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)	$290
Protein/Peptide identification in a complex mixture (e.g., cell lysate, tissue samples)	$360
Protein mapping – Protein sample is digested with multiple enzymes to return comprehensive amino acid sequence information	$750
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) or data-dependent acquisition (DDA; please inform), and includes sample preparation, LC/MS data acquisition, database searching, and basic bioinformatic reporting (e.g. database searches, quantitative and differential abundance analysis and reporting).* *Further sample preparation procedures may be required depending on sample type.* *For best results, 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.)	$395
Protein/Peptide identification and quantification in a high complexity mixture (e.g., cell lysate, tissue samples)	$450
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	$8050

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 a compatible solvent and MS spectra collected. Observed masses are reported and compared to theoretical masses based on empirical formula provided.* *Intact protein mass analysis and native protein analysis (performed in MS compatible physiological pH buffers; e.g.,ammonium acetate) involve proteins 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 (deconvoluted mass only)	$165 per sample,
Top-down protein characterisation of an intact protein	$165 per sample, + $120 p/h for data interpretation
High resolution mass spectrometry of small molecules	$125 per sample
Glycan analysis – reports differential glycan expression in samples by releasing N- and O-linked glycans, or glycopeptide enrichment and analysis. *N- and/or O-linked glycans are released from proteins in samples, analysed by LC/MS and relative abundances of glycan compositions and number of glycan isomers in each sample group are compared and reported.* *For intact N-glycopeptide analysis, purified proteins are digested, glycopeptides are enriched and analysed by LC/MS, searched against databases to identify glycosite and glycan composition, and relative abundance of glycan compositions of each glycosite reported.* *For N-glycosylation site occupancy analysis (e.g., Asp/(Asn + Asp) glycosite comparison), N-glycans are released from the purified protein before protein digestion, and abundance of deaminated glycosite (previously glycosylated) and non-glycosylated Asn glycosite (unoccupied glycosite) are reported.*	
N-linked glycan profile	$465
O-linked glycan profile	$415
N- and O-linked glycan profile	$775
Glycopeptide analysis from purified protein samples	$635
N-glycosylation site occupancy analysis	$750
O-glycopeptide and O-glycosylation site occupancy analysis	Enquire
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

SERVICE	FEE1 A$
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
MASS PHOTOMETRY	
Reports in-solution masses of biomolecules and their complexes. *Mass measurements of biomolecules of interest (e.g. proteins, RNA and their complexes) are performed in-solution at nM concentrations. The technique can measure biomolecular mass, oligomeric state and sample heterogeneity, and is capable of characterising biomolecular interactions.*	
Mass photometry experiment	$150 per sample
BIOINFORMATICS	
Hourly Rate	$190
Quantitative proteomics and differential protein abundance statistical analysis for a single batch (e.g. TMT, DDA, SWATH and DIA)[2]	Incl. with MS project
Combining multiple quantitative proteomics batches analysed with the same MS technology using reference replicate samples [2]	Incl. with MS project
Protein functional enrichment analysis	Enquire
Phosphoproteomics and PTMs analysis (e.g. prediction of upstream kinases)	Enquire
Integrative multi-omics data analysis (e.g. mixOmics and MOFA2)	Enquire
Network visualization (e.g. StringDB and Cytoscape)	Enquire
Custom development of bespoke bioinformatics methods and workflow	Enquire
Machine learning-based discovery and benchmarking	Enquire
AMINO ACID ANALYSIS see here for details of assay	
Amino acid profile (food products - liquid hydrolysis) [3,4]	$185
Amino acid profile with Hydroxyproline & Taurine [3,4]	$200
Tryptophan determination (base hydrolysis) [3]	$215
Cysteine determination (performic acid oxidation) [3]	$215
High sensitivity AAA (purified protein – gas hydrolysis) [3,4]	$185
Free AAA (no hydrolysis, 20aa) [3]	$185
Free AAA (physiological fluids) and aminothiols [3]	Enquire

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LIQUID CHROMATOGRAPHY	
Reversed-phase (RP)-HPLC analysis	$185
A1/A2 beta casein in milk	$185
Lactoferrin analysis	$185
Size exclusion chromatography (SEC)	$135
Size exclusion chromatography (SEC) setup/stds	$185
Method development	Enquire
GEL ELECTROPHORESIS	
Gel Electrophoresis, sample preparation (include extraction, sample cleaning for 2-DE, quantitation)	$230 first sample $60 each additional
1-D gel (up to 18 lanes) stained with Coomassie	$320
MULTIPLEXED IMMUNO-ASSAY (MIA)[8]	
MIA, client performs assay at APAF [6]	$175 per hour
MIA, APAF staff performs assay [5,6]	$990 per plate
MIA, Sample spin filtration (per sample) [7]	$12
MIA, Other service: specify in service request	Enquire
ARRAY TECHNOLOGY	
ELISA [6]	$880/plate [9]
Kit purchase: specify kit in service request	Enquire
ADMINISTRATION	
Biosecurity (international samples) processing	$135
Report administration (chargeable for each additional report prepared)	$40
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. Using robotic platform for liquid delivery, where appropriate; client-supplied kits.
6. 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.
7. No charge where client supplies filtered samples to APAF.
8. Assays are conducted using the Andrew Alliance robotic platform/s for liquid delivery for precision and reproducibility.

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