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 | [ ] include all species in genusFASTA: [ ] Uniprot [ ] TrEMBL [ ] UniREF100 [ ] Isoforms [ ] gene translation |
| Type | [ ] tissue [ ] cell pellet [ ] cell lysate [ ] affinity enrichment [ ] BONCAT[ ] intact protein [ ] digested peptides [ ] other: Click or tap here to enter text. |
| Labeling  [ ] *none* | TMT: [ ] 6-plex [ ] 10/11-plex [ ] 16-plexSILAC: [ ] Arg-6 [ ] Arg-10 [ ] Lys-4 [ ] Lys-8  |
| Preparation | [ ] user *or* [ ] PEL staff (describe below 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. |
| *Samples* | Labels (eg initial\_id) | Click or tap here to enter text. |
| Drop-off Date | Click or tap to enter a date. |
| *Analysis* | Instrument | Preferred: [ ] QExactive HF [ ] Fusion [ ] Eclipse |
| Data Reduction [ ]  *none* | Software: [ ] ProteomeDiscover [ ] MaxQuant [ ] FragPipe [ ] OpenMS  Identification: [ ] top-down [ ] bottom-up Quantitation: [ ] label free [ ] TMT [ ] SILAC quant. abundances: [ ] raw [ ] normalized [ ] scaled |
| Deliverable | Raw LCMS data: [ ] .raw [ ] .mzML [ ] .mzXML [ ] .csv of ms1 scans [ ] .csv of ms2 scansAnalyzed data: Proteins: [ ] .xlsx [ ] .csv [ ] .protXML  expression ratios: [ ] raw [ ] log2 [ ] log10 significance: [ ] p-value [ ] adj. p-value [ ] q-valuemethod: [ ] t-test [ ] Wilcoxon [ ] limma  Peptides: [ ] .xlsx [ ] .csv [ ] .pepXML [ ]  Special Analysis (please describe below) |

# 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. There is no need to do peptide quantification if it is immunoprecipitated or affinity enriched samples.*

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.