

Quantitative Proteomics	
Service Title	iTRAQ based quantitative Proteomics coupled to mass spectrometry analysis. SILAC
Workflow Code	MASS_ITRAQ
Short Service Description	iTRAQ based quantitative analysis of differential expression of proteins
Base Price (Price per unit)	Price on enquiry
Turn Around Time	3 weeks
Detailed Description and background	
<p>The iTRAQ relative quantitation method relies on the tagging of peptides via an amine reactive group. The isobaric tag allows for the simultaneous fragmentation of all labelled peptide and the quantitation based on reporter ions observed in the daughter spectra. In planning and conducting experiments, the CPGR applies G(C)LP principles to ensure that analytical workflows are developed and validated to meet the requirements of type of tissue employed and biological question asked. Experiment design is supported by on-site bio-statistical and bioinformatic expertise to ensure a high level of integration of cross-disciplinary knowledge and dependable outcomes. Raw data generated can feed into further down-stream statistical and bioinformatic analysis, including pathway analysis, data visualisation, and biomarker discovery. Putative protein or peptide ID's can be utilised further to generate to develop assays for validation purposes using the CPGR's protein, peptide or antibody array workflows.</p>	
Service Details	
<p>Extracted protein samples are submitted for digestion and iTRAQ tagging. Alternatively, tissue samples may also be submitted for protein extraction and digestion. After digestion the peptides are separated using two dimensional liquid chromatography and spotted on a MALDI source plate. The data acquired from the MS/MS data acquisition are submitted for database interrogation using ProteinPilot software</p>	
Service Deliverable	
<p>Report includes database search results and relative protein quantitation. Meta-data from the experiments are also available</p>	
Sample/Info Submission Info	
<p>Extracted and pooled samples can be submitted for digest and labelling in either 4-plex or 8-plex format. Alternatively tissue samples may also be submitted for extraction.</p>	
Pricing Details	Price on request
Key Words	Proteomics, Quantitative Proteomics, iTRAQ, MALDI
Sample Shipping Address	Institute of Infectious Disease and Molecular Medicine, UCT, Faculty of Health Sciences, Wernher and Beit Building, Level 2, Lab S2.09, Anzio Road, Observatory, Cape Town 7925, South Africa
Related services	Bioinformatics, protein arrays, protein expression, Luminex

