APAF SERVICE LIST

APAF (Australian Proteome Analysis Facility) is proud to be accredited by the National Association of Testing Authorities (NATA) for compliance with the international standard ISO/IEC 17025.

Refer to Accreditation Number 20344 for APAF's scope of accredited services.

SERVICE	FEE[1] A$
MASS SPECTROMETRY	
Peptide/Protein Identification – reports all detected peptides and proteins in a sample based on a specified database. *Identification is performed by bottom-up proteomics methods using data-dependent MS methods, including sample preparation by trypsin digest, LC/MS data acquisition and database searching. Specialised digests with alternative or multiple enzymes can also be accommodated. Further sample preparation procedures may be required depending on sample type.*	
Protein/Peptide identification in a simple mixture (e.g., purified proteins, immunoprecipitated proteins, low complexity biological samples)	$275
Protein/Peptide identification in a complex mixture (e.g., cell lysate, tissue samples)	$330
Label-free quantitative experiments – reports relative quantities of proteins between sample groups, and identifies proteins that are differentially expressed in sample groups. *Identification is performed using bottom-up proteomics methods using data-independent MS methods (DIA; also known as SWATH), and includes sample preparation, LC/MS data acquisition, database searching, and basic bioinformatic reporting. Alternatively, data-dependent acquisition methods can be used.* *Further sample preparation procedures may be required depending on sample type.* *It is strongly recommended that a 2D library is acquired with DIA experiments to increase protein identification and quantitative robustness.*	
Protein/Peptide identification and quantification in a low complexity mixture (e.g., plasma, saliva, milk etc.)	$295
Protein/Peptide identification and quantification in a high complexity mixture (e.g., cell lysate, tissue samples)	$350
High pH fractionated library (17 fractions) – digested samples are fractionated into 17 individual fractions and LC-MS data acquired to build an ion library for use in DIA peptide identification and quantitation	$3300
TMT-labelled quantitative experiments (10-plex) – reports relative quantities of proteins between sample groups, and identifies proteins that are differentially expressed in sample groups. TMT experiments are limited to experiment sizes of $n = 10$. *Identification and is performed using bottom-up proteomics methods using data-dependent MS methods, and includes sample preparation, TMT labelling, high pH fractionation of samples, LC/MS data acquisition, database searching, and basic bioinformatic reporting.* *Further sample preparation procedures may be required depending on sample type.*	
TMT 10-plex experiment	$7700

SERVICE	FEE1 A$
High resolution mass spectrometry - reports observed m/z and calculated actual masses of species observed in samples. For successful HRMS experiments, high purity samples are required. *Small molecules are dissolved in compatible solvent and MS spectra collected, and reported as ppm observed mass to theoretical mass based on empirical formula provided.* *Proteins to undergo intact mass analysis, which can include native analysis, should be provided in a suitable solvent. Samples are subjected to mass analysis and protein masses are reported. If information pertaining to amino acid sequences, characterisations of protein interactions (e.g., protein-ligand binding), or other in-depth analyses are required, results derived from tandem mass spectrometry (MS/MS) experiments followed by bioinformatics analysis are also reported.*	
Intact protein mass – static spray	$150 per sample, additional $75 p/h for MS/MS data interpretation (if required)
High resolution mass spectrometry of small molecules	$125 for first sample, $25 / additional sample
Glycan analysis – reports differential glycan expression in samples by releasing N- and O-linked glycans, or glycopeptide enrichment and analysis. *N- and O-linked glycans are released from proteins in samples, analysed by LC/MS and relative abundances of glycan in each sample group are compared and reported.* *For glycopeptide analysis, purified proteins are digested, glycopeptides are enriched and analysed by LC-MS, searched against databases to identify glycosite and glycan structure, and relative quantities in different samples reported.*	
N-linked glycan profile	$445
O-linked glycan profile	$395
N- and O-linked glycan profile	$740
Glycopeptide analysis from purified protein samples	$605
Crosslinking mass spectrometry – reports crosslinked peptides from samples treated with a mass spectrometry-cleavable crosslinker *Samples to undergo crosslinking mass spectrometry are treated with a mass spectrometry-cleavable crosslinker (e.g., DSSO, DSBU), followed LC-MS/MS sample preparation and data collection. Crosslinked peptides are identified from the resultant data using a crosslinking mass spectrometry software suite.* *Further sample preparation procedures, such as enrichment of crosslinked peptides, can be incorporated into crosslinking mass spectrometry workflows.*	
Crosslinking mass spectrometry experiment	Enquire
Sample preparation and pre-treatments *For specialized project needs, APAF can assist with a wide range of needs, including specialised protein digestion, extended sample preparation or analysis of post-translational modifications*	
Digestion with additional or alternative enzymes	Enquire
Methanol/chloroform extraction	$170
S-TRAP (or other device) assisted digestion (additional cost)	$95
Sample clean-up (e.g., buffer exchange, detergent removal) *Pricing may vary depending upon required method	$95*
Phosphopeptide enrichment *Phosphopeptide enrichment is compatible with both LFQ and TMT quantitative experiments*	$95 / sample
Other PTM experiments	Enquire
Method development – including relative and absolute quantitation of peptides / protein in samples by ion/reaction monitoring experiments	Enquire

SERVICE	FEE1 A$
BIOINFORMATICS	
Standard single-batch SWATH quantitative proteomics statistical analysis [2]	Incl. with MS project
Standard TMT quantitative proteomics statistical analysis [2]	Incl. with MS project
Multi-batch SWATH differential expression analysis	Enquire
TMT phosphoproteomics statistical analysis	Enquire
Weighted Gene Correlation Network Analysis (WGCNA)	Enquire
Protein functional enrichment analysis	Enquire
Data mining and proteomics-data classification	Enquire
Customised bioinformatics methods and workflow development	Enquire
AMINO ACID ANALYSIS see here for details of assay	
Amino acid profile (food products - liquid hydrolysis) [3,4]	$170
Amino acid profile with Hydroxyproline & Taurine [3,4]	$185
Tryptophan determination (base hydrolysis) [3]	$200
Cysteine determination (performic acid oxidation) [3]	$200
High sensitivity AAA (purified protein – gas hydrolysis) [3,4]	$170
Free AAA (no hydrolysis, 20aa) [3]	$170
Free AAA (physiological fluids) and aminothiols [3]	Enquire
LIQUID CHROMATOGRAPHY	
Reversed-phase (RP)-HPLC analysis	$185
A1/A2 beta casein in milk	$185
Lactoferrin analysis	$185
Size exclusion chromatography (SEC)	$125
Size exclusion chromatography (SEC) setup/stds	$185
Method development	Enquire
GEL ELECTROPHORESIS	
Gel Electrophoresis, sample preparation (include extraction, sample cleaning for 2-DE, quantitation)	$220 first sample $55 each additional
1-D gel (up to 18 lanes) stained with Coomassie	$305
1-D gel - Western blot analysis with client-provided antibodies [5]	Enquire
Gel Electrophoresis, Other service: specify in service request	Enquire
MULTIPLEXED IMMUNO-ASSAY (MIA)	
MIA, client performs assay at APAF [7]	$175 per hour
MIA, client performs assay at APAF, instrument access fee	$185 per day
MIA, APAF staff performs assay [6,7]	$925 per plate
MIA, Sample spin filtration (per sample) [8]	$10
MIA, Conc. of urine by precipitation & filtration prior to cytokine analysis	Enquire
MIA, Other service: specify in service request	Enquire
ARRAY TECHNOLOGY	
ELISA [10]	$810/plate [9]
Array Technology (AT), Other assays [10]	Enquire
Kit purchase: specify kit in service request	Enquire
ADMINISTRATION	
Biosecurity (international samples) processing	$120
Report administration (chargeable for each additional report prepared)	$35
Delivery fee	Enquire

Notes:

1. Prices are exclusive of GST (applicable only to samples originating within Australia).
2. Standalone or additional bioinformatics analyses may incur a cost.

3. Samples are analysed in duplicate. Contact us via e-mail for other Amino Acids (e.g., ornithine, hydroxylysine, GABA) and singlicate/triplicate analysis.
4. Cys and Trp not included.
5. Client must provide the primary antibody for Western Blot Analysis.
6. Using robotic platform for liquid delivery, where appropriate; client-supplied kits.
7. Client may supply the kit or alternatively APAF may purchase the kit in which case the cost of the kit is added to the service fee.
8. No charge where client supplies filtered samples to APAF.
9. Assays are conducted using the Andrew Alliance robotic platform/s for liquid delivery for precision and reproducibility.
10. Client may supply the kit, or alternatively, APAF may purchase the kit in which case the cost of the kit is added to the service fee.

SERVICE REQUESTS

For service enquiries, please email info.apaf@mq.edu.au
For service requests and sample submission, please use the APAF Service Request Form