SEQUENCHER Tech

Découvrir nouvelles sciénce

About Sequencher Tech

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Sequencher Tech Pvt. Ltd. is a Contract Research organization specialized in Products and Services in the area of Biotechnology, Molecular Biology, Animal Biology, Medical Genetics, Agri Genomics, Environment Sciences, Evolutionary Biology, Pharmacogenomics and Personalized Genomics. The Contract research has been our strength with contended customers academic, biotechnology and pharmaceutical researchers worldwide.

We provide all tools of modern genomics and proteomics for our client. We offer high throughput genome sequencing services like whole genome sequencing, Transcriptome analysis, DNA sequencing, Microbial identification, SNP Genotyping, Gene profiling, Oligoneuciotide synthesis from various NexGen Platforms and in Proteomics we offer Protein Sequencing, Characterization, Identification, Mass fingerprinting services.

Sequencher through its collaborators and effective project management skills helps client to compress timelines maintains quality & reduce the cost of commercialization. Sequencher is perfect blend of mix of Products & services and talented team to deliver uncompromising commitment to excellence.

Genomics Services:

Next Gen Sequencing Services:

Whole Genome Sequencing
Transcriptome Analysis
Metagenomics
Amplicon Sequencing
De novo Sequencing
Targeted Resequencing
MicroRNA Expression & Discovery
ChIP Sequencing

Simple Sequencing:

DNA Sequencing
Microbial ID
Microsatellite Discovery
DNA Fingerprinting by RAPD
Nucleic Acid Extraction
Primer Walk
SNP/Microsatellites Discovery & Genotyping
Gene Expression Profiling
DNA Fingerprinting by AFLP

Bioinformatics Services:

Genome Assembly
Clustering & Alignment
Genome Annotation

Proteomics:

Protein Sequencing
Protein Identification
Peptide Mass Fingerprinting
Protein Characterization
Protein Separation

Products

Reagents & Kits
Peptides
Antisera
Plastic Ware
Antibodies
Instruments

Next Generation Sequencing Platform

High throughput long and short read sequencing solutions to accelerate your research goals

Sequencher Tech offers services on three Next Gen Platforms: Solexa/Illumina, ABI SOLiD 3, Roche 454/Titanium. We are contented to offer comprehensive Next Generation sequencing services designed to meet the evolving DNA sequencing needs. Each platform has their own strengths and weaknesses that make it more or less appropriate for your research proposal. It is shown that the use of one technology alone does not necessarily provide the best solution. A combination of these technologies (as well as Sanger sequencing) may provide a more complete, cost-effective sequencing solution.

Illumina GAIIx Sequencing
The Illumina has the highest raw quality scores and its errors are mostly base substitutions. The large number of reads makes the Illumina appropriate for de novo transcriptome studies with simultaneous discovery and quantification of RNAs at qRT-PCR accuracy.

Read lengths - 36 bp, 50 bp or 75 bp for fragment or paired sequencing
Throughput (reads) - >120 million reads per run, fragment
Single read accuracy - >98.5% per base at 2x 50 bp yielding ≥80% perfect reads

Applied Biosystems SOLiD v3 Sequencing
ABI works on Sequencing by Oligonucleotide Ligation and Detection. SOLiD 3 has the shortest but also the highest quantity of reads. The Ultra-high per run throughput of version 3 valuable for counting applications such as Digital Gene Expression. SOLiD has the lowest raw base qualities but the highest processed base qualities when using a reference due to its 2-base encoding.

Read lengths - 50 bp fragment, 25 bp and 35 bp paired
Throughput (reads) - >160 million reads per slide, fragment
System accuracy - >99.94%
Single read accuracy - >98.5% per base at 2x 50 bp yielding ≥80% perfect reads

Roche 454 GS FLX Titanium Sequencing
The Roche/454 FLX with Titanium chemistry generates the longest reads (350-500bp) and the most contiguous assemblies, can phase SNPs or other features into blocks, and has the shortest run times. Errors occur mostly at the ends of long same-nucleotide stretches. Libraries can be constructed with many insert sizes (8kb - 20kb) but at half of the read length for each end and with low efficiency.

Read lengths - Averaging >350 - 400 bp suitable for de novo sequencing projects
Throughput (reads) - ~1 million reads per run
Single read accuracy - 99% at the 400th base and higher for preceding bases
Single read accuracy - >98.5% per base at 2x 50 bp yielding ≥80% perfect reads

Next Generation Sequencing workflow:

Platform	Library Construction	Template Amplification	Sequencing
Illumina GA	Library Construction	Clonal Amplification via bridge amplification	Massively parallel sequencing by synthesis of DNA cluster on a solid support
ABI SOLiD	Library Construction	Clonal Amplification Emulsion PCR	Massively Parallel ligation based sequencing of bead bound DNA Templates
ROCHE 454	Library Construction	Clonal Amplification Emulsion PCR	Massively parallel Pyrosequencing of bead bound DNA Templates

Next Generation Sequencing Services

Whole Genome Sequencing:

The Whole genome sequencing service includes, Fragmentation by nebulization of the genomic DNA, Preparation of a non-cloned single stranded shotgun library (sstDNA) and clonal amplification by emulsion PCR (emPCR), Ultra-high throughput sequencing with Next Generation platform, Assembly with appropriate assembly software, Generation and sequencing of non-cloned paired end libraries, Assembly of the paired ends and scaffolding the contigs, Closing of gaps by designing primer pairs on adjacent contig ends and sequencing PCR amplicons of the genomic region of interest.

De Novo Sequencing

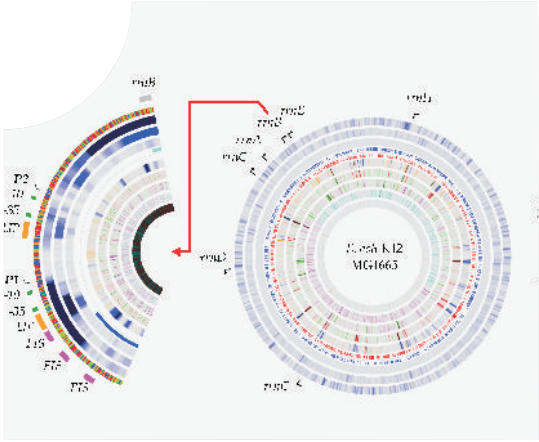
By utilizing long shotgun and large insert paired end reads, contiguous sequence information covering highly repetitive regions of complex genomes can be obtained and assembled.

Targeted Re-sequencing:

Re-sequencing of genomic fragments is the sequencing of presequenced and preselected genomic regions such as exons in order to find a correlation between sequence deviations (e.g. SNPs or indel mutations) and phenotypes. Based on Sanger technology, this service is performed in three phases.

Transcriptome Analysis

The transcriptome analysis service covers the construction and sequencing of standard, normalized or 3'-fragment cDNA libraries and miRNA or sncRNA (small non coding RNA) libraries. New and unknown ESTs (expressed sequence tags) for expression profiling or new rare transcripts can be identified and differential gene expression studies can be performed. Depending on the application, different project strategies are carried out. Transcriptome sequencing encompasses many applications including: mRNA transcript-expression analysis, Novel gene discovery, Gene space identification in novel genomes, Assembly of full-length genes, Single-nucleotide polymorphism (SNP), Insertion - deletion and splice-variant discovery



MicroRNA Expression & Discovery

Small non-coding RNAs are typically only ~18–40 nucleotides in length; however their effect on cellular processes is profound. Small RNA has been shown to play critical roles in developmental timing, cell fate, tumor progression, and neurogenesis. Animals, plants, and fungi contain several distinct classes of small RNA, including: microRNA (miRNA), short interfering RNA (siRNA), piwi-interacting RNA (piRNA), siRNA RNA (rasiRNA).

Metagenomics

By utilizing next-generation sequencing technologies, microorganism communities can be studied in their natural environments thus eliminating the need to culture these organisms. These techniques are particularly useful for those organisms which are difficult to culture.

Amplicon Sequencing

Amplicon sequencing by Next Gen technology refers to ultra-deep sequencing of exons or other PCR products for analyzing genetic variations in eukaryotic or prokaryotic populations, e.g. for SNP or mutation detection or for identifying and qualifying methylation patterns.

ChIP Sequencing

Chromatin immunoprecipitation (ChIP) is a method used to determine the location of DNA binding sites on the genome for a particular protein of interest. This technique gives a picture of the protein-DNA interactions that occur inside the nucleus of living cells or tissues. Determining how proteins interact with DNA to regulate gene expression is essential for fully understanding many biological processes and disease states.

Bioinformatics Support

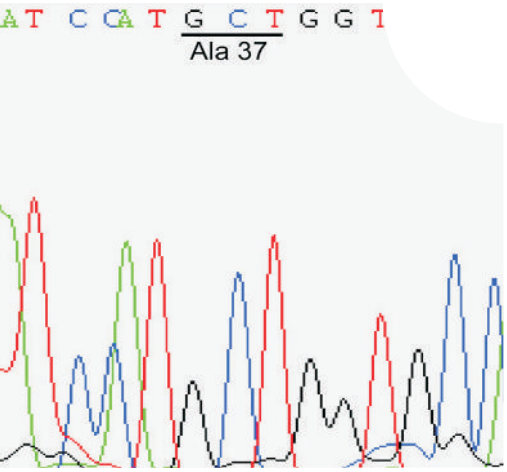
Genomic technologies are generating an extraordinary amount of information, unprecedented in the history of Biology. Thus, a new scientific discipline, Bioinformatics, at the intersection between Biology and Computation, has recently emerged. Bioinformatics addresses the specific needs in data acquisition, storage, analysis and integration that research in genomics generates.

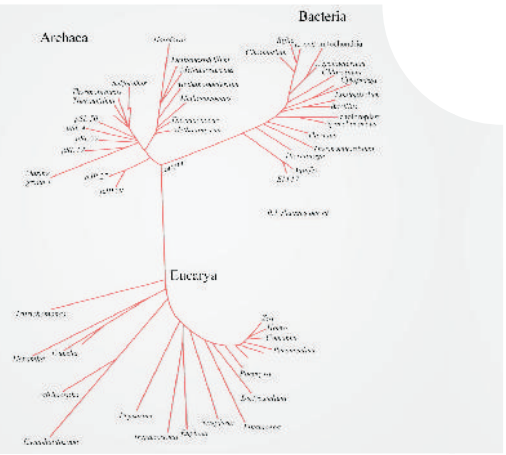
Sequencher Bioinformatics group provides data analysis support for many Genomics applications. Services include:

- Genome assembly and finishing
- Genome annotation
- Web-based EST/Transcriptome annotation database
- Clone like Cosmids & BACs assemblies
- High Throughput SNP discovery
- Clustering and alignment

Simple Sequencing

Trusted partner for superior long read capillary sequencing data





DNA Sequencing

DNA sequencing encompasses biochemical methods for determining the order of the nucleotide bases, in a DNA oligonucleotide. DNA sequence determines the patterns that make up genetic traits and in some cases behaviors. Samples may be submitted in form of cells (glycerol stocks, stabs, plates) or DNA (plasmids, PCR products, BAC/PAC, lambda, cosmids/phosmids).Customers may either provide sequencing primers or provide an e-copy of primer sequences to be synthesized using Sequencher's Oligoneuciotide Sequencing Service. **We provide PCR product / Plasmid, BAC/PAC Sequencing, r-E.coli Sequencing.**

Primer Walk

Primer walking is a method of for sequencing DNA fragments between 1.3 and 7 kb. . The DNA of interest may be either a plasmid insert or a PCR product. The initial sequencing will be performed from each end using either universal primers or designed primers. In order to completely sequence the region of interest Sequencher will design and synthesize primers as necessary to obtain coherent sequence information.
We offer following services.

SSPW - Single Stranded Primer Walk, DSPW - Double Stranded Primer Walk

Microbial ID

Microbial Identification based on gene sequencing has become the essential tool for microbiologists. Sequencher offers 16S and 28S gene sequencing and phylogenetic analysis. The process includes extraction of Genomic DNA, Amplification of desired gene, purification of the Amplicon, Sequence generation, consensus assembly of sequence. The Microbial ID report includes: DNA consensus sequence, Genus & species level identification of top 20 matches with cultured/non cultured sequences, Phylogenetic tree and distance matrix for taxonomy.

Simple Sequencing

SNP/Microsatellites Discovery & Genotyping
Sequencher offer an optimized platform for high-throughput genotype generation based on a novel technology developed. We offer advanced assay design, leading to better clustering of the alleles and easy, high-quality allele calling. This enables to analyze mix and match sets of microsatellites and SNPs, or genotype SNPs alone, for gene studies. Our service includes: Assay development and validation, Primer design and synthesis, PCR amplification and purification, automated fluorescent dye-terminator sequencing, Sequence trace alignment and editing, Mutation/variation identification, Heterozygosity detection via genotyping, Hard copy final report.

Gene Expression Profiling:
The genetic code is "interpreted" by gene expression, and the properties of the expression products give rise to the organism's phenotype. Sequencher provides a comprehensive range of gene expression analysis from bacteria, yeast, fungi, cell line and tissue of plant/animal/human built on multiple platforms including Genome Lab GeXP and QRT-PCR to address researcher's scientific goals.

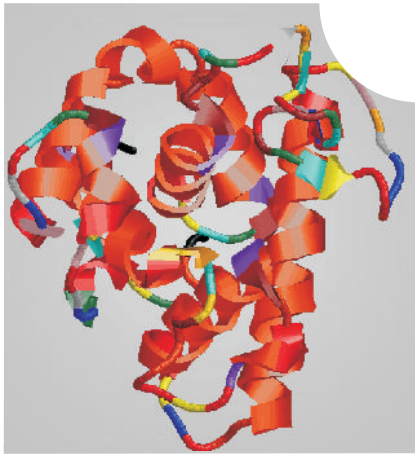
DNA Fingerprinting by RAPD & AFLP:
Random Amplification of Polymorphic DNA is a type of PCR reaction in which the segments of amplified DNA are random. Amplified Fragment Length Polymorphism is a PCR-based method used in genetics research, DNA fingerprinting, and in the practice of genetic engineering.

Nucleic Acid Extraction:
Sequencher has extensive experience in providing nucleic acid extraction and purification services. We worked with a wide range of sample types like whole blood, formalin fixed paraffin-embedded samples, buccal cells and frozen tissues to generate high yields of quality DNA and RNA that is free of PCR inhibitors and other contaminants. Upon completion of extraction and purification projects, Sequencher provides clients a detailed quality report with purity, concentration and yield data.

Proteomics

Proteomics is the deep study of proteins, their structures and functions. After genomics, proteomics is considered the next step in the study of biological systems. Proteomics considered to be much more complicated than genomics mostly because while an organism's genome is more or less constant, the proteome differs from cell to cell and from time to time. This is because distinct genes are expressed in distinct cell types.

Protein Sequencing:
Sequencher offers N-terminal protein and peptide sequencing by using Amino Acid Analyzer. In the first step the free N-terminal amino acid is converted by phenylisothiocyanate to its phenylthiocarbamoyl derivative under mild alkaline conditions. Then this derivative of the N-terminal amino acid is cleaved as a thiazolinone derivative under acidic conditions. After extraction this thiazolinone amino acid it is converted to the more stable phenylthiohydantoin amino acid derivative that can be identified by using chromatography. This procedure is repeated for identification of the next amino acid.



Protein Characterization
Beside proteomics Sequencher offers contract research for complete sequencing of proteins like **antibodies and recombinant or therapeutic proteins** by a comprehensive protein sequencing approach which includes N-terminal and internal Edman protein sequencing, capillary LC separation of proteolytical generated peptides and mass spectrometry including de novo peptide sequencing.

Proteomics

Protein Identification

Sequencher offers protein identification by nanoLC-ESI-MSMS to ensure highest sensitivity and reliability which allows unequivocal identification of one and more proteins within a sample. This is very suitable for analysis of protein bands from SDS-PAGE, protein complexes and other low or medium complex protein samples. The service apply to protein samples delivered as protein gel spot, protein gel band, lyophilized, in solution or bound to blotting membrane. The latter also identification of several protein within a sample due to peptide separation by nanoLC. Protein identification report includes protein name, amino acid sequence and molecular weight.

Protein Separation

Sequencher offers high resolution two dimensional gel electrophoresis (2DE) for separation all kind of protein containing samples and allows separation of up to 10,000 protein spots. This service is used for proteomics, Protein cataloguing, Protein species, isoform distribution analysis, analysis of posttranslational modifications, Western blot, Quality control of proteins.

Peptide Mass Fingerprinting:

Peptide mass fingerprinting is an analytical technique for protein identification the unknown protein of interest is first cleaved into smaller peptides, whose absolute masses can be accurately measured with a mass spectrometer such as MALDI-TOF or ESI-TOF. These masses are then compared to a reference database. Through Bioinformatics analysis translate the known genome of the organism into proteins, then theoretically cut the proteins into peptides, and calculate the absolute masses of the peptides from each protein. They then compare the masses of the peptides of the unknown protein to the theoretical peptide masses of each protein encoded in the genome to know the protein sequence.

Products

Products

We hope to be able to serve our client with highest quality Products that would carry the assurance of performance and ensure total technical satisfaction to the scientists. The technical support team of Sequencher would ensure international quality of after sales services to all establishments worldwide.

We offer below category of products:

- ☞ Reagents & Kits
- ☞ Plastic Ware
- ☞ Peptides
- ☞ Antibodies
- ☞ Antisera
- ☞ Instruments

How can we help!!

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