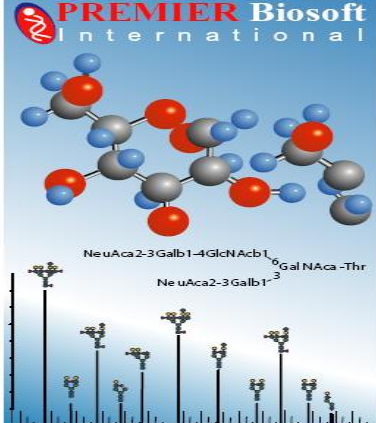


# Software List

## 1. Proteomics




	<p><b>Progenesis SameSpots V.4 (included Progenesis Discovery, PG240)</b>            Progenesis SameSpots is the 2D image analysis product of choice if you use proteomics as a focus of your discovery research. Its unique analysis approach and simplified workflow deliver significant improvements in speed, objectivity and statistics. Progenesis SameSpots is also the only software proven to enable cross lab reproducibility.</p> <p><b>Speed</b> - Typical analysis times of 5 minutes per image with a fast, streamlined workflow. The time you save compared to traditional analysis approaches allows you to focus on further research or run more gels for more reliable conclusions.</p> <p><b>Objectivity</b> - Easy-to-use and highly reproducible results with no post-analysis editing required on the majority of experiments.</p> <p><b>Statistical Power</b> - Increased statistical power for your experiments with 100% matching and no missing values so you can apply multivariate statistics for reliable, unbiased 2D image analysis.</p>
	<p><b>Progenesis SameSpots V.3 (included Progenesis Discovery, PG240)</b>            Progenesis SameSpots is the 2D image analysis product of choice if you use proteomics as a focus of your discovery research. Its unique analysis approach and simplified workflow deliver significant improvements in speed, objectivity and statistics. Progenesis SameSpots is also the only software proven to enable cross lab reproducibility.</p>
	<p><b>Progenesis MALDI</b>            Progenesis MALDI is a simple to use application that gives you high quality proteomics data for biomarker discovery using MALDI-TOF or SELDI analysis. It uses the unique Progenesis workflow and technology to provide:</p> <p><b>Speed</b> - Simple, rapid analysis of large data sets makes it easy for you to run enough replicates in order to minimise false discovery rates</p> <p><b>Objectivity</b> - Guided workflow that helps you apply an objective, statistical-based analysis and run reproducible experiments</p> <p><b>Statistics</b> - Unique spectra alignment process delivers a complete data set for multivariate statistical analysis</p>



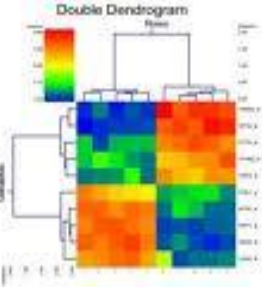
	<p><b>Progenesis PG240</b> The Progenesis range contains advanced analysis solutions for the scientist who requires an in-depth view of their proteomics experiments to drive their research.</p>
	<p><b>DeCyder 2-D Differential Analysis Software v7.0</b> Fully optimized and integrated to the 2-D DIGE platform. Automated analysis, significantly reducing hands-on time. Internal standard approach, increasing accuracy and simplifying gel-to-gel matching. No spot matching within gels, eliminating matching errors. Automatic Oracle client and server installation, offering easy project handling and data security. DeCyder Extended Data Analysis (EDA), a multivariate statistics module for easier and faster biomarker discovery, included as standard.</p>
	<p><b>PDQuest</b> PDQuest offers best-in-class performance for analysis and databasing of 2-D gels. PDQuest software offers powerful comparative analysis and is specifically designed for laboratories that analyze many gels at once.</p>
	<p><b>Melanie v.7</b> ImageMaster™ 2D Platinum v7.0 offers a flexible interface for the comprehensive visualization, exploration, and analysis of 2-D gel data from both 2-D DIGE (2-D Fluorescence Difference Gel Electrophoresis) and non-DIGE technologies.</p>
	<p><b>ImageMaster 2D Platinum v.6</b> ImageMaster™ 2D Platinum offers a flexible interface for the comprehensive visualization, exploration, and analysis of 2-D gel data from both 2-D DIGE (2-D Fluorescence Difference Gel Electrophoresis) and non-DIGE technologies.</p>
	<p><b>CLC Protein Workbench</b> CLC Protein Workbench creates a software environment enabling users to make a large number of advanced protein sequence analyses, combined with smooth data management, and excellent graphical viewing and output options.</p>

	<p><b>SimGlycan</b> SimGlycan™ is an innovative MS/MS data analysis tool. SimGlycan™ predicts the glycan structure, scores it and generates a list of probable glycans that closely match the given MS profile. Both glycopeptide and released glycan profiles are supported.</p>
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## 2. Genomics


### a) Micro array data analysis

	<p><b>Partek Genomics Suite</b> Easily Analyze and Compare a Variety of Genomic Data Using One Complete Package. Partek Genomics Suite can analyze gene expression, exon expression, chromosomal copy number, promoter tiling, and high density SNP data in one application, allowing for analysis of multiple applications in one complete solution. See how Partek GS can work for your data.</p> <ul style="list-style-type: none"> <li>• Gene Expression</li> <li>• Alternative Splicing</li> <li>• Copy Number</li> <li>• Regulation</li> <li>• SNP Association</li> <li>• Next Generation Sequencing</li> </ul>
	<p><b>GeneSpring GX 11</b> Gold standard software for: Micro Array data analysis, Detect alternative splicing events, Identify microRNAs, Analyze real-time PCR data, and Build relevant biological interaction networks &amp; pathway analysis</p>
	<p><b>Agilent Genomic Workbench</b> Three different parts of software: <b>Oligo aCGH Array Solution:</b> Agilent's microarray-based</p>

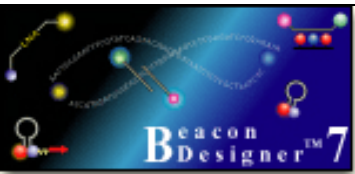
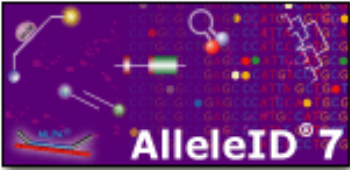
	<p>comparative genomic hybridization (aCGH) technology is a powerful solution to your research in cancer and developmental disorders. Agilent's CGH end-to-end solution consists of flexible microarray formats, optimized and easy-to-use protocol, high resolution microarray scanning, and powerful analytics software to give you the best quality results.</p> <p><b>ChIP-on-chip Solution:</b> The ChIP-on-chip DNA microarrays allow the monitoring of binding events of DNA-binding proteins to areas around the human and mouse promoters, yeast genome and defined regions such as the Human ENCODE region. In addition, custom ChIP-on-chip arrays can be constructed from almost any organism including Zebrafish, Drosophila, Arabidopsis, and more.</p> <p><b>DNA Methylation Solution:</b> The DNA methylation microarrays allow the monitoring of methylation events in CpG Islands, areas around the human and mouse promoters, and defined regions such as those found in Human ENCODE. In addition, custom tiling arrays can be constructed from almost any organism including Zebrafish, Drosophila, Arabidopsis, and more.</p>
	<p><b>Array Designer</b> A microarray software for fast, efficient design of specific oligos for making whole genome arrays, tiling arrays and resequencing arrays.</p>
	<p><b>TMA Foresight</b> TMA Foresight is a statistical tool for tissue microarray data analysis designed to explore the relatedness of prognostic marker expression and clinico-pathological variates with the outcome.</p>
	<p><b>GESS &amp; NCSS Package</b> <b>GESS:</b> Microarray Data Analysis software Following is a comprehensive list of all microarray data analysis procedures that are available in the latest release of GESS. If you would like to see full details on a procedure, we suggest that you download the trial version and look at the Help file. <b>NCSS:</b> Comprehensive and easy to use statistical analysis software. NCSS has specialized in providing statistical analysis software to researchers, businesses, and academic institutions. Our current release, is comprehensive and easy to use. NCSS includes over 230 statistical procedures and plots. NCSS imports and exports all major spreadsheet, database, and statistical file formats. NCSS easily produces sharp, flexible graphics. NCSS output is easily transferred to popular word processors and presentation software such as PowerPoint.</p>

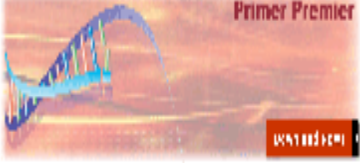


## b) 1D gel analysis & quantification

	<p><b>Phoretix 1D Pro - (replacing TotalLab TL120DM)</b> Phoretix 1D Pro allows you to perform large dataset investigations in a fast and easy to use interface. It includes <b>Phoretix 1D</b> and <b>Phoretix Quant</b> analysis software together with a robust database to create a powerful analysis platform. <i>Phoretix 1D is the premium 1D Gel analysis product on the market.</i> As well as all of the automated features available in the 1D Gel analysis module of TotalLab Quant it can also perform complex band pattern matching across a gel essential in sample strain analysis, such as cultivar experiments, evolutionary biology and population genetics.</p>
	<p><b>Phoretix 1D - (replacing TotalLab TL120)</b> Phoretix 1D is the premium 1D Gel analysis product on the market. As well as all of the automated features available in the 1D Gel analysis module of TotalLab Quant it can also perform complex band pattern matching across a gel essential in sample strain analysis, such as cultivar experiments, evolutionary biology and population genetics.</p>
	<p><b>Phoretix Quant - (replacing TotalLab TL100)</b> TotalLab Quant contains modules for:</p> <ul style="list-style-type: none"> <li>• 1D electrophoresis gel and Western blot analysis</li> <li>• Array / dot blot / slot blot analysis</li> <li>• Colony counting &amp; basic 2D spot measurement</li> <li>• General feature-based image analysis</li> </ul>
	<p><b>Bio Rad Quantity One</b> Quantity One is a powerful, flexible software package for imaging and analyzing 1-D electrophoresis gels, dot blots and other arrays, and colonies.</p>




	<p><b>GeneTools</b></p> <p>It is an advanced 1D gel and 2D spot blot analysis software for use with any gel documentation system. This highly automated software can rapidly analyze a gel from loading an image to output of results in a matter of seconds. With an extensive and flexible array of options you can handle a range of media including gels, plates, films and blots, making GeneTools one of the most versatile packages of its type. For speed, accuracy and ease of use GeneTools is a must for any gel documentation system GeneTools functions:</p> <ul style="list-style-type: none"> <li>• 1D analysis</li> <li>• Molecular weight</li> <li>• Quantity analysis</li> <li>• Spot blot</li> <li>• Colony counting</li> <li>• Gel scoring</li> <li>• Band matching</li> <li>• Manual band quantification</li> </ul>
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## c) Primer & Probe design and analysis





	<p><b>Beacon Designer</b></p> <p>Design successful SYBR Green, TaqMan, MethyLight TaqMan, LNA™ spiked TaqMan, molecular beacons for both standard and NASBA assays, Scorpions and FRET assays by automatically interpreting BLAST results and avoiding template structures.</p>
	<p><b>AlleleID</b></p> <p>AlleleID is a comprehensive desktop tool designed to address the challenges of bacterial identification, pathogen detection or species identification. With ClustalW multiple sequence alignment at its core, AlleleID can be used to design species identification/cross species probes for microarrays or real time PCR including SYBR Green, TaqMan MGB, TaqMan probes, Molecular Beacons and real time PCR primers. AlleleID also offers support for designing microarray experiments for detecting alternative splicing events.</p>

	<p><b>Primer Premier</b> A Comprehensive PCR Primer Design Software Primer Premier's search algorithm finds optimal PCR, multiplex and SNP genotyping primers with the most accurate melting temperature using the nearest neighbor algorithm. Primers are screened for secondary structures, dimers, hairpins, homologies and physical properties before reporting the best ones for your sequence, in a ranked order. Load the gene of interest from NCBI, select a search range, sit back and let Primer Premier pick the best possible primers for you.</p>
	<p><b>Primer Express Software</b> Primer Express software is a primer and probe design tool. Primer Express software lets you independently design oligonucleotides (oligos) for PCR applications using a customized application specific document for each of the following assay types:</p> <ul style="list-style-type: none"> <li>• Absolute/Relative Quantification</li> <li>• Allelic Discrimination</li> </ul>
	<p><b>OLIGO Primer Design</b> OLIGO performs a range of functions for researchers in PCR and related technologies; consensus, multiplex and degenerate primers, oligonucleotide database, secondary structure, LCR and more.</p>



## d) Sequence analysis




	<p><b>CLC Genomics Workbench</b> (Including CLC <b>Main</b>, <b>DNA</b>, <b>RNA</b> and <b>Protein</b> workbench software) CLC Genomics Workbench, for analyzing and visualizing Next Generation Sequencing data, incorporates cutting-edge technology and algorithms, while also supporting and integrating with the rest of your typical NGS workflow. Some of the key works are: Reference assembly / mapping De novo assembly Support for analysis of hybrid data SNP detection Identifying genomic rearrangements Digital Gene Expression Discovery of novel transcript variants Expression profiling by tags EST library construction Epigenomics analyses Classical Sequence Analysis and database Integration</p>
	<p><b>CLC Main Workbench</b> (CLC Main Workbench includes all features and functions of CLC DNA Workbench, CLC RNA Workbench, and CLC Protein Workbench.) CLC Main Workbench creates a software environment enabling users to make a large number of advanced DNA, RNA, and protein sequence analyses, combined with gene expression analysis, smooth data management, and excellent graphical viewing and output options.</p>
	<p><b>Lasergene DNASTAR v. 8.1</b> Comprehensive Software for DNA &amp; Protein Sequence Analysis, Contig Assembly and Sequence Project Management DNASTAR Lasergene software consists of an integrated suite of <b>seven</b> modules that can be purchased in any combination. The modules of Lasergene are: <b>SeqBuilder</b> - Sequence editing, mapping, annotation, and automated virtual cloning <b>SeqMan Pro</b> - Sequencing Manager, Sequence Assembly, Contig Management, and SNP Discovery <b>MegAlign</b> - Multiple and Pairwise Sequence Alignment <b>PrimerSelect</b> - Oligonucleotide Primer and Probe Design and Analysis <b>Protean</b> - Protein Structure Analysis, Prediction and Annotation <b>GeneQuest</b> - Gene Discovery and Sequence Annotation <b>EditSeq</b> - Utility for Editing and Importing Unusual File Type</p>

	<p><b>DNASIS MAX v.3</b> Bioinformatics software for DNA/RNA/Amino Acid sequence analysis. DNASIS MAX bioinformatics software helps life scientists edit, annotate and analyze DNA, RNA and amino acid sequences. It includes a comprehensive set of analytical tools and can be expanded with optional homology search, multiple alignment and base calling and sequence assembly (Phred/Phrap) modules.</p>
	<p><b>Vector NTI Advance v.11</b> Vector NTI is a professional multi-purpose bioinformatics software package.</p> <ol style="list-style-type: none"> <li>1. Create, annotate, analyse, and share DNA/protein sequences</li> <li>2. Perform and save BLAST searches</li> <li>3. Design primers for PCR, cloning, sequencing or hybridisation experiments</li> <li>4. Plan cloning and run gels in silico</li> <li>5. Align multiple protein or DNA sequences</li> <li>6. Search NCBI's Entrez, view, and save DNAs, proteins, and citations</li> <li>7. Edit chromatogram data, assemble into contigs</li> </ol>
	<p><b>Geneious Pro</b> Geneious is an integrated, cross-platform bioinformatics software suite for manipulating, finding, sharing, and exploring biological data such as DNA sequences or proteins, phylogenies, 3D structure information, publications, etc. It features sequence alignment and phylogenetic analysis, contig assembly, primer design and cloning, access to NCBI and UniProt, BLAST, protein structure viewing, automated PubMed searching, and more. It even includes an API for creating your own plugins.</p>
	<p><b>Sequencher 4.1.4</b> DNA Sequence Assembly Software Sequencher includes: Multiple, configurable DNA assembly algorithms Comprehensive DNA sequence editing tools Full support of sequence data confidence values Powerful Reference Sequence and the Variance Table find SNPs quickly and easily. Comprehensive Restriction Mapping Specialized tools for Forensic mtDNA profiling</p>


	<p><b>CLC DNA Workbench</b> CLC DNA Workbench creates a software environment enabling users to make a large number of advanced DNA sequence analyses, combined with smooth data management, and excellent graphical viewing and output options.</p>
	<p><b>CLC RNA Workbench</b> The CLC RNA Workbench gives the user easy access to a range of complex algorithms and options. RNA secondary structures can be predicted using state-of-the-art free energy minimization algorithms.</p>
	<p><b>ABI DNA Sequence Analysis</b> This software is designed to display, edit, basecall, trim and print sequencing sample files generated from ABI PRISM® 310, 377, 3100-Avant, 3100, 3700 Genetic Analysis instruments and Applied Biosystems 3730/3730xl DNA Analyzers. This software reads ONLY the following file types: AB1, .seq files and .fasta files. This software generates the following file types: .AB1, .seq, .fasta, .scf and .phd.1 files.</p>
	<p><b>DNAMAN for windows</b> DNAMAN is a one-for-all software package for molecular biology applications. This package provides an integrated system with versatile functions for high efficiency sequence analysis. You no longer need one program for restriction analyses and others for multiple sequence alignment, designing PCR primers, protein sequence analysis or drawing plasmids...</p>

## e) Mutation, SNP and RFLP analysis

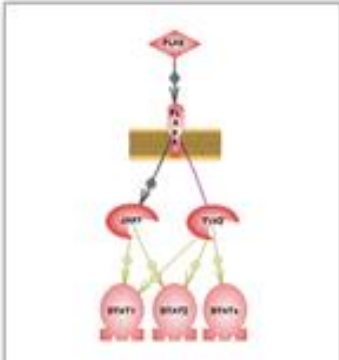
	<p><b>Mutation Surveyor</b> A Unique tool for DNA Variant Analysis from Sanger Sequence Traces with Detection Sensitivity to 5%; Accuracy greater than 99%. Provides highly accurate discovery of DNA Variants from Sanger Sequencing traces. Compatible with outputs from Applied Biosystems, Beckman-Coulter and MegaBace systems, Mutation Surveyor rapidly locates all variants and SNPs &amp; Indels between reference traces and sample/patient traces with excellent accuracy and sensitivity. Mutation Surveyor Capabilities:</p> <ul style="list-style-type: none"> <li>• Detection Sensitivity &amp; Accuracy</li> <li>• Somatic Mutation Detection</li> <li>• Mutation Quantification</li> <li>• Methylation Analysis</li> <li>• Hypervariable Region Variant Detection</li> <li>• Base Calling</li> <li>• Analysis Review Tool</li> <li>• <i>de novo</i> Assembly</li> <li>• Whole Gene Assembly</li> <li>• Custom Reporting Options</li> </ul>
	<p><b>GeneMarker</b> GeneMarker has been designed to provide genetic researchers with a biologist friendly genotyping tool. Their main requirements were ease-of-use, high accuracy, flexibility and low acquisition cost. GeneMarker can perform analysis on up to 1,000 lanes of four or five color data sets generated by either slab gel or capillary electrophoresis. It is a unique genotyping tool as it is compatible with files from all major capillary and slab gel electrophoresis systems including ABI files (*.FSA, *.AB1, *.ABI), SCF files, MegaBACE™ files (*.RSD, *.ESD), SpectruMedix files (*.SMD, *.SMR), Beckman files, and slab gel image files (TIFF,BIP,JPEG and TXT). GeneMarker is a replacement for such software packages as SAGA from LI-COR, TrueAllele from Cybergenetics, GeneMapper, Genotyper, and GeneScan from Applied Biosystems, MegaBACE Genetic Profiler and Fragment Profiler software.</p>

	<p><b>GeneMarker HID</b> STR Human Identity Software which is an excellent choice for all forensic profiling applications. This software can be employed as a "biologist friendly" replacement for GeneScan/GenoTyper or as an alternative to GeneMapper ID. GeneMarker HID Provides:</p> <ul style="list-style-type: none"> <li>• Meets the requirements of an expert system with single source samples</li> <li>• Mixture Analysis module</li> <li>• Kinship/Relationship/Pedigree Testing Module</li> <li>• 40% Faster Analysis</li> <li>• Increased Accuracy - 45% Fewer Extraneous allele calls</li> <li>• Reduced Analyst Fatigue</li> <li>• Results Concordant with GeneMapper ID</li> <li>• Customize stutter filter for each Marker</li> </ul>
	<p><b>ABI Seqscape v.2.6</b></p> <ul style="list-style-type: none"> <li>• Comprehensive reference sequence handling—Helps interpret the role of each polymorphism</li> <li>• Accurate data analysis—Detects heterozygous indels and provides quality values</li> <li>• Two-tier analysis—Reduces analysis time and complexity; identifies best sequence matches from a sequence library</li> <li>• Assists with 21 CFR Part 11 compliance —Provides data security, an audit trail of data changes, and electronic signatures</li> <li>• Detailed reports—Generates comprehensive reports with detailed results describing data quality</li> <li>• Automation—Integrated with Data Collection Software to analyze raw data generated from Applied Biosystems genetic analyzers</li> </ul>
	<p><b>ABI GeneMapper ID</b> GeneMapper ID Software combines the precision-sizing capabilities of GeneScan software with the allele-calling power of Genotyper software. Making accurate allele calls for human identification applications has never been easier. The software defined by Applied Biosystems for human identification laboratories analyzing forensic, paternity, databasing, and single-source samples.</p>

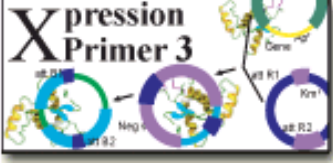
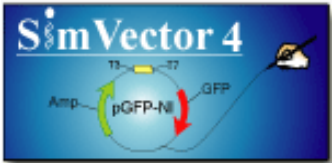
## f) Real time PCR data analysis

	<p><b>GENEX Pro</b> The ultimate software for real-time PCR gene expression analysis. Optimal use of real-time PCR measurements requires proper analysis of real-time PCR data. GenEx provides the appropriate tools to analyze real-time PCR gene expression data and to extract valuable information from the measurements.</p>
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## g) Pathway analysis software

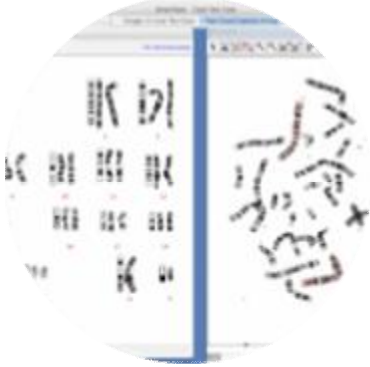

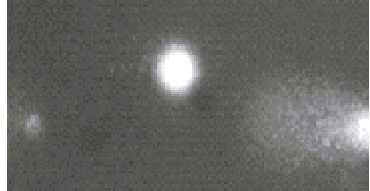
	<p><b>Pathway Studio 7</b> Pathway Studio pathway analysis software helps you to:</p> <ul style="list-style-type: none"><li>• Interpret gene expression and other high throughput data</li><li>• Build, expand and analyze pathways</li><li>• Find relationships among genes, proteins, cell processes and diseases</li><li>• Draw publication-quality pathway diagrams</li><li>• Build and visualize pathways</li><li>• Analyze and curate pathways</li><li>• Import and analyze gene &amp; protein lists</li><li>• Interpret microarray gene expression data</li><li>• Analyze proteomics, metabolomics, and other high throughput data</li></ul>
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## h) Cloning and Expression


	<p><b>Xpression Primer</b> Extensive Assay Support for Tagged Primer design Use the sophisticated algorithm of Xpression Primer to design thousands of tagged primers for expression cloning systems such as Gateway, BD In-Fusion, epitope and TOPO Tools. You can choose to amplify an entire ORF or generate N terminal or C terminal fusion proteins. Xpression Primer ensures that the reading frame of the amplified ORF is conserved.</p>
	<p><b>SimVector</b> An exceptional tool for drawing publication and vector catalog quality maps and designing cloning experiments. The software includes:</p> <ul style="list-style-type: none"> <li>• Exceptional Publication Quality Plasmid Maps</li> <li>• Multiple Cloning Site (MCS) Display is Unique to SimVector</li> <li>• Lightning Fast Cloning Simulation</li> <li>• Restriction Enzyme Analysis</li> <li>• Biologist-designed Intuitive Interface</li> </ul>

## 3. Medical genetics


### a) Karyotyping



	<p><b>SmartType</b> Powerful, Simple to Use Karyotyping software. SmartType is a robust, simple-to-use karyotyping system complete with everything needed to start karyotyping immediately.</p> <p><b>Feature List:</b></p> <ul style="list-style-type: none"> <li>•Simple To Use Interface</li> <li>•Compatible with any Laboratory Microscope</li> <li>•Integrated Patient Data Recording</li> <li>•FISH &amp; M-FISH Options</li> <li>•G, R, Q &amp; Dapi-band Classifiers</li> <li>•Trainable Classifiers</li> <li>•Simple Annotation Tools</li> <li>•Fast Onscreen Focussing</li> <li>•Multi Step Undo</li> <li>•Flexible Report Printing</li> <li>•Smart Editing Tools</li> <li>•Database Integration</li> </ul>
	<p><b>KARIO Software</b> KARIO is a karyotyping software developed to support genetists during the exacting work of karyotype reconstruction. The KARIO software was designed to reduce waiting and wasted time and to be more user friendly. The system may be fully personalized to meet your needs.</p>
	<p><b>COMET</b> The software uses the "<i>Comet-Assay</i>", a fast, highly sensitive fluorescent method, to examine damage and/or repair of DNA at an individual cell level. This assay has critically important applications in the fields of toxicology and epidemiology. These range from aging and clinical investigations to genetic toxicology and molecular epidemiology.</p>

## b) Patient databank management



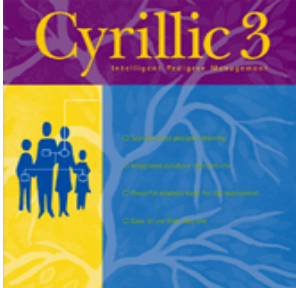

	<p><b>Progeny Suite (LIMS, Clinical, LAB)</b>            Complete Clinical and Pedigree Management            Complete Genotype Management            Complete Sample Inventory Tracking</p> <p><b>Clinical:</b> Multi-user clinical and pedigree management designed for collaboration and large-scale research teams. Ideal for family-based studies featuring a fully customizable relational database with user-based security and integrated pedigree drawing component.</p> <p><b>Lab:</b> Complete multi-user genotype data management for whole genome association, targeted or linkage studies. Track all genotypic and phenotypic data in one centralized, secure database, with ability to manage genotypes, samples, plates, SNP/STR maps, output to analysis packages and more.</p> <p><b>LIMS:</b> Complete multi-user LIMS system with advanced, multi-level sample inventory management. Generate and record barcodes, create custom workflows, and track chain of custody with full security compliance. Includes support for wireless hand-held devices.</p>
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## c) Genetics counseling

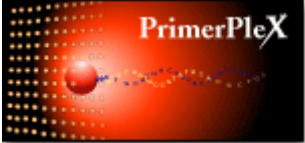

	<p><b>London Medical Database (LMD) Dysmorphology &amp; Neurogenetics</b></p> <p><b>The Winter-Baraitser Dysmorphology Database (WBDD):</b> currently contains information on over 4450 dysmorphic, multiple congenital anomaly and mental retardation syndromes. It includes single gene disorders, sporadic conditions, and those caused by environmental agents. WBDD mainly contains information about non-chromosomal multiple congenital anomaly syndromes, it also includes information about distinctive microdeletion syndromes and those resulting from uniparental disomy. WBDD contains over 44000 fully searchable references, linked to the appropriate syndromes.</p> <p><b>The Baraitser-Winter Neurogenetics Database (BWND):</b> currently contains information on over 4000 syndromes involving the central and peripheral nervous system seen in adults and children. Like the WBDD, it contains information on single gene disorders, sporadic conditions, and those caused by some environmental agents. BWND contains around 47000 fully searchable references, linked to the appropriate syndromes.</p> <p><b>The Photo Library:</b> Now integrated into WBDD and BWND, the Photo</p>
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	<p>Library is a superb collection of over 19300 photographs that show the main dysmorphic features of the syndrome and other relevant images, such as skeletal radiographs, hair microscopy, etc. In the case of neurogenetic syndromes, there are CT and MRI images showing their characteristic neuroradiological features, examples of EEG changes or the changes observed on other key electrophysiological investigations and, where relevant, pictures of the characteristic neuropathology, including nerve and muscle biopsy.</p>
	<p><b>London Ophthalmic Genetics Database (GENEEYE)</b>          GENEYE is a comprehensive database of over 2750 genetic ophthalmic conditions. Ophthalmological features have been considerably extended and all the syndromes from WBDD and BWND with an eye feature extracted and reclassified according to their features. To this has been added many single congenital anomalies both genetic and sporadic, including all the corneal dystrophies, macular dystrophies, the scores of different rod-cone dystrophies and much else. GENEYE contains over 36000 fully searchable references, linked to the appropriate syndromes, and an image library of around 13000 photographs. GENEYE has been developed with the support and assistance of Hans Møller, Isabelle Russell-Eggitt and David Taylor.</p>
<p><small>pictures of standard syndromes and undiagnosed malformations</small></p> 	<p><b>POSSUM</b>          POSSUM is a computer-based system that helps clinicians to diagnose syndromes in their patients. It contains information on more 2800 syndromes, including multiple malformation chromosomal abnormalities and skeletal dysplasias. The comprehensive mediabase includes x-rays, diagrams, histopathology slides and video clips.</p>

## d) Pedigree drawing

	<p><b>Progeny Suite (LIMS, Clinical, LAB)</b>          Complete Clinical and Pedigree Management          Complete Genotype Management          Complete Sample Inventory Tracking</p>
	<p><b>PED</b>          PED is a fast interactive pedigree drawing software for Windows. PED complies with the "Recommendations for standardized human pedigree nomenclature. Among other enhancements, PED now can fetch family information from a data file with LINKAGE or CSV (comma separated values) format, where each line describes an individual by the pedigree ID, the individual's ID, the IDs of his/her father and mother, the gender, the phenotype or affection status, and any other data related to the individual (like haplotypes, or clinical characteristics).</p>
	<p><b>Cyrillic 3 Standard Version</b>          Pedigree Draw and Risk Calculation Tool          Cyrillic 3 Standard Version calculates risks for breast cancer using BRCAPRO. Cyrillic also includes MENDEL, which has served practitioners of genetic counseling and genetic epidemiology for many years.</p>
	<p><b>Cyrillic 2 Linkage Version</b>          Pedigree Draw and Linkage Analysis Tool</p>

## 4. Luminex & ELISA data analysis

	<p><b>PrimerPlex</b></p> <p>PrimerPlex is an efficient and sophisticated tool for designing oligos for multiplex analysis on suspension array systems such as Luminex 100, Luminex 200 and Bio-Plex 200. Based on Luminex xMAP technology, these systems offer a versatile platform for multiplex nucleic acid detection in the 96-well format.</p> <p>PrimerPlex designs specific capture probes for direct hybridization assays and primer for Allele Specific PCR Extension (ASPE) assays. The assays are used for high throughput SNP applications such as genotyping, pathogen detection, strain typing, and haplotyping. To ensure specificity, the oligos are designed after avoiding the regions of homologies identified by a BLAST search.</p> <p>PrimerPlex then checks the oligos for cross reactivity and minimizes T<sub>m</sub> mismatches to give you the best possible multiplex set. In the process, it analyzes millions of possible multiplex sets in a few seconds and presents a list of alternate sets to you as well.</p>
	<p><b>MasterPlex Package</b></p> <p>A complete set for Luminex &amp; ELISA data analysis including:</p> <p><b>MasterPlex GT</b> simplifies genotyping and haplotyping analyses from multiplexed data generated with the Luminex® xMAP Platform. Integrating a wide variety of graphical data presentations as well as advanced statistics, MasterPlex GT provides rapid screening and analysis for all genomic laboratories.</p> <p><b>MasterPlex QT:</b> By the Only Software Company Focused on the Luminex xMAP Platform.</p> <p>Curve-fitting has never been easier with full support for the 4 Parameter Logistic (4-PL) and 5 Parameter Logistic (5-PL) model equations and much more!</p> <p><b>MasterPlex ReaderFit:</b> Software dedicated to ELISA Data Analysis. Get Fast Accurate Results Like Never Before.</p> <p>Curve-fitting for ELISA analysis has never been easier with full support for the 4 Parameter Logistic (4-PL) and 5 Parameter Logistic (5-PL) model equations and automatic EC<sub>50</sub> &amp; IC<sub>50</sub> calculations for Dose Response Curves.</p>

## 5. Flowcytometry



### **FlowJo**

FlowJo software reads flow cytometry data and facilitates complex data analysis in a graphically intuitive way.

## 6. Chemo / Bioinformatics


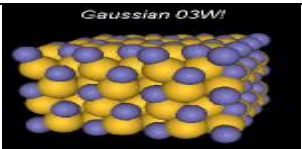


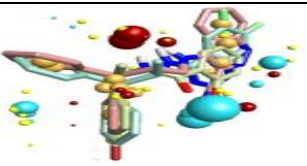


### **ChemBioOffice Ultra 2010 Suite**

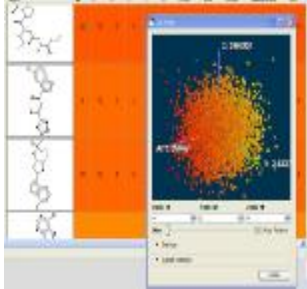
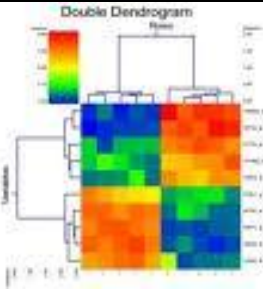
ChemOffice is a powerful suite of software, consisting of ChemDraw, Chem3D, ChemFinder and ChemACX for chemists, BioOffice, BioAssay, BioViz, and BioDraw for biologists, and Inventory, E-Notebook and The Merck Index for scientists.

BioDraw is a desktop application for drawing, sharing, and presenting biological pathways. BioDraw makes it easy to draw biological pathways. ChemDraw includes Struct=Name, ChemDraw/Excel and ChemNMR. Create stereochemically correct structures from chemical names, and get accurate IUPAC names for structures.

## 7. Molecular Modeling

	<p><b>Molegro Virtual Docker</b> Molegro Docker is an integrated platform for predicting protein – ligand interactions. It handles all aspects of the process, from preparing the molecules to determining the potential binding site of the target protein, and predicting the binding mode of the ligand. Molegro Virtual Docker offers high-quality docking based on a novel optimization technique combined with a user interface experience focusing on usability and productivity.</p>
	<p><b>Gaussian</b> Software for Computational Chemistry which is used by chemists, chemical engineers, biochemists, physicists and others for research in established and emerging areas of chemical interest.</p>
	<p><b>Diamond</b> Crystal and Molecular Structure Visualization <i>Diamond</i> is outstanding molecular and crystal structure visualization software. It integrates a multitude of functions, which overcome the work with crystal structure data - in research and education as well as for publications and presentations.</p>
	<p><b>Accelrys Discovery Studio</b> Discovery Studio provides the most advanced software solutions for life science researchers available today. Application Areas:</p> <ol style="list-style-type: none"> <li>1. ADMET Descriptors</li> <li>2. Biopolymer Building and Analysis</li> <li>3. Pharmacophore Modeling and Analysis</li> <li>4. Predictive Toxicology</li> <li>5. Protein Modeling and Sequence Analysis</li> <li>6. Simulations</li> <li>7. Structure Based Design and Visualization</li> </ol>
	<p><b>FieldTemplater</b> FieldTemplater allows the modeller or medicinal chemist to generate hypotheses for the bioactive conformation of ligands from 2D structures alone. Given three or more active molecules, FieldTemplater can suggest not only what the bioactive conformation of the molecules is, but also the relative alignment of the different molecules in the binding site.</p>

## 8. Biostatistics

	<p><b>Molegro Data Modeller</b></p> <p>Data Modeller is a cross-platform application for data mining, data modelling, and data visualization. The highly interactive user interface is ideal for fast and intuitive data exploration, as opposed to complex workflow based solutions or commanddriven statistical products. Create regression and classification models using partial least squares, neural networks, multiple linear regression, or support vector machines. Models are saved together with relevant normalization information making them easy to apply to new datasets. Cross-validation and feature selection can be applied using the built-in wizards. Automatic search for optimal model parameter settings.</p>
	<p><b>GESS &amp; NCSS Package</b></p> <p><b>GESS:</b> Microarray Data Analysis software</p> <p>Following is a comprehensive list of all microarray data analysis procedures that are available in the latest release of GESS. If you would like to see full details on a procedure, we suggest that you download the trial version and look at the Help file.</p> <p><b>NCSS:</b> Comprehensive and easy to use statistical analysis software.</p> <p>NCSS has specialized in providing statistical analysis software to researchers, businesses, and academic institutions. Our current release, is comprehensive and easy to use. NCSS includes over 230 statistical procedures and plots. NCSS imports and exports all major spreadsheet, database, and statistical file formats. NCSS easily produces sharp, flexible graphics. NCSS output is easily transferred to popular word processors and presentation software such as PowerPoint. NCSS is fully-documented; all help manuals are available online for download.</p>