



**CPGR**

CENTRE FOR PROTEOMIC  
& GENOMIC RESEARCH



## **Services 2016**

**Your gateway to Complete Genomics & Proteomics on the African continent!**





CPGR

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The CPGR is a specialist not-for-profit contract research organization established in South Africa through funding by the Technology Innovation Agency (TIA) to provide support and services to the life science and biotech community. It is based on an initiative by the Department of Science and Technology (DST) to boost the development of a bio-economy in South Africa.

The CPGR combines state-of-the-art information rich genomic and proteomic ('omics') technologies with bio-computational pipelines, and biological models, to create unique solutions in the human health and the agri-biotech sectors.

### Value proposition

To use our expertise in high-quality genomic and proteomic data generation, analysis and interpretation to deliver outstanding value to customers and partners in Medicine and Health, on the African continent. To stimulate, support and drive innovation in Precision Medicine, biomarker and drug development.

### Background

- ⊕ Situated in **Cape Town** and built with a vision to contribute towards growing the **South African bio-economy**
- ⊕ **Affymetrix GS 3000** and **Affymetrix GeneTitan** for genotyping and gene-expression analysis; **Tecan LS** and **Tecan hyb station** for protein array analysis, **Genetix Qarray 2** for protein array printing; **ABI 4800 MALDI-ToF/ToF** and **Thermo Q Exactive** for MS-Proteomics; **ABI 7900** and **Roche LC 480** for qRT-PCR applications; **Bioplex** system for multiplex immunoassays; **liquid handling**, extraction, **DNA/RNA QC**, library handling and other ancillary support systems; dedicated **IT infrastructure** and **bioinformatic applications** for data analysis and interpretation
- ⊕ Track record of **over 800 projects since 2007**
- ⊕ Active across the **African continent** (for example, Tunisia, Nigeria, Zimbabwe) and with clients/collaborators all over the **globe**
- ⊕ Strongly **networked** with stakeholders across the **life science innovation chain**, including academic researchers, clinical scientists, state funders, technology providers, private investors and life science industry
- ⊕ Legally setup as a **non-profit** with **strong corporate governance** systems and record and **hybrid social enterprise model** (mixing a strong public benefit mandate and commercial activities)
- ⊕ State of the art **quality management** (ISO 9001:2008 certification; GLP principles adhered to in study design)
- ⊕ Strong focus on **regional capacity** building through training, clustering and networking

## GENOMICS

### Affymetrix cartridge arrays

| Assay   | Lab workflow  | Data Analysis   | Output  |
|---|---|---|---|
| <b>CHIP-on-Chip</b>                                     | Large-scale (to genome-wide) profiling of DNA (e.g. promoter) binding proteins  | None  | <ul style="list-style-type: none"> <li>Analytical data QC Report</li> </ul>   |
| <b>DNA methylation</b>                                  | Genome-wide detection of methylation patterns in the plant and animal kingdom   | None  | <ul style="list-style-type: none"> <li>Analytical data QC report</li> </ul>   |
| <b>Genotyping</b>                                       | Genotyping / genome-wide association studies on SNP 6.0 arrays or Axiome (Gene Titan high throughput) arrays. High throughput custom arrays | <ul style="list-style-type: none"> <li>Genotype calls</li> <li>Copy number/LOH</li> <li>Copy Number Segments Data (SNP6)</li> <li>Copy Number Variation Analysis</li> </ul>   | <ul style="list-style-type: none"> <li>Analytical Data QC Report</li> <li>Genotyping calls</li> <li>Annotated gains and losses</li> <li>Copy number</li> </ul>                  |
| <b>Exon expression</b>                                  | Exon-specific RNA profiling for human, mouse and rat on high-density GeneChip arrays  | <ul style="list-style-type: none"> <li>Gene level and alternative splicing analysis</li> </ul>  | <ul style="list-style-type: none"> <li>Analytical Data QC Report</li> <li>Annotated gene lists for differentially expressed and alternatively spliced genes</li> </ul>          |
| <b>Gene expression</b>                                  | Largest variety of eukaryotic and prokaryotic arrays  | <ul style="list-style-type: none"> <li>Data Quality assessment, normalization, data filtering, outlier identification.</li> <li>Differentially expressed annotated genes, clustering, gene set enrichment (GSE) analysis, classification</li> </ul> | <ul style="list-style-type: none"> <li>Analytical Data QC Report</li> <li>List of differentially expressed genes</li> </ul>   |
| <b>miRNA expression</b>                                 | miRNA expression analysis on high-density arrays  | <ul style="list-style-type: none"> <li>Extract expressed miRNA values</li> <li>Extract relevant species data</li> </ul>   | <ul style="list-style-type: none"> <li>Analytical Data QC Report</li> <li>List of differentially expressed miRNAs</li> <li>MicroRNA integration with gene expression</li> </ul> |
| <b>DMET Plus</b>  | Query 1,936 known ADME markers in a single GeneChip™ assay  | <ul style="list-style-type: none"> <li>Genotyping Call and copy number</li> <li>Generation of marker lists or pathways</li> </ul>   | <ul style="list-style-type: none"> <li>Analytical data QC Report</li> <li>Phenotype Report</li> <li>Star Allele Translation</li> </ul>  |
| <b>CytoScan HD/750K<br/>CytoScan Optima (pre-natal)</b> | Ultra-high density analysis of chromosomal aberrations, CNV and LOH   | <ul style="list-style-type: none"> <li>Genotyping, LOH, Copy number,</li> <li>Uniparental Disomies (UPDs)</li> </ul>  | <ul style="list-style-type: none"> <li>Analytical Data QC Report</li> <li>Segment Report</li> </ul>   |

## Affymetrix GeneTitan arrays

| Assay   | Lab workflow   | Data Analysis  | Output  |
|---|--|--|---|
| <b>Gene expression profiling</b>                        | <ul style="list-style-type: none"> <li>• Exploration of gene expression profiles relating to important biological phenotypes such as disease or drug response in 16-, 24- and 96-well array formats</li> <li>• Available for human, model and applied research organisms</li> </ul>              | <ul style="list-style-type: none"> <li>• Data Quality assessment, normalization, data filtering, outlier identification</li> <li>• Differentially expressed annotated genes, clustering, gene set enrichment (GSE) analysis, classification</li> </ul> | <ul style="list-style-type: none"> <li>• Analytical Data QC Report</li> <li>• Annotated Gene lists</li> </ul>     |
| <b>Genome-wide analysis and genotyping applications</b> | <ul style="list-style-type: none"> <li>• Population genetics, targeted genotyping (human) and marker-assisted breeding (model and applied organisms)</li> </ul>  | <ul style="list-style-type: none"> <li>• SNP calls, single/multiple SNP association tests performed on allele, genotype, and dominant/recessive models</li> </ul>  | <ul style="list-style-type: none"> <li>• Analytical Data QC Report</li> </ul>                                     |
| <b>Custom arrays</b>                                    | <ul style="list-style-type: none"> <li>• MyGeneChip Expression array plates for human and model and applied research organisms.</li> <li>• Axiom® myDesign™ Genotyping array plates – genomic coverage tailored for human and agricultural populations, focussing on SNPs of interest</li> </ul> | <ul style="list-style-type: none"> <li>• To be discussed with bioinformaticist</li> </ul>  | <ul style="list-style-type: none"> <li>• Depending on application</li> <li>• Analytical data QC report</li> </ul> |

## qRT-PCR

| Assay                | Lab workflow   | Bioinformatics         | Output   |
|----------------------|--|------------------------|--|
| <b>Genotyping</b>    | High-throughput (large sample over low gene number) TaqMan- based genotyping assays in 384 MTPs                    | None                   | Genotype clustering graphs to determine allelic discrimination |
| <b>qRT-PCR</b>       | High-throughput quantitative gene-expression profiling   | qBasePlus (BioGazelle) | Relative gene expression                                       |
| <b>TLDA</b>          | Pre-designed and custom TaqMan Low-Density Arrays (TLDA) for quantitative RNA profiling (e.g. cytokine expression) | qBasePlus (BioGazelle) | Relative gene expression                                       |
| <b>Compatibility</b> | ABI, Superarray, Sybr Green, Roche   |                        |  |
| <b>Viral titres</b>  | Determine titres of baculovirus stocks through Sybr Green assay  | None                   | Relative abundance   |

## Next Generation Sequencing

| Assay   | Lab workflow  | Data Analysis   | Output   |
|---|---|---|--|
| <b>Microbial Genome Sequencing</b><br><br><b>16S Metagenomics</b> | <ul style="list-style-type: none"> <li>Sample QC &amp; Library Preparation</li> <li><b>Ion PGM</b> <ul style="list-style-type: none"> <li>-Viral &amp; Bacterial</li> <li>- 30 samples for 16S metagenomics on an Ion chip 318v2 @ 183k reads/sample</li> </ul> </li> <li>Illumina MiSeq                             <ul style="list-style-type: none"> <li>-Viral, bacterial &amp; Fungal</li> <li>- 200 samples for 16S metagenomics on V3 (600 cycle kit) @ 125k reads per sample</li> </ul> </li> </ul> | <ul style="list-style-type: none"> <li>Experimental design support</li> <li>Read QC and data filtering</li> </ul> | <ul style="list-style-type: none"> <li>Raw sequence reads</li> <li>Detailed analysis report</li> </ul> |
| <b>Exome sequencing</b>   | <ul style="list-style-type: none"> <li>Sample QC</li> <li>Library preparation</li> <li><b>Platforms</b> <ul style="list-style-type: none"> <li>-Ion Proton, 2exomes per run with 92% covered @20x</li> </ul> </li> </ul>  | <ul style="list-style-type: none"> <li>Experimental design support</li> <li>Read QC and data filtering</li> </ul> | <ul style="list-style-type: none"> <li>Raw sequence Reads</li> <li>Detailed Analysis Report</li> </ul> |
| <b>Targeted Panels</b>  |   |   |  |
| <b>Human Genome Sequencing</b>                                    | Collaboration with NYGC   |   |  |



# PROTEOMICS

## Mass spectrometry

### Instrumentation – Q Exactive Orbitrap Thermo Fisher

| Assay  | Lab workflow   | Bioinformatics   | Output  |
|--|--|--|---|
| <b>Sample Fractionation</b>                              | <ul style="list-style-type: none"> <li>Upstream fractionation of complex protein/peptide samples</li> <li>Samples fractionated by variety of methods including strong cation exchange chromatography, high pH reverse phase chromatography and 1 D SDS page</li> </ul>   | <ul style="list-style-type: none"> <li>None</li> </ul>   | <ul style="list-style-type: none"> <li>Simplified fractions for MS analysis</li> </ul>                                      |
| <b>Simple and complex mixture protein identification</b> | <ul style="list-style-type: none"> <li>Purified protein identification and identification of 100s to 1000s of proteins in complex whole tissue extractions</li> </ul>  | <ul style="list-style-type: none"> <li>Mascot, Byonic and Scaffold</li> </ul>  | <ul style="list-style-type: none"> <li>Lists of identified proteins with confidence levels</li> </ul>                       |
| <b>Label based relative quantification</b>               | <ul style="list-style-type: none"> <li>Isobaric isotope labels that can be attached to peptides prior to LC-MS allowing relative (or absolute if an internal standard is available) quantitation of up to 8 protein samples</li> <li>Ideally suited for protein biomarker discovery with small sample sizes</li> </ul> | <ul style="list-style-type: none"> <li>Mascot and Scaffold</li> </ul>  | <ul style="list-style-type: none"> <li>Relative abundance of proteins present in the sample</li> </ul>                      |
| <b>Label free relative quantification</b>                | <ul style="list-style-type: none"> <li>MS1 signal intensity used to quantify peptides/proteins</li> <li>Suited to biomarker discovery with large sample size (&gt;8)</li> </ul>  | <ul style="list-style-type: none"> <li>Power analysis to determine significant fold change threshold<br/>Mascot, Sieve and Progenesis</li> </ul> | <ul style="list-style-type: none"> <li>Relative abundance of proteins present in the sample</li> </ul>                      |
| <b>Phospho-proteome analysis</b>                         | <ul style="list-style-type: none"> <li>Specific enrichment for phosphopeptides prior to LCMS</li> <li>Can be applied to both qualitative and quantitative analyses</li> </ul>  | <ul style="list-style-type: none"> <li>Mascot and Byonic open source workflows</li> </ul>  | <ul style="list-style-type: none"> <li>Identity of phosphorylated proteins</li> </ul>                                       |
| <b>Data analysis</b>                                     | <ul style="list-style-type: none"> <li>Assessment of quality of identification.</li> <li>Processing of data to reveal regulated proteins</li> <li>Statistical testing</li> <li><b>Pathway analysis using IPA</b></li> </ul>  | <ul style="list-style-type: none"> <li>Mascot, ProgenesisQI, Byonic &amp; Scaffold</li> </ul>  | <ul style="list-style-type: none"> <li>Identity of proteins and for quantitative studies also relative abundance</li> </ul> |
| <b>Protein QC/QA</b>                                     | <ul style="list-style-type: none"> <li>Quality control analysis for protein and peptide products can be developed to customers specifications.</li> </ul>  | <ul style="list-style-type: none"> <li>None</li> </ul>   | <ul style="list-style-type: none"> <li>Confirmation of sample integrity</li> </ul>  |
| <b>Protein purification</b>                              | <ul style="list-style-type: none"> <li>Tailor made separation solutions can be developed</li> </ul>  | <ul style="list-style-type: none"> <li>None</li> </ul>   | <ul style="list-style-type: none"> <li>Purified protein</li> </ul>  |

|                           |   |  |   |
|---------------------------|---|--|---|
|                           | according to customer needs.  |  |   |
| <b>Protein extraction</b> | <ul style="list-style-type: none"> <li>A variety of validated extraction protocols exists at the CPGR and new methods can be developed according to the customer's needs</li> </ul> | <ul style="list-style-type: none"> <li>None</li> </ul> | <ul style="list-style-type: none"> <li>Protein extracts suitable for MS analysis</li> </ul> |

## Metabolomics

LCMS/MS based targeted metabolite quantification in serum/plasma using Biocrates kits.

| Assay                      | Lab workflow   |
|----------------------------|--|
| <b>Absolute IDQ p150</b>   | <ul style="list-style-type: none"> <li>The kit measures up to 163 analytes from four substance classes (i.e. acylcarnitines, amino acids, hexoses, phospho- and sphingolipids).</li> </ul>                                 |
| <b>AbsoluteIDQ Stero17</b> | <ul style="list-style-type: none"> <li>Simultaneous identification and quantification of 17 steroid hormones from 3 classes: (sex steroids, mineralocorticoids, glucocorticoids).</li> </ul>                               |
| <b>Absolute IDQ p180</b>   | <ul style="list-style-type: none"> <li>Quantify up to 188 endogenous metabolites from 5 different compound classes (i.e. acylcarnitines, amino acids, hexoses, phospho- and sphingolipids and biogenic amines).</li> </ul> |
| <b>Vitamin D</b>           | <ul style="list-style-type: none"> <li>Quantitative measurement of 25-hydroxyvitamin D2 and 25-hydroxyvitamin D3.</li> </ul>   |





## HUMAN CAPITAL DEVELOPMENT

### Internships

| Course/training type                                 | Description  | Outcome   |
|--|--|---|
| <b>Technology Innovation Agency (TIA) Internship</b> | <ul style="list-style-type: none"> <li>The TIA internship programme is aimed at postgraduate MSc students training in bioinformatics, statistics, mathematics, biology or any relevant field</li> <li>The programme is eligible to South African citizens</li> </ul> | <ul style="list-style-type: none"> <li>In addition to the skills and knowledge acquired, at the end of the program interns are required to produce a technical report, poster and a presentation</li> </ul> |
| <b>National Research Foundation (NRF) Internship</b> | <ul style="list-style-type: none"> <li>The National Research Foundation (NRF) internship programme targets undergraduate students' specifically South African citizens</li> </ul>  | <ul style="list-style-type: none"> <li>Interns are required to produce a technical report, poster and a presentation</li> </ul>   |

### Programmes

| Course/training type                      | Description  | Outcome  |
|---|--|--|
| <b>Foundation in Genomics</b>             | <ul style="list-style-type: none"> <li>Project Design and Ethics considerations</li> <li>Effective sample preparation &amp; troubleshooting (Including practical lab workshop)</li> <li>The importance of quality management to generate reliable "omics" results</li> <li>An introduction* to:               <ol style="list-style-type: none"> <li>1) Real time PCR (including practical lab workshop)</li> <li>2) Array Technologies – theory and applications</li> <li>3) Next Generation Sequencing</li> </ol> </li> <li>Bioinformatics - an introduction to data analysis</li> </ul> | <ul style="list-style-type: none"> <li>From standard molecular technology to 'omics' application in 3 days</li> </ul>                                      |
| <b>Knowledge Transfer Programme (KTP)</b> | <ul style="list-style-type: none"> <li>The Knowledge Transfer Programme (KTP) is an initiative to bring together experts and associates facilitated by a host institution to pursue specific projects with the aim of transferring knowledge in a natural and cost effective way. It targets postgraduates, post-doctoral and researchers</li> </ul>   | <ul style="list-style-type: none"> <li>The programme produces either a publication, patent or intellectual properties depending on the project.</li> </ul> |

## Other training

| Course/training type         | Description   | Outcome   |
|------------------------------|---|---|
| <b>Specialised Workshops</b> | <ul style="list-style-type: none"> <li>Workshops in bioinformatics led by international experts and targeted at life scientists, biologists, bioinformaticians, biostatisticians, physicists and computer scientists in academia and industry</li> <li>A typical workshop stretches over five consecutive days.</li> </ul>                | <ul style="list-style-type: none"> <li>Training in cutting-edge omics technologies, tools/software/pipelines, methodologies, data analysis and advanced bioinformatics applications</li> <li>Theoretical knowledge and practical skills</li> <li>Certification awarded</li> </ul> |
| <b>Online Training</b>       | <ul style="list-style-type: none"> <li>Free online training offered in Ingenuity Pathway Programme (IPA), available at <a href="http://www.cpgr.org.za/bixhcd.html">http://www.cpgr.org.za/bixhcd.html</a></li> <li>System requirements: Internet connection, web browser, IPA registration</li> <li>Runs several times a year</li> </ul> | <ul style="list-style-type: none"> <li>A variety of core and custom modules</li> <li>Live or pre-recorded</li> <li>Internationally recognized IPA certification awarded</li> <li>Software Licenses offered to scientists in South Africa</li> </ul>                               |



# Foundations In 'omics' Education







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