/var/folders/mm/d1t9xlqs7w9_10l252n5gbx80000gn/T/com.microsoft.Word/Content.MSO/A36402B1.tmpProteome 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 genus  FASTA: 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-plex  SILAC: Arg-6 Arg-10 Lys-4 Lys-6 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 data | .raw .mzML .mzXML  .csv of ms1 scans .csv of ms2 scans |
| Biological data | Proteins: .xlsx .csv .protXML  Peptides: .xlsx .csv .pepXML |
| 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. 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.