APAF
australian proteome
analysis facility

MACQUARIE
University
SYDNEY·AUSTRALIA

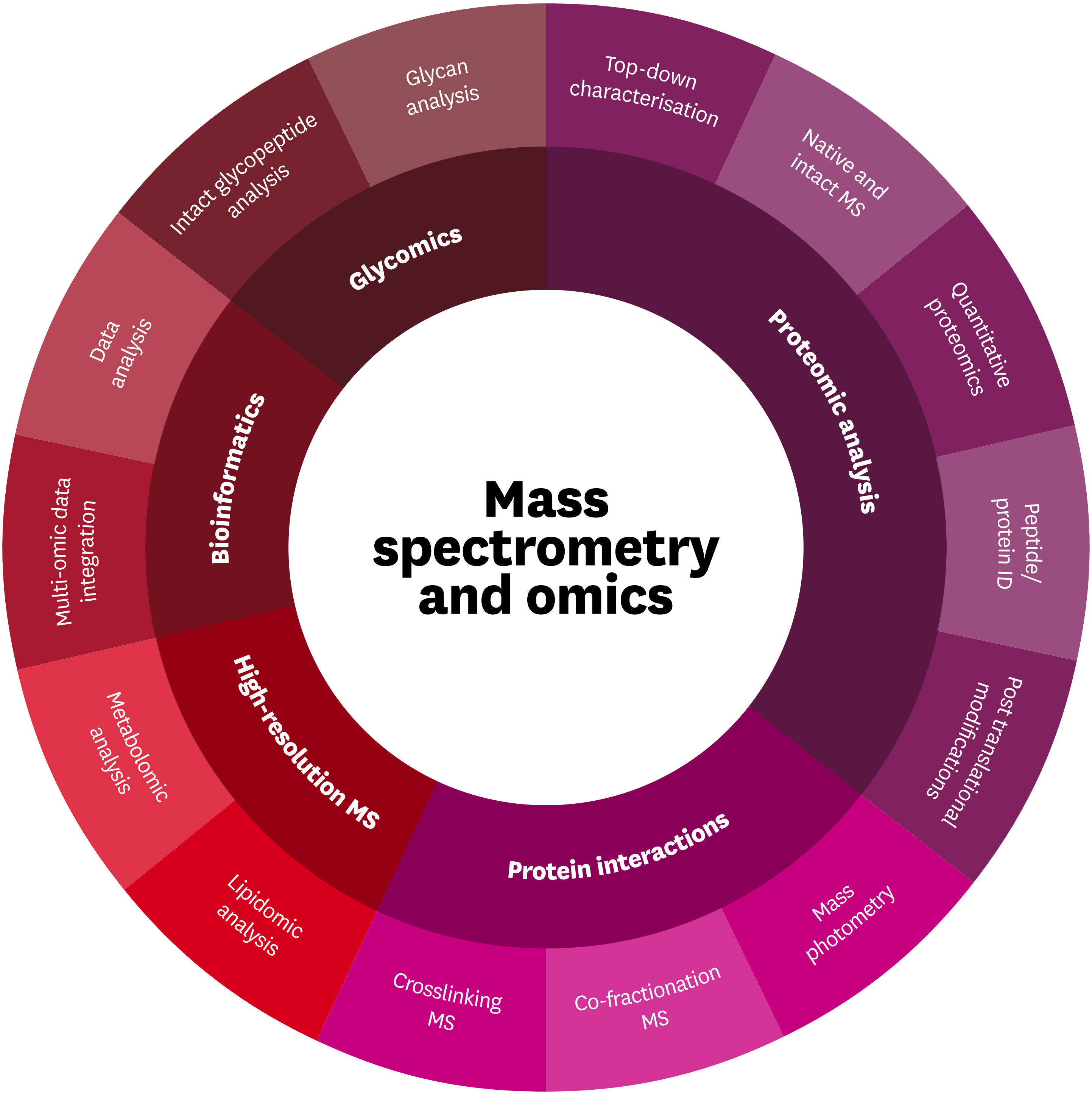
APAF service list

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.

Effective date: 1 January 2026

SERVICE REQUESTS
For service enquiries, email **info.apaf@mq.edu.au**
For service requests and sample submission, use the **APAF service request form**


Mass spectrometry and omics
Proteomic analysis
Top-down characterisation
Native and intact MS
Quantitative proteomics
Peptide/ protein ID
Post translational modifications
Protein interactions
Mass photometry
Co-fractionation MS
Crosslinking MS
High-resolution MS
Lipidomic analysis
Metabolomic analysis
Bioinformatics
Multi-omic data integration
Data analysis
Glycomics
Intact glycopeptide analysis
Glycan analysis

Service[*]	FEE[1] AUD
PROTEOMICS ANALYSIS	
Peptide/Protein identification: reports all detected peptides and proteins (and relative abundances if requested) 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.*	
Peptide/protein identification from one sample	\$320 per sample
Protein mapping – protein sample is digested with multiple enzymes to return comprehensive amino acid sequence information	\$850 per sample
Post translational modification analysis (PTMs)	Enquire
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 (eg quantitative and differential abundance analysis and reporting).* *Further sample preparation procedures may be required depending on sample type.*	
Peptide/protein identification and quantification for 6 samples (3 v 3 comparison)	\$2500 per n = 6 experiment \$360 per additional sample
Peptide/protein identification and quantification for large sample sets (20 samples or more, minimum 3 samples per group)	\$7800 per n > 20 experiment \$320 per additional sample
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	\$3500 per experiment
Labelled quantitative experiments: 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 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	\$8500 per experiment
Intact protein analysis: reports observed m/z and calculated actual masses of species observed in samples. For successful experiments, high purity samples are required. *Intact protein mass analysis and native protein analysis (performed in MS compatible physiological pH buffers; eg, 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 (eg, 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)	\$200 per experiment
Intact protein mass – LC/MS; up to 10 proteins per sample (deconvoluted mass only)	\$250 per sample
Top-down protein characterisation of an intact protein	\$2000 per sample

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[*] Additional administrative fees may apply – see end of Protein Analysis service list for details

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Service*	FEE[1] AUD
PROTEIN INTERACTION ANALYSIS	
Crosslinking mass spectrometry: reports crosslinked peptides from samples treated with a mass spectrometry-cleavable crosslinker *Samples to undergo crosslinking mass spectrometry that have been treated by client with a mass spectrometry-cleavable crosslinker (eg, 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	$300 per sample
Co-fractionation mass spectrometry: reports protein complexes on a whole proteome scale *Co-fractionation mass spectrometry (CF-MS) involves extensive fractionation of cellular lysates – and the protein complexes therein – using one or more non-denaturing separation techniques (eg size exclusion chromatography). The resulting fractionation profiles of individual protein complex subunits are measured using quantitative proteomics. As subunits of intact complexes will co-fractionate, protein complexes can then be predicted using bioinformatics techniques which make use of correlations between fractionation profiles.*	
Co-fractionation mass spectrometry experiment	$6000 per experiment
Mass photometry: Reports in-solution masses of biomolecules and their complexes. *Mass measurements of biomolecules of interest (eg 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
OTHER BIOMOLECULAR ANALYSIS	
High resolution mass spectrometry: reports observed m/z and calculated actual masses of species observed in samples. For successful 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.*	
High resolution mass spectrometry of small molecules	$175 per sample
Metabolomics analysis: reports all detected metabolites (and relative abundances if requested) in a sample based on a specified database. *Identification is performed by data-dependent MS methods and includes sample preparation, LC/MS data acquisition and database searching. Data should be collected in both positive and negative mode for comprehensive analysis. Further sample preparation procedures may be required depending on sample type.*	
Single polarity (positive mode or negative mode)	$220 per sample
Dual polarity (positive mode and negative mode)	$320 per sample
Metabolomics data analysis (Client-provided data)	Enquire
Lipidomics analysis: reports all detected metabolites (and relative abundances if requested) in a sample based on a specified database. *Identification is performed by data-dependent MS methods and includes sample preparation, LC/MS data acquisition and database searching. Data should be collected in both positive and negative mode for comprehensive analysis and a standard should be included in the analysis. Further sample preparation procedures may be required depending on sample type.*	
Single polarity (positive mode or negative mode)	$250 per sample
Dual polarity (positive mode and negative mode)	$350 per sample
Standard analysis	$50 per sample
Lipidomics data analysis (client-provided data)	Enquire
Multiomics packaging: reports all detected metabolites (and relative abundances if requested) in a sample based on a specified database. *Identification is performed by data-dependent MS methods and includes sample preparation, LC/MS data acquisition and database searching. Data should be collected in both positive and negative mode for comprehensive analysis and a standard should be included in the analysis. Further sample preparation procedures may be required depending on sample type.*	
Multiomics (includes proteomics, metabolomics, and lipidomics) analysis package; minimum 6 samples (3 v 3 comparison)	$6000 per experiment $600 per additional sample

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GLYCOMICS AND GLYCOPROTEOMICS	
Glycan analysis from purified proteins or complex mixture: *N- and/or O- linked glycans are released from purified glycoproteins or complex mixtures such as serum, plasma etc. Released glycans are analysed by LC/MS followed by manual data annotation. Report includes relative abundance of released N- or O-glycan, corresponding glycan-compositional and basic structural information.*	
N-linked (released) glycan analysis	$465 per sample
O-linked (released) glycan analysis	$415 per sample
N- and O- (released) glycan analysis	$775 per sample
N- and O- (released) glycan analysis with structural characterisation and glycan isomer information	Enquire
Intact N-linked glycopeptide analysis from purified protein samples: *Purified glycoprotein is digested using Trypsin or multiple enzymes for glycopeptide identification. Glycopeptides are enriched and analysed by Data Dependent Acquisition (DDA method) on LC/MS, searched against database to identify N-glycopeptides and corresponding glycan compositions. Label free quantitation reports relative abundance of glycan composition observed on each glycosylation site.*	
Qualitative N-glycopeptide identification and glycan composition	$635 per sample
Qualitative and label free relative abundance of N-glycopeptides (number of N-glycosylation sites ≤ 5)	$750 per sample
N-glycopeptide analysis for glycoproteins with more than 5 glycosylation sites	Enquire
Qualitative O-glycopeptide identification and glycan composition	Enquire
Qualitative and label free relative abundance of O-glycopeptides	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	$100 per sample
S-TRAP (or other device) assisted digestion (additional cost)	$100 per sample
Sample clean-up (eg, buffer exchange, detergent removal)	$100[†] per sample
Phosphopeptide enrichment (compatible with both LFQ and TMT quantitative experiments)	$100 per sample
Other PTM experiments	Enquire
Method development – including relative and absolute quantitation of peptides/protein in samples by ion/reaction monitoring experiments	Enquire
BIOINFORMATICS	
Bioinformatics services are designed to translate complex, high-dimensional data from mass spectrometry experiments into meaningful biological insights. We employ robust statistical methods and advanced computational tools to process, analyse, and visualise your proteomics, metabolomics, and lipidomics data and perform integrative multi-omics analyses.	
Model organism SWATH or TMT data analysis (stand-alone data project)	$585 per project
Non-model organism SWATH or TMT data analysis (stand-alone data project)	$1170 per project
Standalone proteomics functional enrichment analysis	$390 per project
Model organism TMT phosphoproteomics statistical analysis	$1755 per project
Multi-omics data integration (from three to five types of -omics)	$1270 per project
Weighted gene correlation network analysis (WGCNA)	Enquire
Customised bioinformatics methods and workflow development	Enquire

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† Pricing may vary depending upon required method

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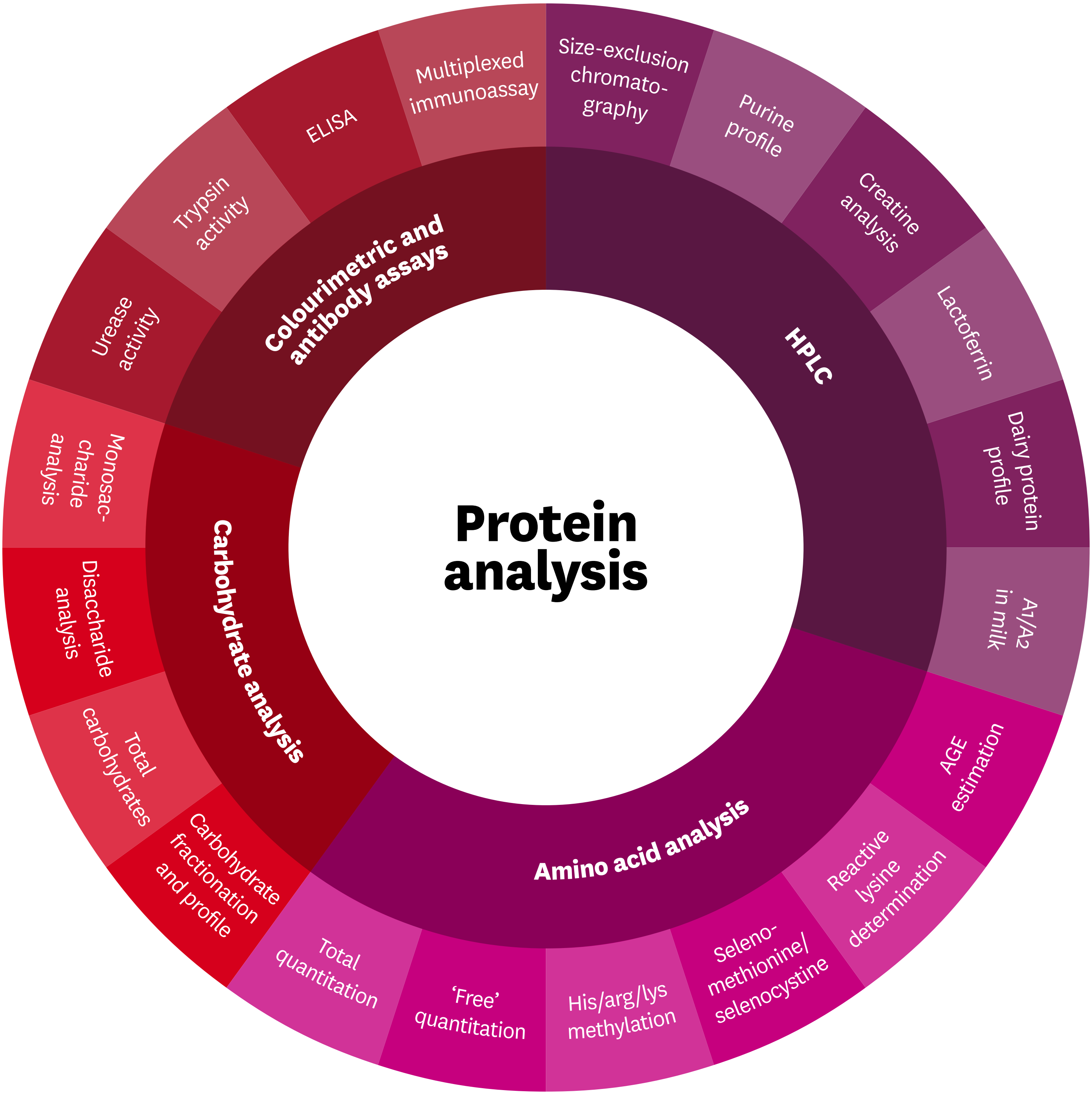
Protein analysis
HPLC
Size-exclusion chromato-graphy
Purine profile
Creatine analysis
Lactoferrin
Dairy protein profile
A1/A2 in milk
Amino acid analysis
AGE estimation
Reactive lysine determination
Seleno-methionine/ selenocystine
His/arg/lys methylation
'Free' quantitation
Total quantitation
Carbohydrate analysis
Carbohydrate fractionation and profile
Total carbohydrates
Disaccharide analysis
Monosac-charide analysis
Colourimetric and antibody assays
Urease activity
Trypsin activity
ELISA
Multiplexed immunoassay

Service*	FEE[1] AUD
AMINO ACID ANALYSIS (see **here** for details of assay)	
Amino acid profile (food products – liquid hydrolysis)[3,4]	$195 per sample
Amino acid profile with hydroxyproline & taurine[3,4]	$210 per sample
Amino acid profile with additional amino acids	Enquire
Tryptophan determination (base hydrolysis)[3]	$225 per sample
Cysteine determination (performic acid oxidation)[3]	$225 per sample
High sensitivity AAA (purified protein – gas hydrolysis)[3,4]	$195 per sample
Free AAA (no hydrolysis, 20aa)[3]	$195 per sample
Free AAA (physiological fluids) and aminothiols[3]	Enquire
Reactive (available) lysine determination	$440 per sample
MODIFIED AMINO ACID PROFILING	
Sample suitability trial (profile and concentration estimation)	$220 per sample
Selenomethionine determination	$380 per sample
Selenocysteine determination	Enquire
Selenomethionine and selenocysteine ratio (SeMet/total Met, and SeCys/total Cys)	Enquire
Histidine methylation profile (1-methyl/3-methyl/total His)	$380 per sample
Arginine methylation profile (Rme1/aRme2/sRme2/total Arg)	$420 per sample
Lysine methylation profile (Kme1/Kme2/Kme3/total Lys)	$420 per sample
Modified amino acid quantitation – method development[‡]	$195 per hour
Advanced glycation end-product estimation (carboxymethyl-lysine)	Enquire
LIQUID CHROMATOGRAPHY	
Reversed-phase (RP)-HPLC analysis	$195 per sample
Sample fractionation by RP-HPLC, collection of 4x injections, pooling of wells of interest, and vacuum centrifugation	$360 per sample
Custom (RP)-HPLC method for fractionation	Enquire
A1/A2 beta casein in milk	$195 per sample
Dairy protein profile (α-casein, β-casein, κ-casein, β-lactoglobulin and α-lactalbumin)	$220 per sample
Lactoferrin analysis	$195 per sample
Creatine analysis	$215 per sample
Purine profiling	$215 per sample
Size exclusion chromatography (SEC; see **here** for details of assay)	$145 per sample
Size exclusion chromatography (SEC) setup/stds	$185 per project
Method development	Enquire

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‡ Does not include procurement of specialist reagents.

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[3] Samples are analysed in duplicate. Contact us via e-mail for other Amino Acids (eg, ornithine, hydroxylysine, GABA) and singlicate/triplicate analysis.

[4] Cys and Trp not included.

Service*	FEE[1] AUD
CARBOHYDRATE ANALYSIS (see **here** for details of assay)	
Monosaccharide analysis – instrumental set-up and running of standards	$195 per method
Free monosaccharide analysis (no hydrolysis, triplicate analysis)	$270 per sample
Amino monosaccharide analysis (eg, glucosamine, galactosamine; triplicate analysis)	$270 per sample
Neutral monosaccharide analysis (eg, galactose, glucose, mannose, fucose, ribose, rhamnose, arabinose, xylose; triplicate analysis)	$270 per sample
Neutral disaccharide analysis (eg, fructose, maltose, lactose, sucrose; triplicate analysis)	$270 per sample
Acidic monosaccharide analysis (eg, galacturonic acid, glucuronic acid; triplicate analysis)	$270 per sample
Sialic monosaccharide analysis (eg, N-acetylneuraminic acid and N-glycolylneuraminic acid, 2-keto-3-deoxy-D-glycero-D-galacto-nononic acid (KDN); triplicate analysis)	$270 per sample
Custom monosaccharide profile (eg, trehalose, maltotriose)	Enquire
Total carbohydrates quantitation	$450 per 96-well plate
Carbohydrate fractionation and quantification (simple sugars, starch and structural carbohydrates)	$780 per 96-well plate
GEL ELECTROPHORESIS	
Gel electrophoresis, sample preparation (including extraction, sample clean up and in-gel digestion)	$230 first sample $60 per additional sample
1-D gel (up to 18 lanes) stained with Coomassie	$320 per 18-lane gel
MULTIPLEXED IMMUNO-ASSAY (MIA) [8]	
MIA, client performs assay at APAF[6]	$175 per hour
MIA, APAF staff performs assay[5 6]	$990 per 96-well plate
MIA, sample spin filtration (per sample)[7]	$12 per sample
MIA, other ancillary services	Enquire
ARRAY TECHNOLOGY	
ELISA[6]	$880 per 96-well plate
Kit purchase: specify kit in service request	Enquire
Trypsin activity assay	Enquire
Urease activity assay	Enquire
Colourimetric assay quantitation[9]	$540 per 96-well plate
Experimental design consultation and method development	$195 per hour
ADMINISTRATION	
Use of the AQIS biosecurity import (international samples)	$145 per use
Additional reporting charge	$45 per each additional report
Delivery fee	Enquire

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[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.

[9] Price does not include sourcing of the assay kit or specialised reagent/s.