenous Lysyl Oxidase in Clear Cell Renal Cell Carcinoma Progression and Collagen Stiffness Revealed by Primary Cell Cultures" (http://europepmc.org/abstract/MED/27449199) to extract all the information needed for submission to ArrayExpress.

Let's log in to Annotare to start our submission!

Choose the submission type

- What is the experiment type of this experiment?
- How many hybridisations did you performed?
- What array did you use?
- What label did you use?

Describe your experiment

- Informative title highlighting the intention of your experiment
- Background biology and aim of the experiment
- Experiment type
- Choose your experiment design
- Date of public release
- Add your contact details
- Add publication details

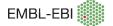At this stage, you can start uploading the raw data files (*.CEL files).

Sample annotation

Extract as many metadata as you can from the publication to describe your samples and define the experimental variable. When annotating samples you can use the Ontology Look-up Service (OLS; https://www.ebi.ac.uk/ols/index).

Information about protocols

Find information about the following protocols:

- Sample collection protocol
- Nucleic acid extraction protocol
- Nucleic acid labeling protocol
- Nucleic acid hybridisation to array protocol
- Array scanning and feature extraction protocol

Upload files and assign samples

This table will help you to assign each sample to the corresponding microarray raw data file (*.CEL file).

Samples	Microarray raw data
106CS	106CS_PrimColt_C_08i22156_Exon1.0_13.04.11.CEL
121GIC	121GIC_PrimColt_C_09i14599_Exon1.0_18.04.11.CEL
143PG	143PG_PrimColt_C_10i4386_Exon1.0_18.04.11.CEL
148GB	148GB_PrimColt_C_10i10898_Exon1.0_13.04.11.CEL
66SML	66SML_PrimColt_C_06i10962_Exon1.0_18.04.11.CEL
70LS	70LS_PrimColt_C_06i17914_Exon1.0_14.04.11.CEL
72FG	72FG_PrimColt_C_06i19711_Exon1.0_14.04.11.CEL
95RA	95RA_PrimColt_C_08i8806_Exon1.0_13.04.11.CEL
106CS	106CS_PrimColt_T_08i22156_Exon1.0_13.04.11.CEL
121GIC	121GIC_PrimColt_T_09i14599_Exon1.0_18.04.11.CEL
124LR	124LR_PrimColt_T_09i16420_Exon1.0_14.04.11.CEL
143PG	143PG_PrimColt_T_10i4386_Exon1.0_18.04.11.CEL
148GB	148GB_PrimColt_T_10i10898_Exon1.0_13.04.11.CEL
66SML	66SML_PrimColt_T_06i10962_Exon1.0_14.04.11.CEL
70LS	70LS_PrimColt_T_06i17914_Exon1.0_14.04.11.CEL
95RA	95RA_PrimColt_T_08i8806_Exon1.0_13.04.11.CEL

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