

**Omics Studies**

**Case Report Form: 2 CRF – Proteomics.docx**

**CRF module: proteomics**

Date that this CRF was filled out:

Name of person filling out CRF:

Project name/Identifier:

Animal/ID:

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<u>CDE Name</u>	<u>Data Collected</u>
<b>Experiment type</b>	
Omics level	<input type="checkbox"/> Proteomics
Input type	<input type="checkbox"/> Bulk primary tissue <input type="checkbox"/> Selected cell-types from primary tissue <input type="checkbox"/> Cell-cultures <input type="checkbox"/> Single-cell/single nuclei <input type="checkbox"/> Cerebrospinal fluid <input type="checkbox"/> Whole blood <input type="checkbox"/> Plasma <input type="checkbox"/> Serum <input type="checkbox"/> Saliva <input type="checkbox"/> Sweat <input type="checkbox"/> Urine <input type="checkbox"/> Feces <input type="checkbox"/> Other
If other, please specify	
If bulk primary tissue, specify tissue type	
If bulk primary tissue, specify tissue localization	
<b>Sample preparation</b>	

Quality control date and time MM/DD/YYYY hh:mm:ss	
Quality assessment type	<input type="checkbox"/> Hemolytic <input type="checkbox"/> Icteric <input type="checkbox"/> Lipemic <input type="checkbox"/> Unknown <input type="checkbox"/> Other
If other, please specify	
Sample preparation date and time MM/DD/YYYY hh:mm:ss	
Sample preparation	<input type="checkbox"/> Protein precipitation <input type="checkbox"/> Ultrafiltration <input type="checkbox"/> Solid phase extraction <input type="checkbox"/> Liquid-liquid extraction <input type="checkbox"/> Derivatization <input type="checkbox"/> Tissue homogenization <input type="checkbox"/> Tissue pulverization <input type="checkbox"/> Centrifugation <input type="checkbox"/> Unknown <input type="checkbox"/> Other
If other, please specify	
Internal standards used	<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/> Unknown
If internal standards were used, specify name(s)	
If internal standards were used, specify vendor(s)	
If internal standards were used, specify cat no	
If internal standards were used, specify concentration(s)	
External standards (calibrators) used	<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/> Unknown
If external standards were used, specify name(s)	
If external standards were used, specify vendor(s)	
If external standards were used, specify cat no	
If external standards were used, specify concentration(s)	
Label-free approach used	<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/> Unknown
Quality control samples used	<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/> Unknown
If quality control samples were used, specify name(s)	
If quality control samples were used, specify vendor(s)	

If quality control samples were used, specify cat no	
If quality control samples were used, specify concentration(s)	
If quality control samples were used, specify matrix/solvent	
<b>Sample preparation method</b>	
Specify protein precipitation precipitant	
Specify volume of precipitant	
Specify volume of sample added to precipitant	
Specify ultrafiltration device	
Specify centrifugation speed	
Specify centrifugation duration	
Specify centrifugation temperature	
Specify solid phase extraction cartridge vendor	
Specify solid phase extraction cartridge cat no	
Specify liquid-liquid extraction kit vendor	
Specify liquid-liquid extraction kit cat no	
Specify derivatization kit vendor	
Specify derivatization kit cat no	
Specify homogenizer vendor	
Specify homogenizer cat no	
Specify sample tubes vendor	
Specify sample tube cat no	
Specify beads vendor	
Specify beads cat no	
Specify homogenizing solution vendor	
Specify homogenizing solution cat no	
Specify volume of homogenizing solution	
Specify tissue weight that was homogenized	
<b>Liquid chromatography method</b>	

Instrument used, specify vendor	
Specify instrument used	
Specify instrument cat no	
Chromatography	<input type="checkbox"/> Reverse phase <input type="checkbox"/> HILIC <input type="checkbox"/> Ion exchange <input type="checkbox"/> Mixed-mode <input type="checkbox"/> Unknown <input type="checkbox"/> Other
If other, please specify	
Column used, specify vendor	
Specify column used	
Specify column cat no	
Specify column stationary phase	
Specify column inner diameter	
Specify column length	
Mobile phase A used	
Mobile phase B used	
Gradient used	
Flow rate used	
Column temperature used	
Injected sample volume used	
<b>Mass spectrometry method</b>	
Instrument used, specify vendor	
Specify instrument used	
Specify instrument cat no	
Instrument type	<input type="checkbox"/> TOF <input type="checkbox"/> Q-TOF <input type="checkbox"/> Single quad <input type="checkbox"/> Triple quad <input type="checkbox"/> Ion trap <input type="checkbox"/> Fourier transform <input type="checkbox"/> Unknown <input type="checkbox"/> Other
If other, please specify	
Proteomics mode	<input type="checkbox"/> Untargeted <input type="checkbox"/> Targeted <input type="checkbox"/> Unknown

Ionization mode	<input type="checkbox"/> ES+; <input type="checkbox"/> ES-; <input type="checkbox"/> APCI+; <input type="checkbox"/> EI; <input type="checkbox"/> CI-; <input type="checkbox"/> CI+; <input type="checkbox"/> Unknown <input type="checkbox"/> Other
If other, please specify	
MS mode	<input type="checkbox"/> Full scan <input type="checkbox"/> MS <sup>e</sup> <input type="checkbox"/> MRM <input type="checkbox"/> SIM <input type="checkbox"/> Unknown <input type="checkbox"/> Other
If other, please specify	
Specify peak detection and processing software	
<b>Data annotation</b>	
Peak/spectral identification	<input type="checkbox"/> Reference to known standards <input type="checkbox"/> Rule-based fragmentation annotation <input type="checkbox"/> Database search <input type="checkbox"/> Self-established spectral library <input type="checkbox"/> Unknown
Database used	<input type="checkbox"/> MASCOT <input type="checkbox"/> SEQUEST <input type="checkbox"/> Proteome Discoverer <input type="checkbox"/> Peaks DB <input type="checkbox"/> Unknown <input type="checkbox"/> Other
Database version	
If other, please specify	
If self-established spectral library, specify availability	
Manual data curation	<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/> Unknown
Database used for pathway analysis	<input type="checkbox"/> Ingenuity Pathway <input type="checkbox"/> Wikipathways <input type="checkbox"/> Pathway Tools <input type="checkbox"/> PANTHER <input type="checkbox"/> STRING <input type="checkbox"/> KEGG <input type="checkbox"/> Unknown <input type="checkbox"/> Other
If other, please specify	
Database version	
<b>Data quantification</b>	
Quantification strategy	<input type="checkbox"/> Relative quantification <input type="checkbox"/> Untargeted quantification <input type="checkbox"/> Absolute targeted quantification – label-free data <input type="checkbox"/> Labeled quantification (isotope tag-based, TMT) <input type="checkbox"/> Unknown <input type="checkbox"/> Other
If other, please specify	

Class or subclass-specific protein internal standards	
Pooled samples	<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/> Unknown
Internal standards	<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/> Unknown
Candidate identification criteria	<input type="checkbox"/> p-value <input type="checkbox"/> Log2 (fold change) <input type="checkbox"/> Unknown <input type="checkbox"/> Other
If other, please specify	
If p-value, specify value used	
If Log2 (fold change), specify value used	
<b>Data validation</b>	
Proteome confirmation by second method	<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/> Unknown
If yes, specify method	
Independent biological replicates for validation	<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/> Unknown
If yes, specify number	
<b>Data statistical processing</b>	
Statistical tests	<input type="checkbox"/> PCA <input type="checkbox"/> T-test + FDR <input type="checkbox"/> ANOVA <input type="checkbox"/> Regression <input type="checkbox"/> Unknown <input type="checkbox"/> Other
If other, please specify	

**Instructions:** Please check boxes where applicable. If none of the predetermined options is appropriate use the default space to specify your answer.

This form is to be filled in for one individual animal.

Abbreviations: ANOVA, analysis of variance; APCI, atmospheric pressure chemical ionization; CI, chemical ionization; EI, electron ionization; ES, electrospray ionization; FDR, false discovery rate correction; HILIC, hydrophilic interaction liquid chromatography; KEGG, Kyoto Encyclopedia of Genes and Genomes; MRM, multiple reaction monitoring; MS, mass spectrometry; PCA, principal component analysis; Q-TOF, quadrupole time-of-flight; SIM, single ion monitoring; TOF, time-of-flight