Proteome Exploration Laboratory

Sample Submission Form

Please fill out the form and save as PEL\_[PI Last Name]\_[User Initials]\_yyyymmdd. Email to tfchou@caltech.edu.

|  |  |  |
| --- | --- | --- |
| *User**Info* | Submission Date | Click or tap to enter a date. |
| Name | Click or tap here to enter text. |
| Email | Click or tap here to enter text. |
| Phone # | Click or tap here to enter text. |
| PI name | Click or tap here to enter text. |
| *Account* | Account Type | [ ]  TSA or [ ]  PTA no: Click or tap here to enter text. |
| Recharge | [ ]  collaboration *or* [ ]  fee for service |
| *Project* | Reference String | Click or tap here to enter text. (i.e. LastNameYYYYMMDD) |
| Description | Click or tap here to enter text. |
| Analytical Goal | Click or tap here to enter text. |
| Organism | Click or tap here to enter text.  |
| Proteome  | FASTA: [ ] Uniprot [ ] Swiss-Prot [ ] TrEMBL [ ] Isoforms [ ] Gene translation |
| Type | [ ] tissue [ ] cell pellet [ ] cell lysate [ ] affinity enrichment [ ] BONCAT[ ] intact protein [ ] digested peptides [ ] other:  |
| Labeling  [ ] *none* | TMT: [ ] 6-plex [ ] 10/11-plex [ ] 18-plexSILAC: [ ] Arg-6 [ ] Arg-10 [ ] Lys-4 [ ] Lys-6 [ ] Lys-8  |
| Preparation | [ ] user *or* [ ] PEL staff (describe on next page or attach doc) |
| Digestion [ ] *none* | [ ] trypsin [ ] chymotrypsin [ ] CNBr [ ] PepsinA[ ] arg-c [ ] asp-n [ ] lys-c [ ] lys-n [ ] other: Click or tap here to enter text. |
| Labels (eg initial\_id) | Click or tap here to enter text. |
| *Samples* | Drop-off Date | Click or tap to enter a date. |
| Instrument | Preferred: [ ] Astral [ ] Stellar [ ] Eclipse [ ] Fusion  |
| *Analysis* | Data Reduction [ ]  *none* | Software: [ ] ProteomeDiscover [ ] MaxQuant [ ] FragPipe [ ] OpenMS  Identification: [ ] top-down [ ] bottom-up Quantitation: [ ] label free [ ] TMT [ ] SILAC quant. abundances: [ ] raw [ ] normalized [ ] scaled |
| Raw data | [ ] .raw [ ] .mzML [ ] .mzXML |
| *Deliverable* | Biological data | Proteins: [ ] .xlsx [ ] .csv [ ] .protXML Peptides: [ ] .xlsx [ ] .csv [ ] .protXML |
| Statistical data[ ]  *Special Analysis (please describe below)* | expression ratios: [ ] raw [ ] log2 [ ] log10 significance: [ ] p-value [ ] adj. p-value [ ] q-value* method: [ ] t-test [ ] Wilcoxon [ ] limma

pathway: [ ]  GO analysis [ ]  GSEA |

# User sample preparation details

*Please describe the buffers used in each step, any desalting methods, the final peptide concentration, and a description of how it was determined.*

*\*For immunoprecipitated or affinity enriched samples, there is no need to do peptide quantification.*

*\*For gel band samples, please attach an image of your gel with the bands of interest CLEARLY indicated with your submission. Cut the band of interest and put it in a tube with some dH2O.*

Click or tap here to enter text.

# User requested special analysis

*Please describe any special analysis requests. Specifically, if protein expression ratios are to be calculated describe the normalization procedure (basic between samples, via a specific protein) and the specific pairwise comparisons while noting the denominator.*

Click or tap here to enter text.