GELBANK

ARGONNE NATIONAL LAB
PROTEIN MAPPING GROUP

GELBANK

OVERVIEW   PROTEOMES   2D GELS   TOOLS   UPLOAD   BIO-BAG

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GELBANK

A database of annotated 2-dimensional gel
electrophoresis patterns of biological systems
with completed genomes

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Introduction

- Gelbank is database with 2-dimensional gel
  electrophoresis (2DE) of proteomes from organisms with
  known genome information.
- The website contains 233 identifications for 81 gel
  patterns for Homo Sapiens e.a.

What are proteomes?
What is a 2-dimensional gel electrophoresis?

Proteomes

The term "proteome" has been used to refer to the
collection of proteins found in a particular cell type under a
particular set of environmental conditions . (Wikipedia.org)

The proteome of an organism is the collection of potential
open reading frames (ORFs)

Some Theory, ORFs

By examining the DNA sequence alone we can determine
the sequence of amino acids that will appear in the final
protein.

In translation codons of three nucleotides determine which
amino acid will be added next in the growing protein chain.
But you will need to decide on which nucleotide to start
translation, and when to stop, this is called
an *open reading frame*.

Example ORF

atgcccaagctgaatagcgtagaggggtttttcatcatttgaggacgatgtataa

1 atg ccc aag ctg aat agc gta gag ggg ttt tca tca ttt gag gac gat gta taa
   M P K L N S V E G F S S F E D D V *
2 tgc cca agc tga ata gcg tag agg ggt ttt cat cat ttg agg acg atg tat
   C P S * I A * R G F H H L R T M Y
3 gcc caa gct gaa tag cgt aga ggg gtt ttc atc att tga gga cga tgt ata
   A Q A E * R R G V F I I * G R C I

ATG is a start condon,
TAA,TGA & TAG are stop condons

Proteome Analysis

Proteome Analysis requires the isolation of the complete proteome, separation of complex protein mixtures into discrete protein components measurement of relative abundance and identification of each protein Component.

The most widely used separation method is:

2-dimensional gel electrophoresis

What is 2D Gel Electrophoresis?
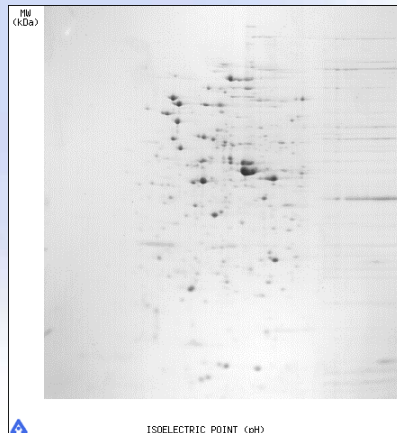
Back to 2DE

2DE is a separation method for proteome-analysis. Proteins are separated according to their isoelectric piont (pI) and their molecular weight (MW).

It's a combination of 2 techniques:
- Isoelectric focusing
- SDS Polyacrylamide Gel Electrophoresis

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Isoelectric focusing

Because of the amino acids in proteins, they have amphoteric properties and will be positively charged at pH values below their IpH and negatively charged above.
This means that proteins will migrate toward their IpH.
Most proteins have a IpH in the range of 5 to 8.5.
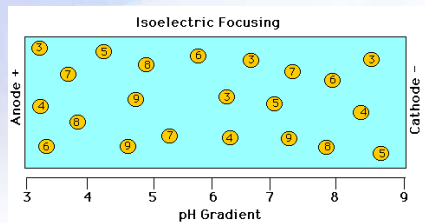
SDS Polyacrylamide Gel Electrophoresis

The proteins are inserted into a (flat) gel and an electrical current is applied.
Due to their linear form and negative charge, the proteins move through the gel .
Large proteins will move slowly through the gel, constrained by bulk, while small proteins will slip from pore to pore easily and move quickly.
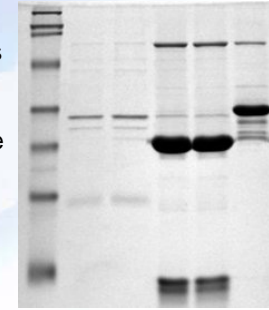
Thus proteins may be separated roughly according to size (molecular weight).

Proteome Analysis

Then we can identify our proteins with peptide mass fingerprinting by comparing them peptide masses of ours proteins with the predicted peptide masses.

Gelbank can now answer 2 questions:

Given a genome and potential ORF information, what is the most likely identity of a protein at a given location on a gel?

What are the predicted proteins resolved in a given pI and MW range?

Gelbank features

1. Proteomes: collection of interfaces for proteome queries.
2. 2D Gels: interfaces for 2D gel queries.
3. Tools: tools for proteome analysis by 2DE.
4. Upload: registered users can manipulate their 2DE patterns.
5. Bio-bag: a "shopping" basket for easy storage of items from the website.
6. FTP site: for access of data in various formats

Proteomes

- Search by description

Proteomes

- Search by sequence fragment

Proteomes

- Search by mW and pI

Use of tools

- ClustalW
- Titration
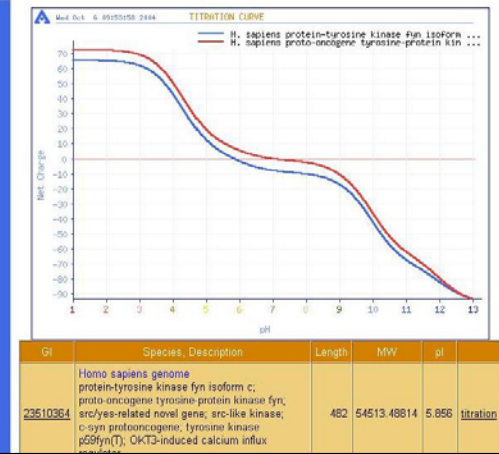
2DE gels

2DE gels-Simple search

2DE gels-Simple search

- Profiled Gel
- ClustalW
- Titration
- Size till 1500
- animation
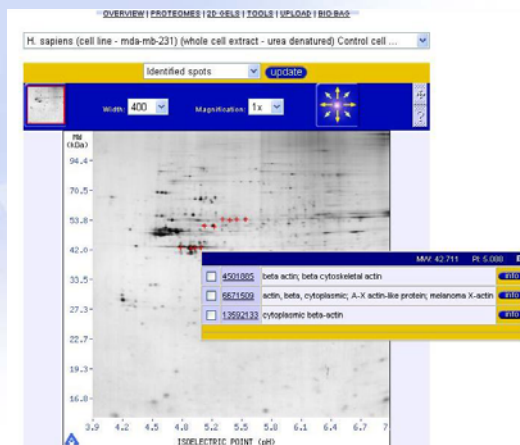
2DE gels – Complex search

- Species
- Tissue
- Sample type
- Staining
- First Dimension
- PH range
- Second Dimension

Tools

Bio-Bag

- Storage of object for later use
- Deleted after 30 min of inactivity
- Tools: multiple sequence alignment, titration curves ORFS, animation, etc.
- Contents can be deleted

Tools

- Selecting and saving patterns
- ClustalW (alignment)
- Titration curve
- Images animation
- Selecting sub-region
- Saving animations to BioBag

Upload

- PNG (8-bit), 1,4Mb max
- Profiling (markers, assigning MW pI values)
- ORACLE9i
- Assigning ORF's to a protein spot
- Adding new properties

FTP-site

- Entire content website
- Tab-delimited file
- Flat text format
- ORACLE9i database dumps
- 2DE patterns
- Weekly updated

References

- http://www.aber.ac.uk/parasitology/Proteome/Tut_2D.html #Section%201
- http://bioweb.uwlax.edu/GenWeb/Molecular/Seq_Anal/Translation/translation.html
- http://www.kennislink.nl/web/show?id=89064&showframe=content&vensterid=70344&prev=89059
- http://http://gelbank.anl.gov/
- www.ipn.uni-kiel.de/eibe/UNIT14NL.PDF
- http://en.wikipedia.org