Proteome Exploration Laboratory/var/folders/mm/d1t9xlqs7w9_10l252n5gbx80000gn/T/com.microsoft.Word/Content.MSO/A36402B1.tmp

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-plex  SILAC: 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.