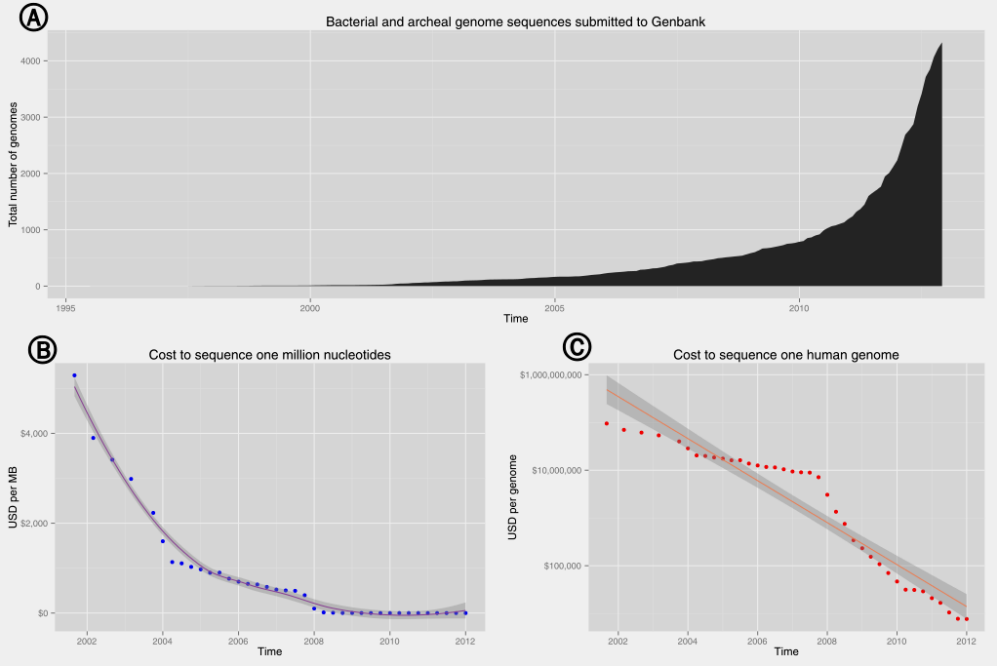
OMİK(S)LER
Genomik(s), Transkriptomik(s), Proteomik(s)

Doç. Dr. Murat Kasap
KOU Tıp Fak. Tıbbi Biyoloji AD

Genomiks

Temeli DNA'nın dizilenmesi ve elde edilen dizilerin biyoinformatiksel metotlar kullanılarak anlamlı hale getirilmesine dayanır.

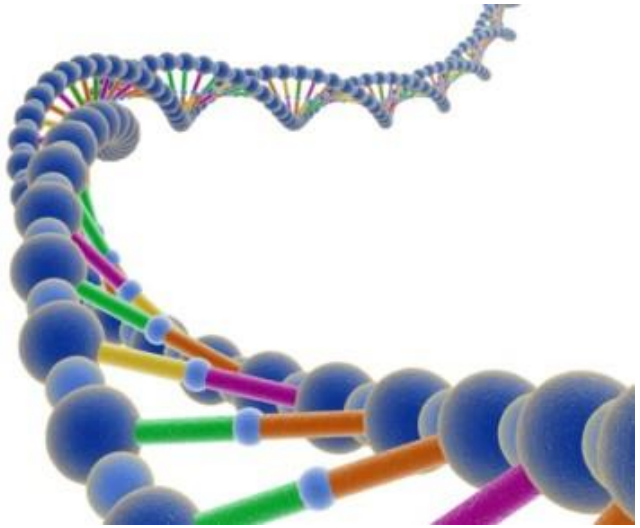
1964- Robert W. Holley- Alanin tRNA'ya ait ilk nükleik asit dizisi
1972- Walter Fiers Bakterifajı MS2'ye ait bir proteinin gen dizisi
1976- Wlater Fiers Bakterifajı MS2'nin tüm genomuna ait dizi (3569 bç)
1977-Alan Coulson Bakterifajı X174'ün tüm genom dizisi (5386bç)



Tamamlanmış Genom Projeleri

1981-İnsan mitokondri DNA'sı (16568 bç)
1986-Kloroplast DNA'sı
1992- S. cerevisiae'nın III. Kormozomunun dizisi (315 kbç)
1995- H. İnfluenza genom dizisi (1.8Mbç)
1996- S. cerevisiae genom dizisi (12.1 Mbç)

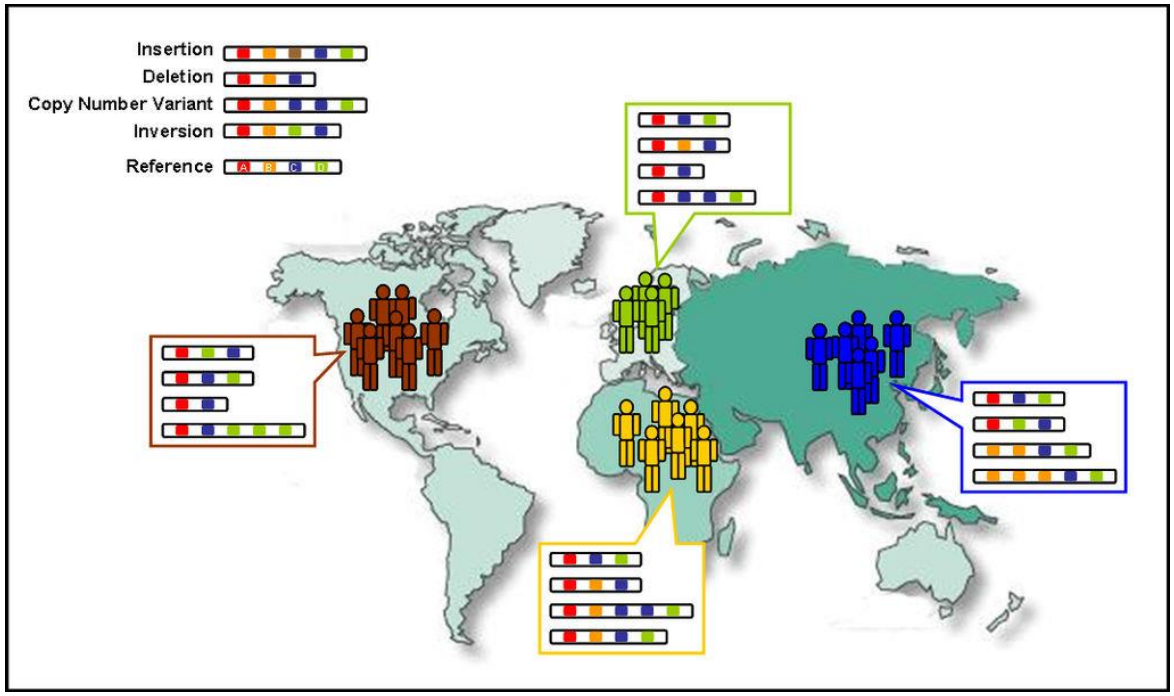
21.05.2015 itibarı ile
4691 viral genom dizisi
34845 Bakterial genom dizisi
2247 Ökaryotik genom dizisi



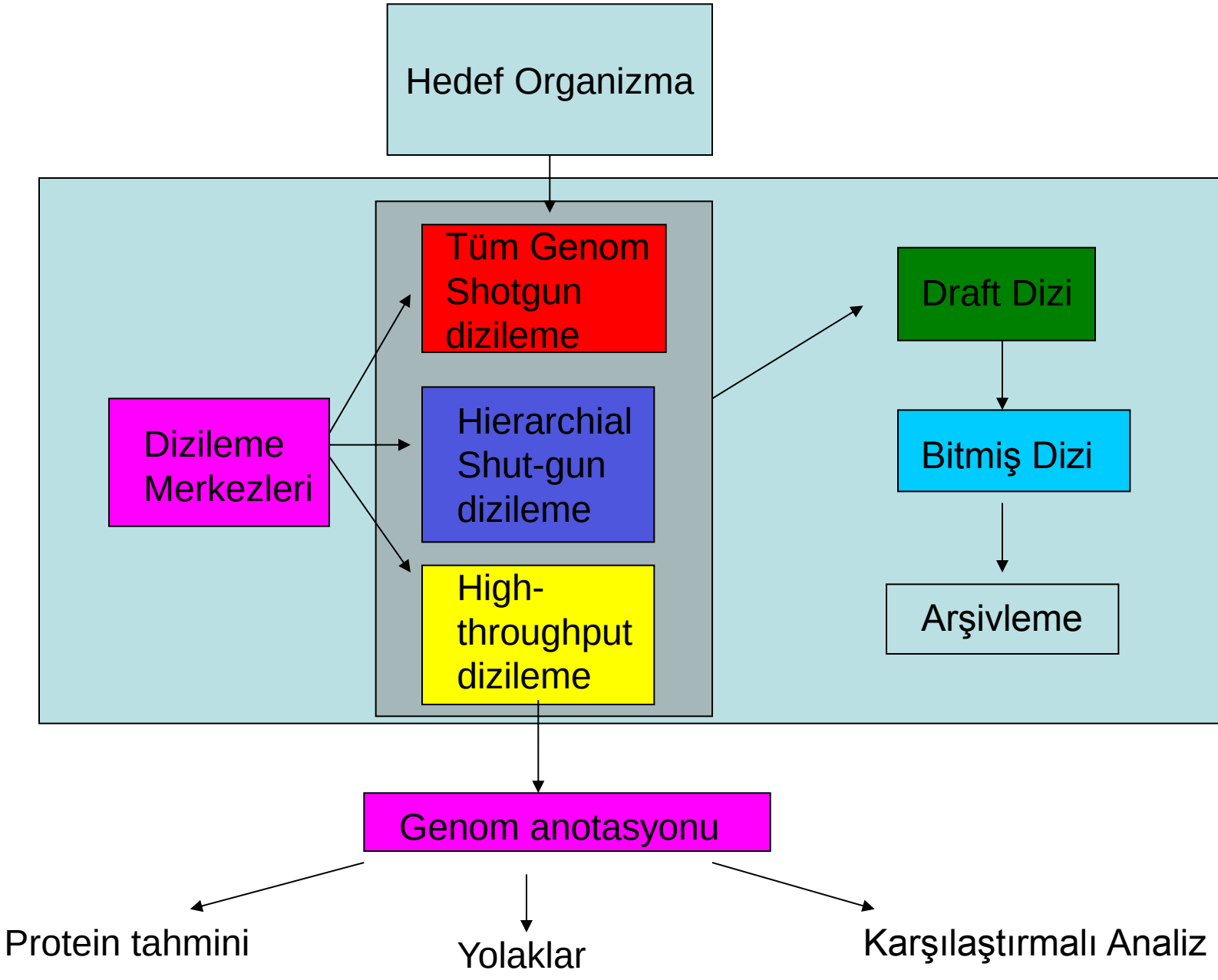
Neler Dizilenmiş:

1. Patojenler
2. Model organizmalar
3. İnsan genomu
4. Endüstriyel önemi olan organizmalar

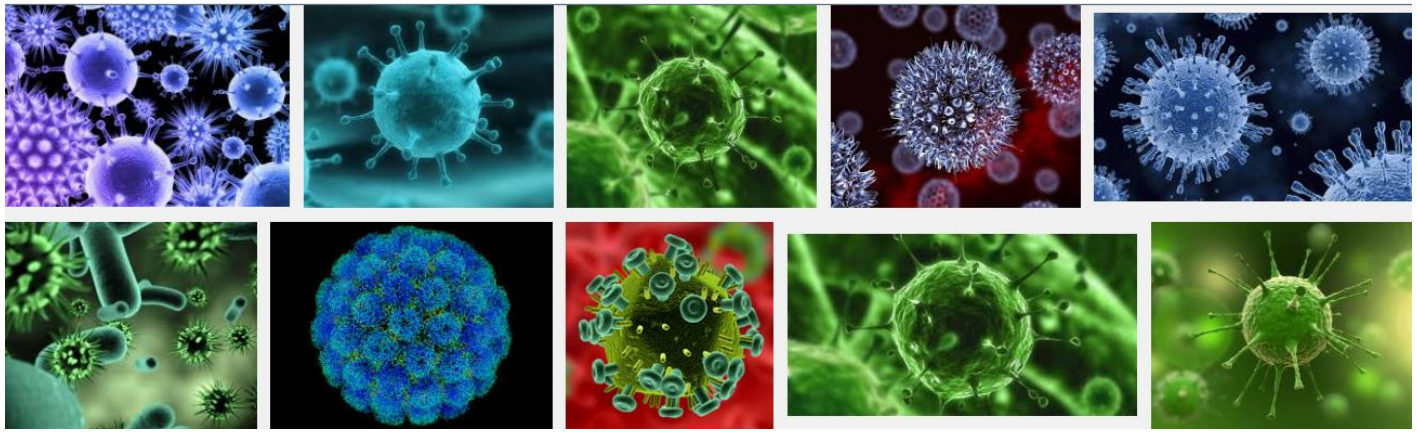
1000 Genom Projesi



Insandaki genetik varyasyonları ortaya çıkarmak için gerçekleştirilmiştir. SNP'ler, CNV'ları ve indel'ları belirlemek için yapılmıştır.


Hedef Organizma
Tüm Genom Shotgun dizileme
Hierarchial Shut-gun dizileme
High-throughput dizileme
Dizileme Merkezleri
Draft Dizi
Bitmiş Dizi
Arşivleme
Genom anotasyonu
Protein tahmini
Yolaklar
Karşılaştırmalı Analiz

Viral Genomiks



Viral enfeksiyonlar insan ve hayvan hastalıklarının temel nedenleri arasındadır.

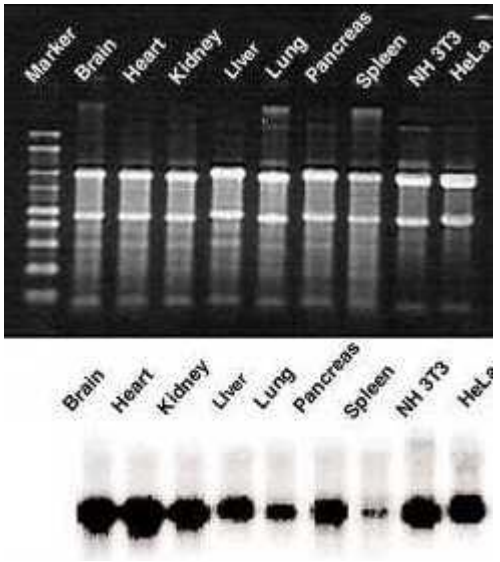
1. Virüs genom çeşitliliğinin ortaya çıkartılması
2. Dinamik genom varyasyonlarını belirlemek
3. Hastalıkların patogenezi ve epidemiyolojisini anlamak
4. Virüs replikasyonunun inhibisyonu
5. Virüs enfeksiyonlarının biyolojisinin anlaşılması

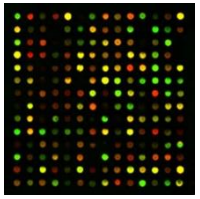
Transkriptomiks çalışmaları

“The sequence tells us what the cell could possibly do, while the expression profile tells us what it is actually doing at a point in time.”

Amaç:
Up-regülsyon
Down regülasyon

Northorn blotlama
Reverse-transcriptase PCR
Real-time PCR
SAGE (Serial Analysis Of Gene Expression)
Array teknolojileri
……
…….
……..





Avantajları

• Tek bir deneyle global gen ekspresyon profili elde edilebilir. Oysaki bir proteomiks çalışmalarında 200 civarında proteinin seviyesinde değişim görülebilir ki bu da toplam protein sayısının % 0.2'si demektir.
•Gen expresyon profili bir hücre tipinin çevresindeki değişikliklere vermiş olduğu tepkinin ölçümünde kullanılabilir.
• Ekspresyon profili iki yada daha fazla deneysel şart altında relatif olarak değişen mRNA seviyelerinin tespitinde kullanılabilir.

Limitasyonları/Dezavantajları

•Aktif olarak transkripte edilemeyen gen seviyelerindeki değişiklikleri görmek mümkün değil (Snap-shot picture).
•Genler sabit bir düzeyde eksprese edilirken protein seviyelerinde değişiklikler gözlemlenebilir.
•Yapılan deneylerin pahalı olması nedeni ile isatistiksel olarak güçlü sonuçlar elde etmek kolay değildir.
•Birçok genin düzeyindeki değişimler çalışılmış olsa da, araştırmacıların bir çoğu çalışilan transkriptlerin sadece çok az bir miktarı üzerine yoğunlaşırlar.

Proteomiks

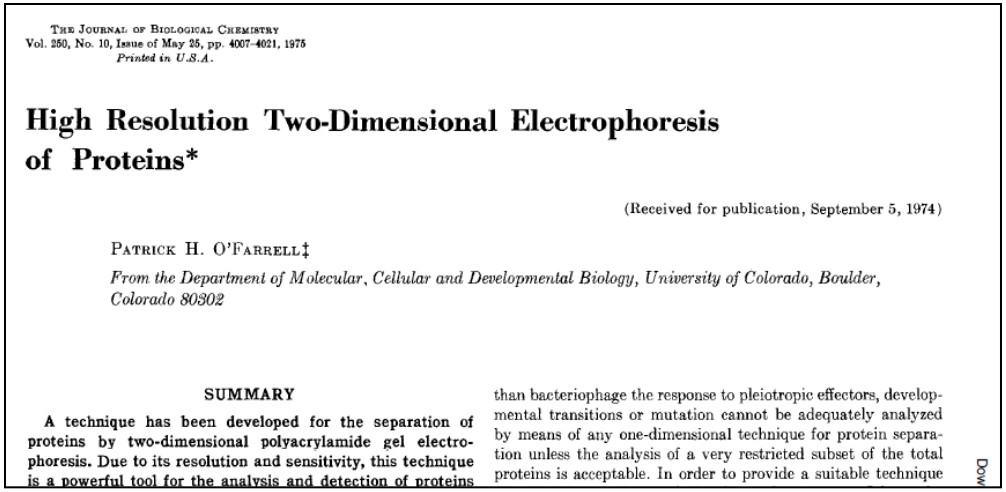





Proteomiks nedir?

Proteinlerin rollerinin tam olarak anlaşılması, diğer proteinlerle olan ilişkileri, hücrede nerede, ne kadar süre ile ve ne şekilde bulunduğu ve tüm organizma açısından öneminin vurgulandığı bir biyolojik çalışma alanıdır.

Proteomiğin kökleri her ne kadar 1975'li yıllara uzansa da (OFarrel, 1975), Proteomik kelimesi ilk kez bir doktora öğrencisi tarafından tez savunması sırasında kullanılmıştır.



THE JOURNAL OF BIOLOGICAL CHEMISTRY
Vol. 250, No. 10, Issue of May 25, pp. 4007–4021, 1975
Printed in U.S.A.

High Resolution Two-Dimensional Electrophoresis of Proteins*

(Received for publication, September 5, 1974)

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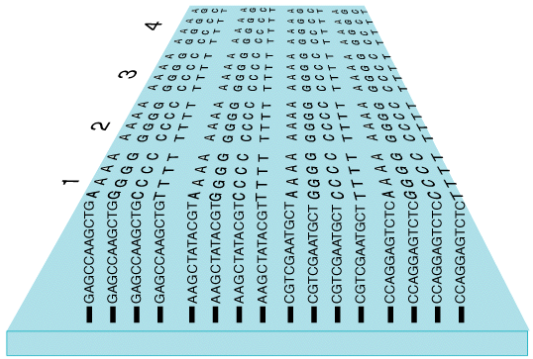
From the Department of Molecular, Cellular and Developmental Biology, University of Colorado, Boulder, Colorado 80302

SUMMARY

A technique has been developed for the separation of proteins by two-dimensional polyacrylamide gel electrophoresis. Due to its resolution and sensitivity, this technique is a powerful tool for the analysis and detection of proteins than bacteriophage the response to pleiotropic effectors, developmental transitions or mutation cannot be adequately analyzed by means of any one-dimensional technique for protein separation unless the analysis of a very restricted subset of the total proteins is acceptable. In order to provide a suitable technique

Neden çalışılmalıdır?



Genomik Çalışmaları

Faydalı bilgiler üretilmekte ancak çoğunlukla statik bir yapıdan bahsediyoruz.

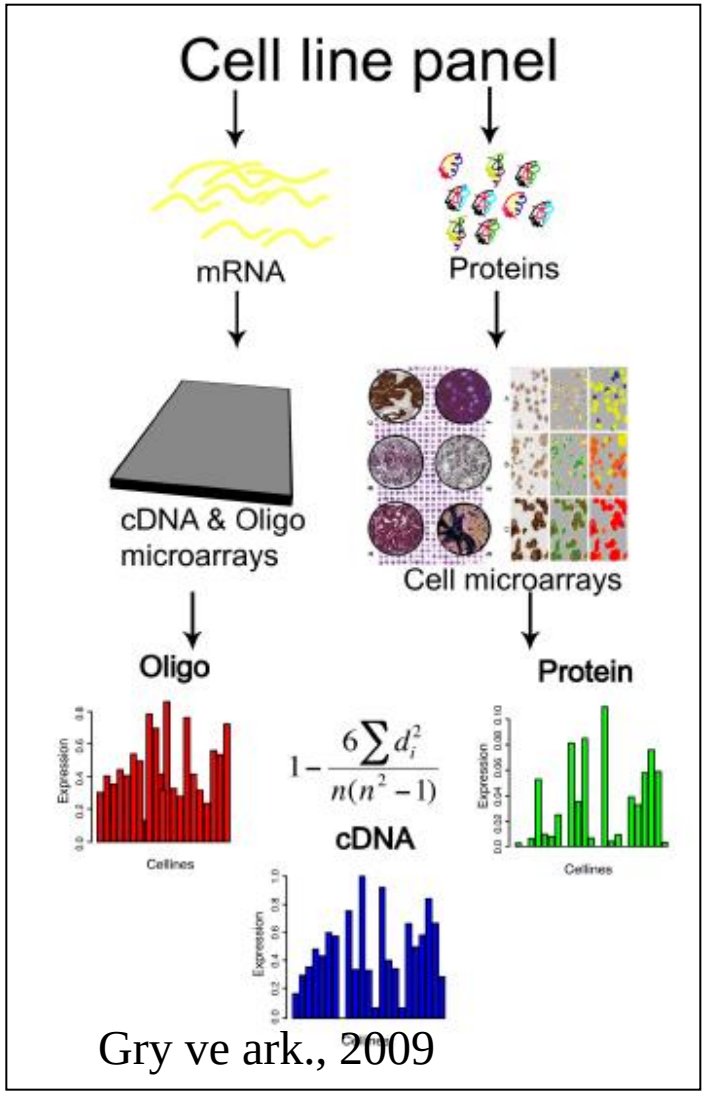
Ancak:

Genomdaki değişiklikler proteinlere nasıl yansımakta sorusuna cevap verememekte.

Ancak RNA ekspresyon profilleri yalnız başına genlerin fonksiyonlarını ve biyolojik prosesleri anlamada yeterli değil.

•Gry ve ark., 2009. Correlations between RNA ve protein expression profiles in 23 human cell lines. *BMC Genomics*.

•Çalışılan 1066 genden sadece üçte birinde (%33) RNA ve protein seviyeleri arasında ciddi manada ilişki bulunmuştur.



Gry ve ark., 2009

Neden Viral Proteomiks?

1. Virüslerin kodladığı proteinleri tanımlamak amaçlı (MALDI-TOF ya da LC-MS ile). (Zarsız virüsler, Zarlı RNA virüsleri, Herpes virüsleri, Poxvirüsler, Bakteri fajları)
2. Yapısal proteomiks (PDB databankası)
3. Viral proteinler arasındaki etkileşimler (TAP tag, IP, Maya sistemi)
4. Virüs-virüs etkileşimleri
5. Virüs-host etkileşimleri
6. Virüslerin host proteomu üzerinde sebep oldukları değişiklikler

Proteomiğin Alt Grupları

1. Ekspresyon proteomiği
   Hangi gen ürünleri, ne zaman ve neden yapılmakta?

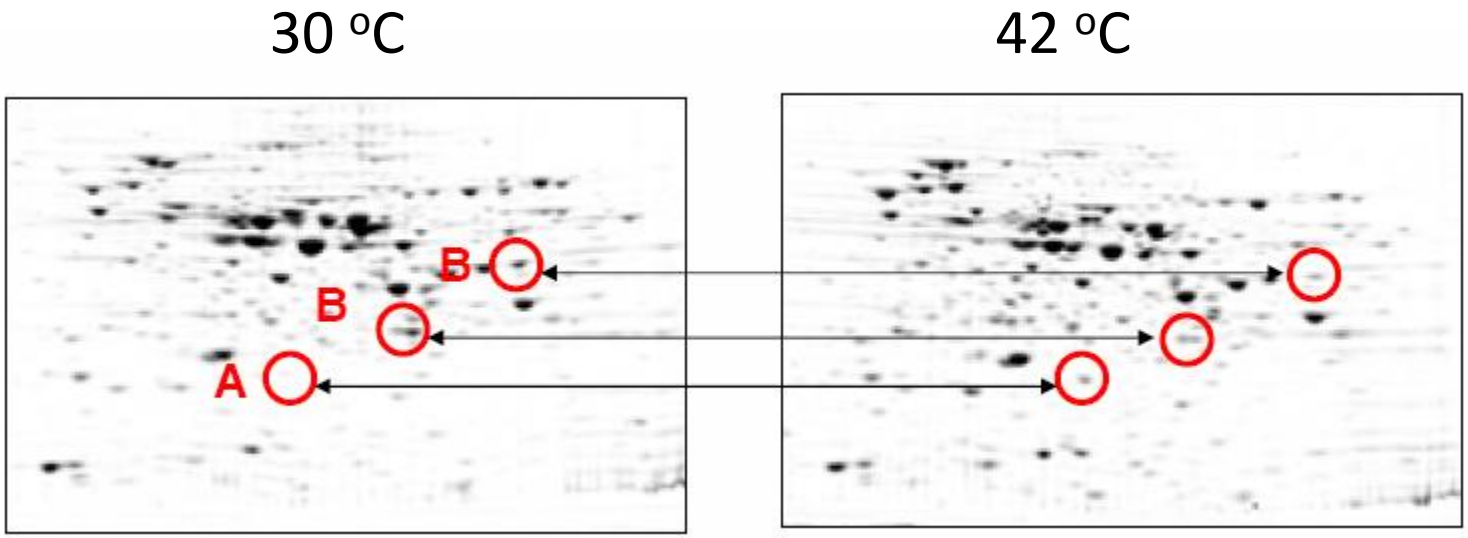
2. PTM-omics- modifikomiks
   Proteinlerin hangi varyantları var, nerede ve nasıl lokalize olmaktalar?

3. Cell-Map proteomiks
   Hangi proteinler etkileşmekte, nerede ve ne zaman?

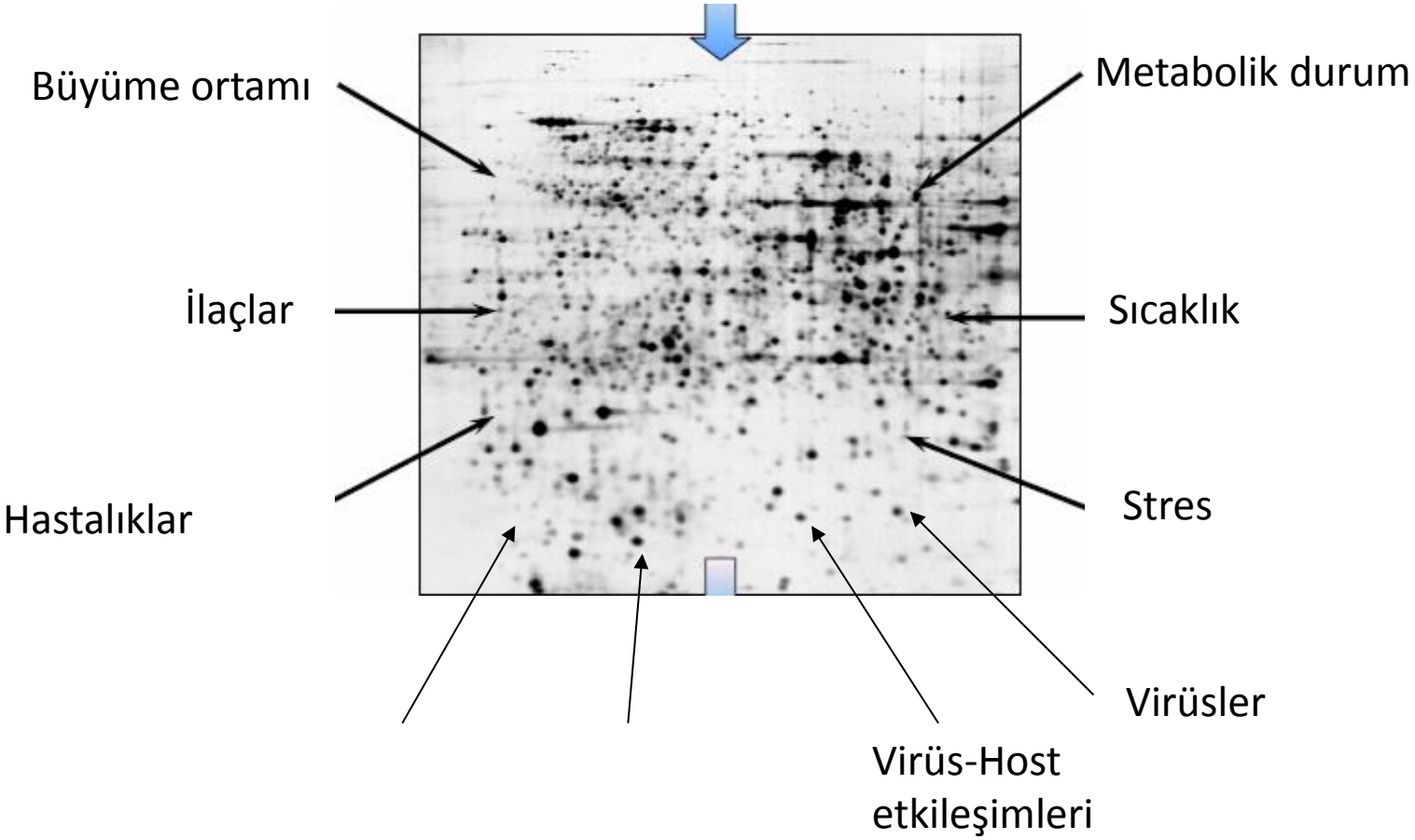
4. Fonksiyonel proteomiks
   Fazla yada az ifade edilen proteinlerin aktiviteleri nelerdir?

2D Tabanlı Proteomiks (Ekspresyon Proteomiği)

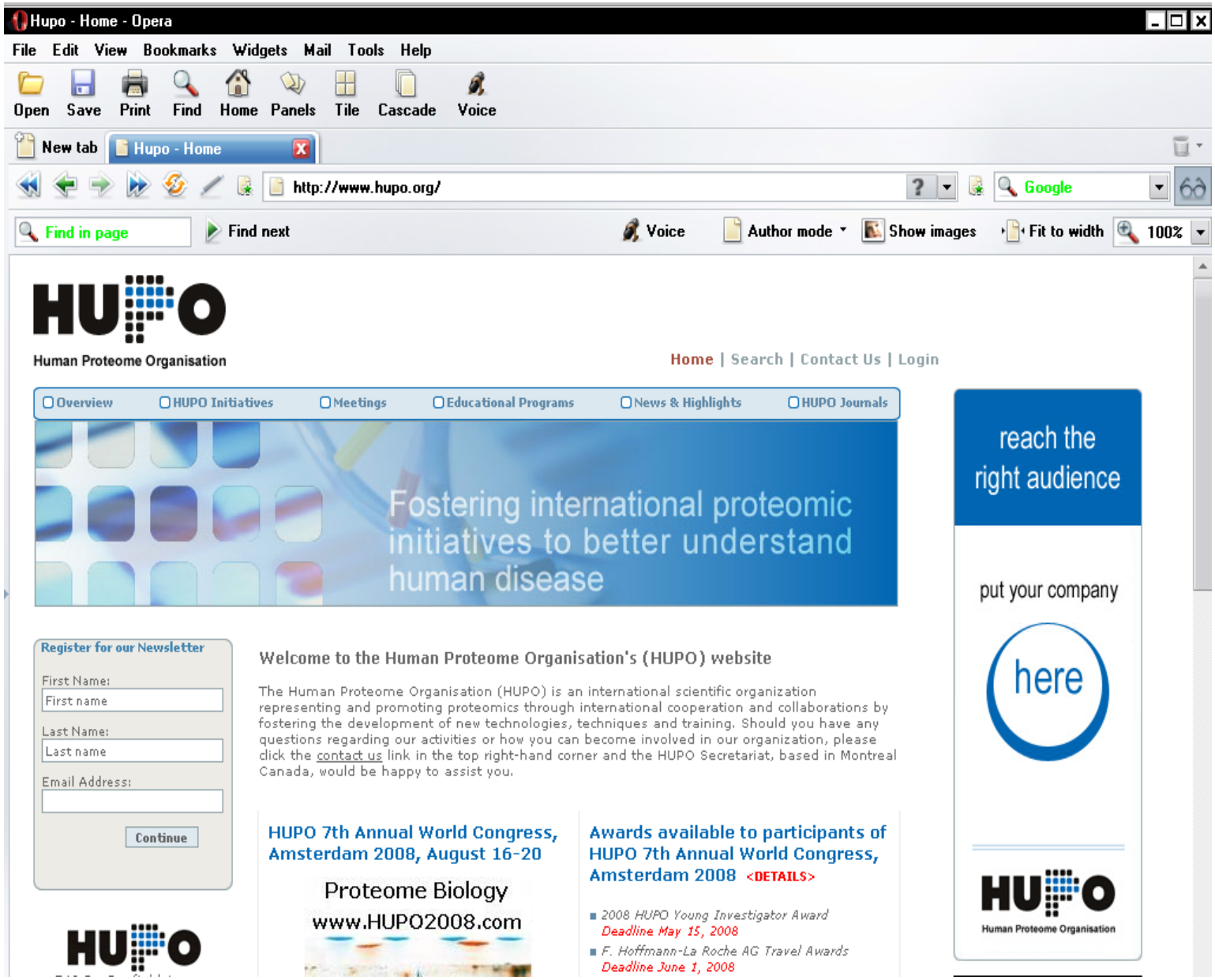
İki farklı ortamda büyütülmüş *E. coli* DH10B hücrelerinin protein profilleri



Neler çalışılabilinir?



Dünya Nerede????



HUPO

Human Proteome Organisation

Human Liver Proteome Project (HLPP)

Human Brain Proteome Project (HBPP)

Proteomics Standards Initiative (PSI)

Human Antibody Initiative (HAI)

Human Plasma Proteome Project (HPPP)

Human Disease Glycomics / Proteome Initiative (HGPI)

HUPO CardioVascular Initiative (HCVI)

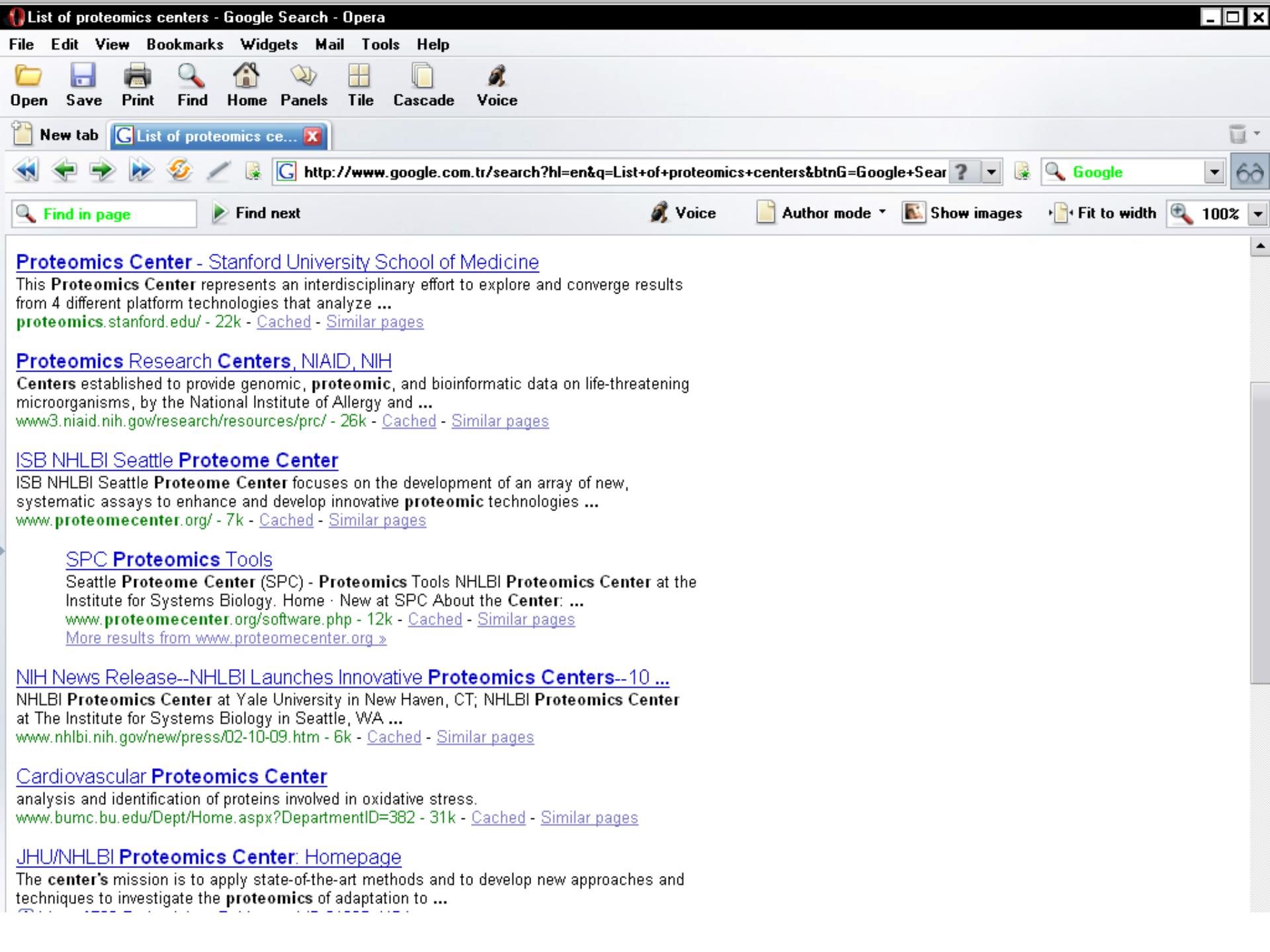
Proteome Biology of Stem Cells Initiative

Research Projects

Presently, there are eleven HUPO-sponsored Scientific Initiatives:

- Human Liver Proteome Project (HLPP)
- Human Brain Proteome Project (HBPP)
- Proteomic Standards Initiative (PSI)
- Human Antibody Initiative (HAI)
- Plasma Proteome Project (PPP)
- Human Disease Glycomics/Proteome Initiative(HGPI)
- HUPO Cardiovascular Initiative (HUPO CVI)
- Proteome Biology of Stem Cells Initiative
- Disease Biomarkers Initiatives (DBI)
- Mouse Models of Human Disease (MMHD)
- Kidney and Urine Initiative (HKUPP)

Each of these global initiatives is based in one country, but includes subprojects that involve international research laboratories. Funding for these projects has come from National Granting Agencies and industry.


List of proteomics centers - Google Search - Opera
File Edit View Bookmarks Widgets Mail Tools Help
Open Save Print Find Home Panels Tile Cascade Voice
New tab
List of proteomics ce...
http://www.google.com.tr/search?hl=en&q=List+of+proteomics+centers&btnG=Google+Sear
Google
Find in page
Find next
Voice
Author mode
Show images
Fit to width
100%
Proteomics Center - Stanford University School of Medicine
This Proteomics Center represents an interdisciplinary effort to explore and converge results from 4 different platform technologies that analyze ...
proteomics.stanford.edu/ - 22k - Cached - Similar pages
Proteomics Research Centers, NIAID, NIH
Centers established to provide genomic, proteomic, and bioinformatic data on life-threatening microorganisms, by the National Institute of Allergy and ...
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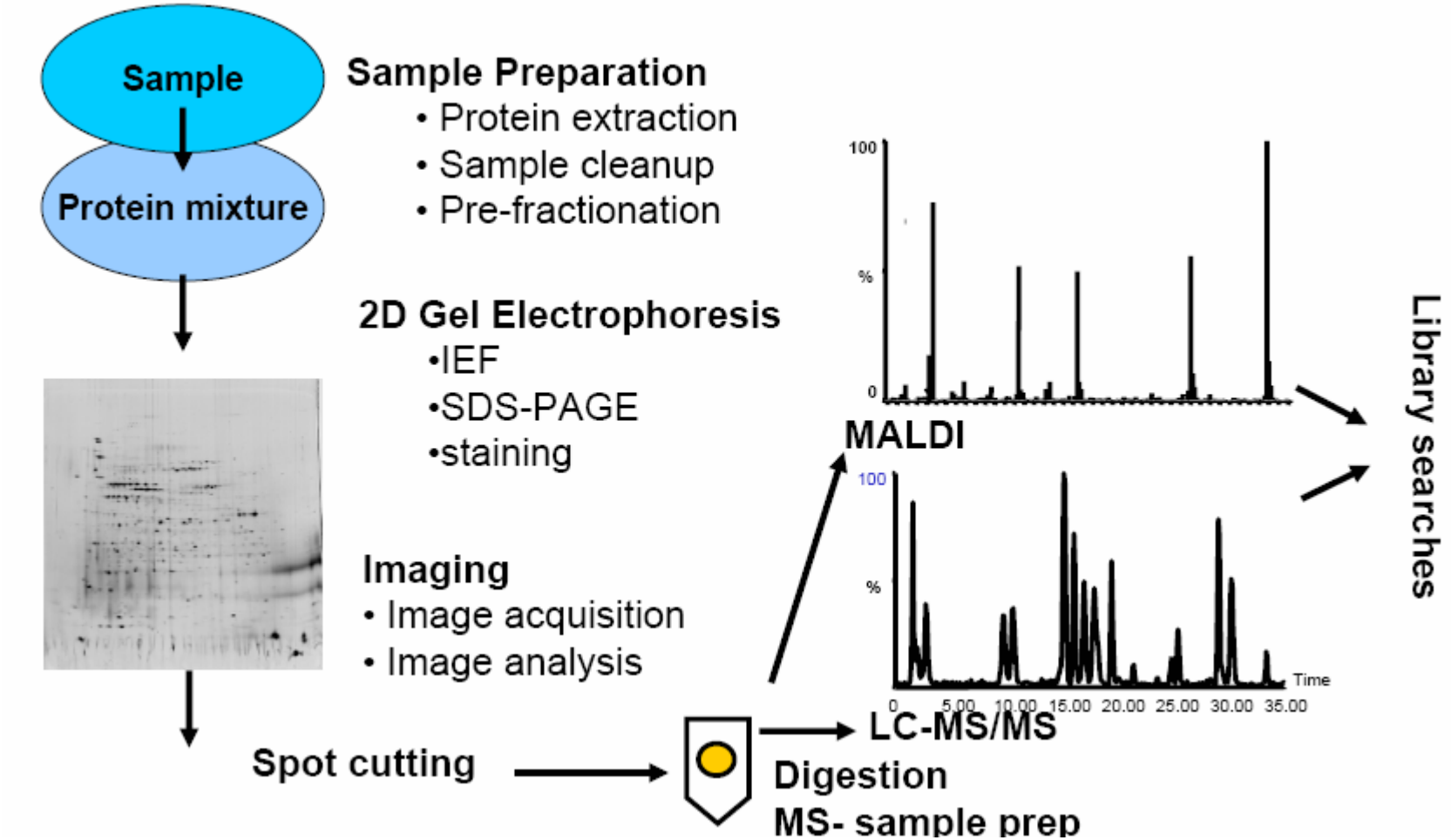
ISB NHLBI Seattle Proteome Center
ISB NHLBI Seattle Proteome Center focuses on the development of an array of new, systematic assays to enhance and develop innovative proteomic technologies ...
www.proteomecenter.org/ - 7k - Cached - Similar pages
SPC Proteomics Tools
Seattle Proteome Center (SPC) - Proteomics Tools NHLBI Proteomics Center at the Institute for Systems Biology. Home · New at SPC About the Center: ...
www.proteomecenter.org/software.php - 12k - Cached - Similar pages
More results from www.proteomecenter.org »
NIH News Release--NHLBI Launches Innovative Proteomics Centers--10 ...
NHLBI Proteomics Center at Yale University in New Haven, CT; NHLBI Proteomics Center at The Institute for Systems Biology in Seattle, WA ...
www.nhlbi.nih.gov/new/press/02-10-09.htm - 6k - Cached - Similar pages
Cardiovascular Proteomics Center
analysis and identification of proteins involved in oxidative stress.
www.bumc.bu.edu/Dept/Home.aspx?DepartmentID=382 - 31k - Cached - Similar pages
JHU/NHLBI Proteomics Center: Homepage
The center's mission is to apply state-of-the-art methods and to develop new approaches and techniques to investigate the proteomics of adaptation to ...

DEKART
Protein araştırmaları ve Proteomiks Laboratuarı

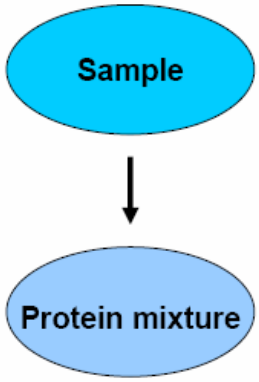
http://kabiproteomics.kocaeli.edu.tr/index-2.php

2DE- tabanlı proteom çalışmalarında ÇALIŞMA AKIŞI



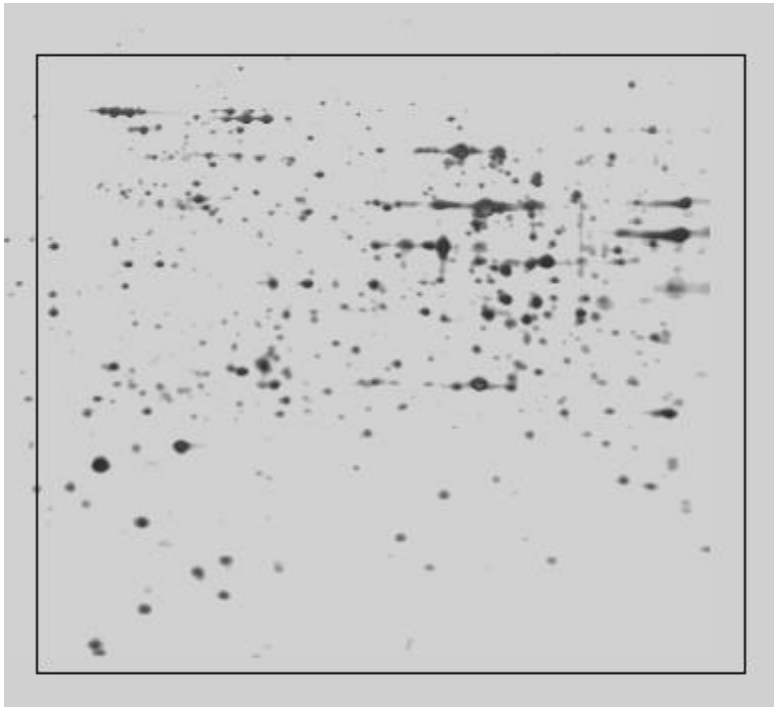
ADIM 1. ÖRNEK HAZIRLAMA

En önemli adımdır.

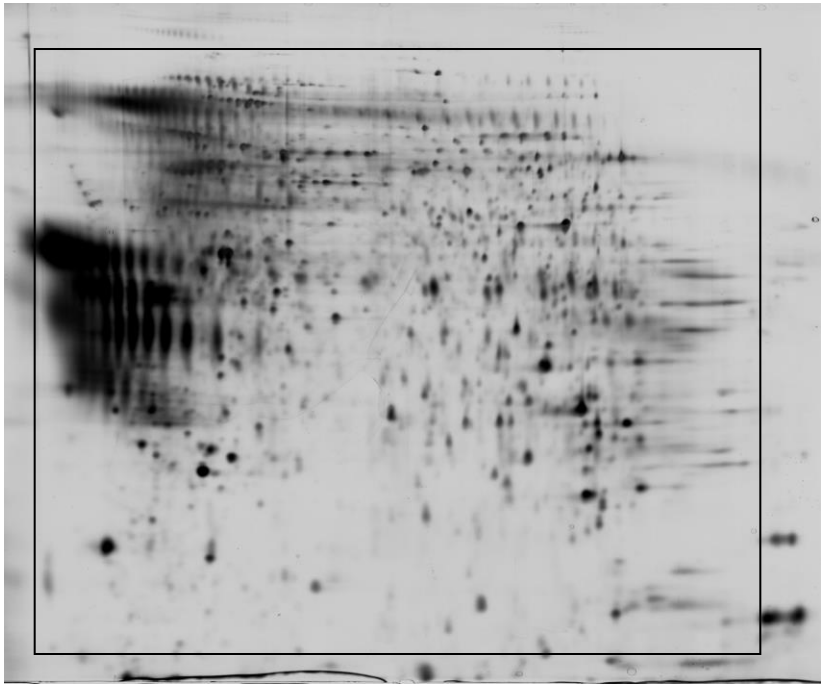


- Hücre parçalama/Liziz
- Protein ekstraksiyonu ve solubilizasyonu
- Kontaminantların yok edilmesi ve temizleme
- Fraksiyonlama
  - Protein karışımını basitleştirme
  - Düşük miktardaki proteinleri zenginleştirme

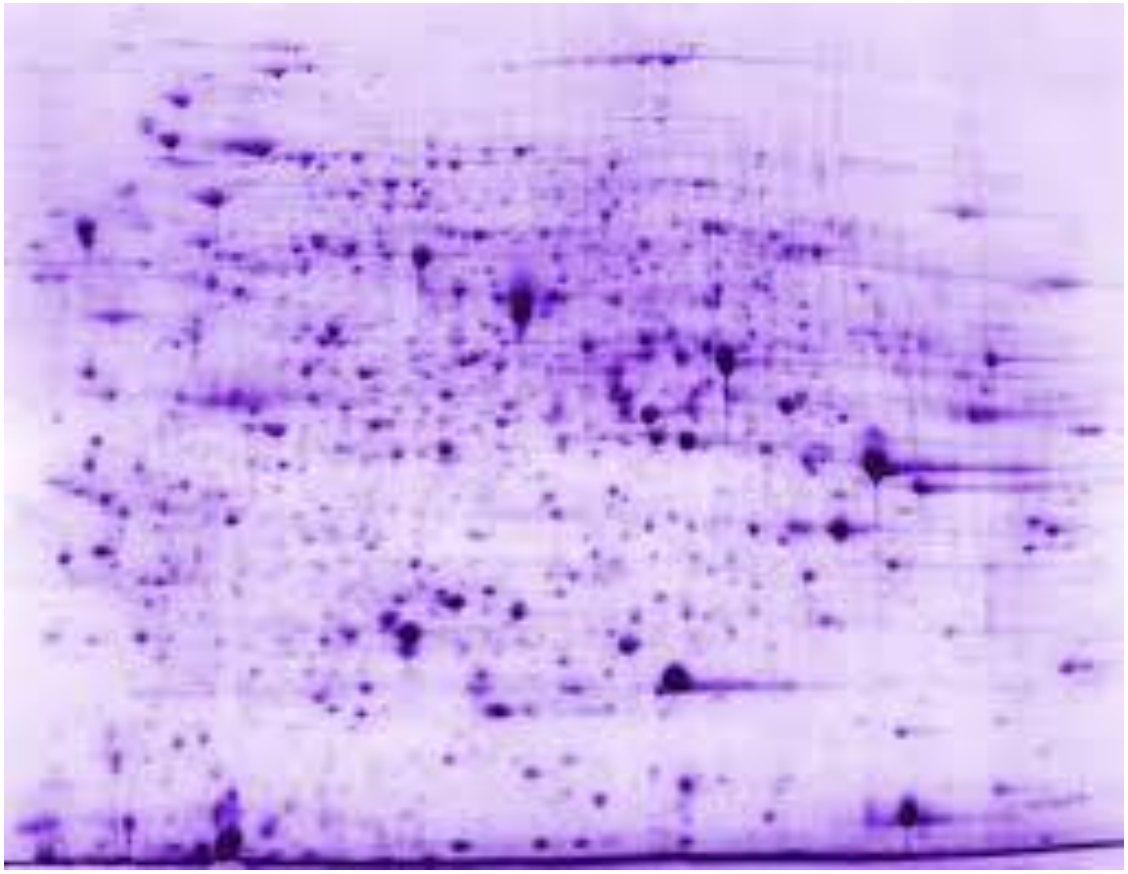
İyi Örnek



Kötü Örnek

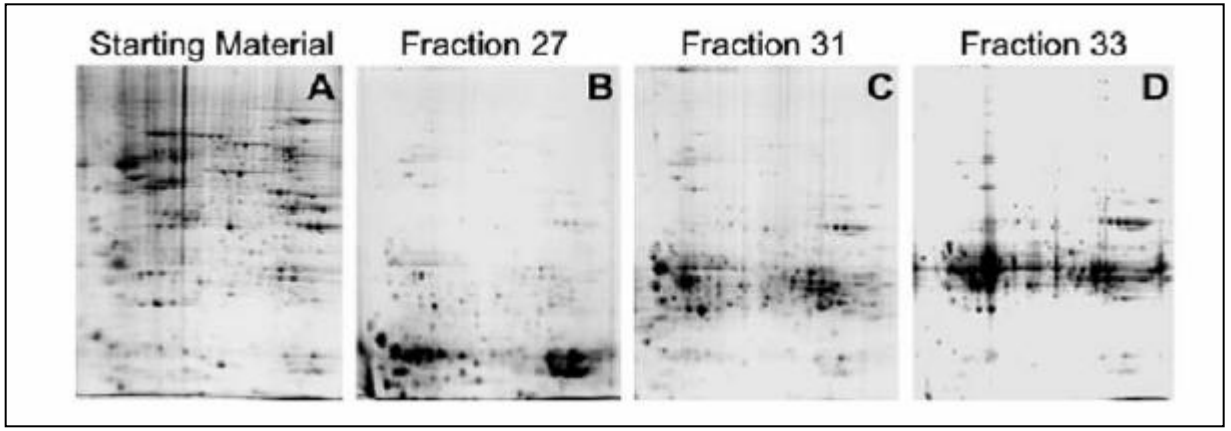


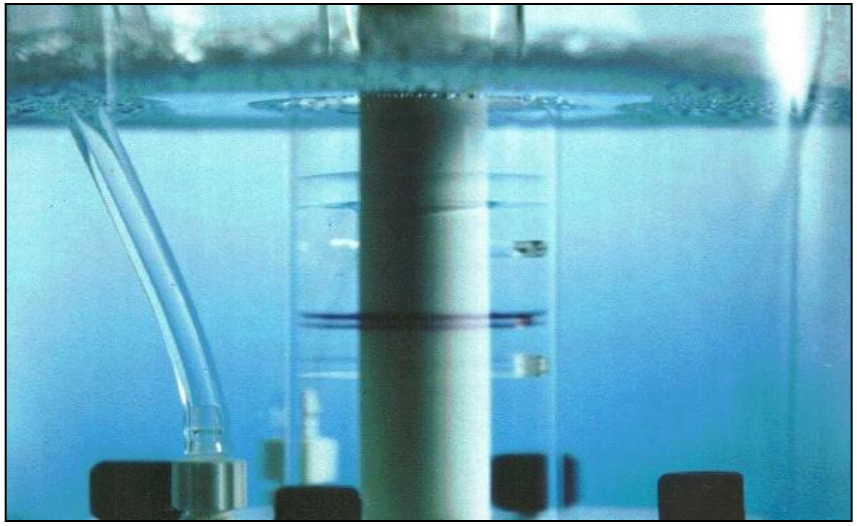
Komplex Protein Karışımlarından Detaylı Bilgi Elde Edebilmek İçin Fraksiyonlama yapmak gerekmekte

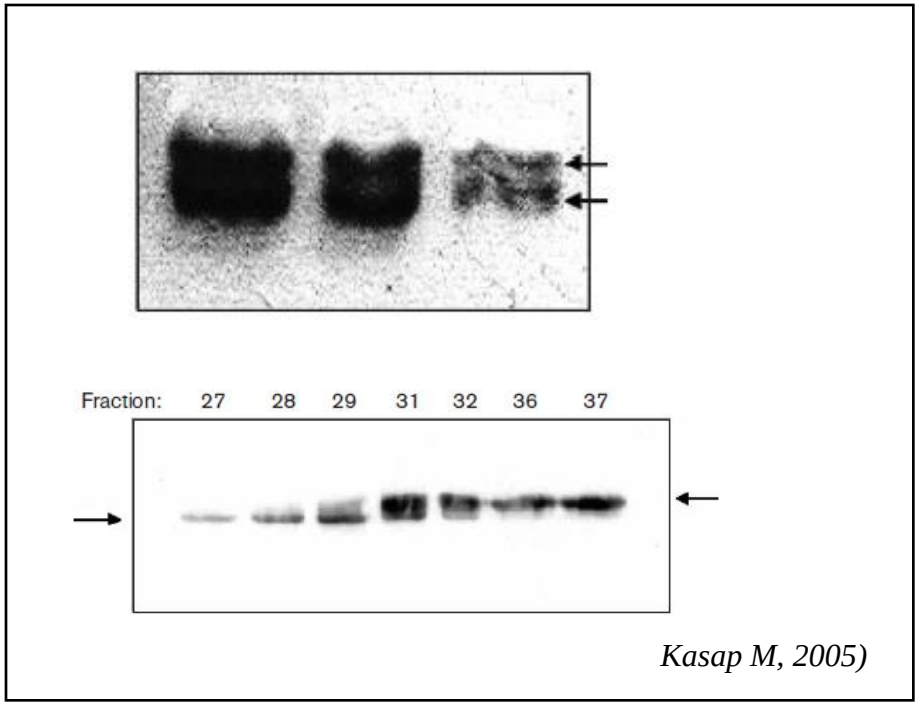


FRAKSİYONLAMA TEKNİKLERİ NELERDİR?

PrepCell-Preparative tube electrophoresis

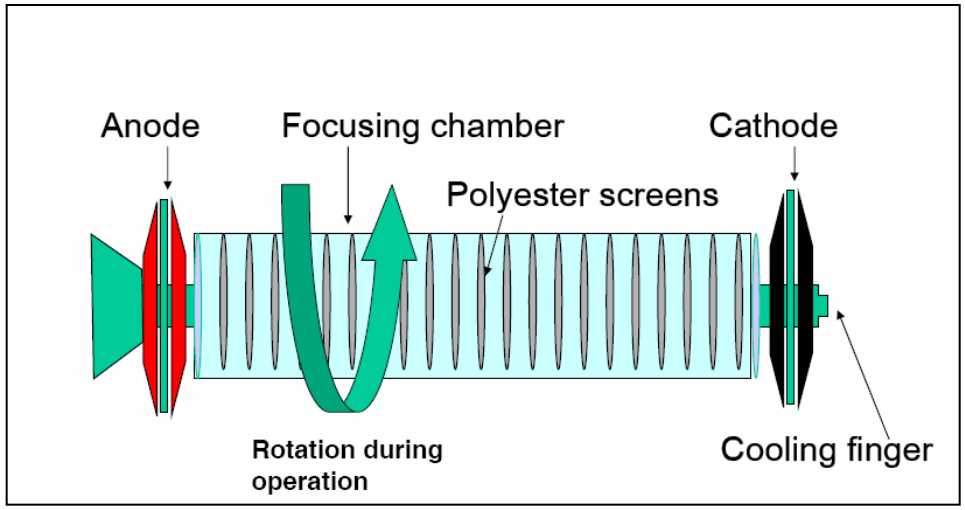


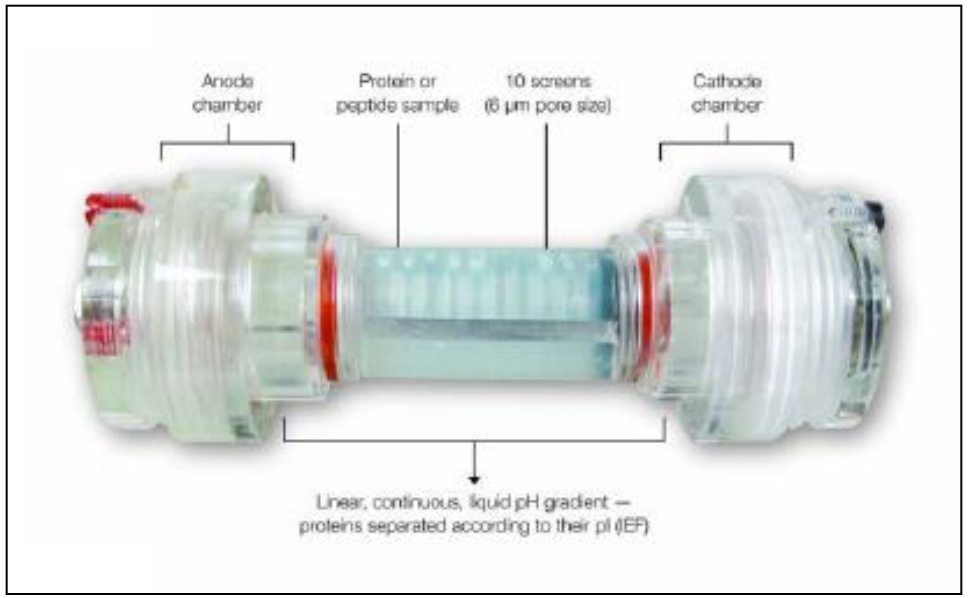


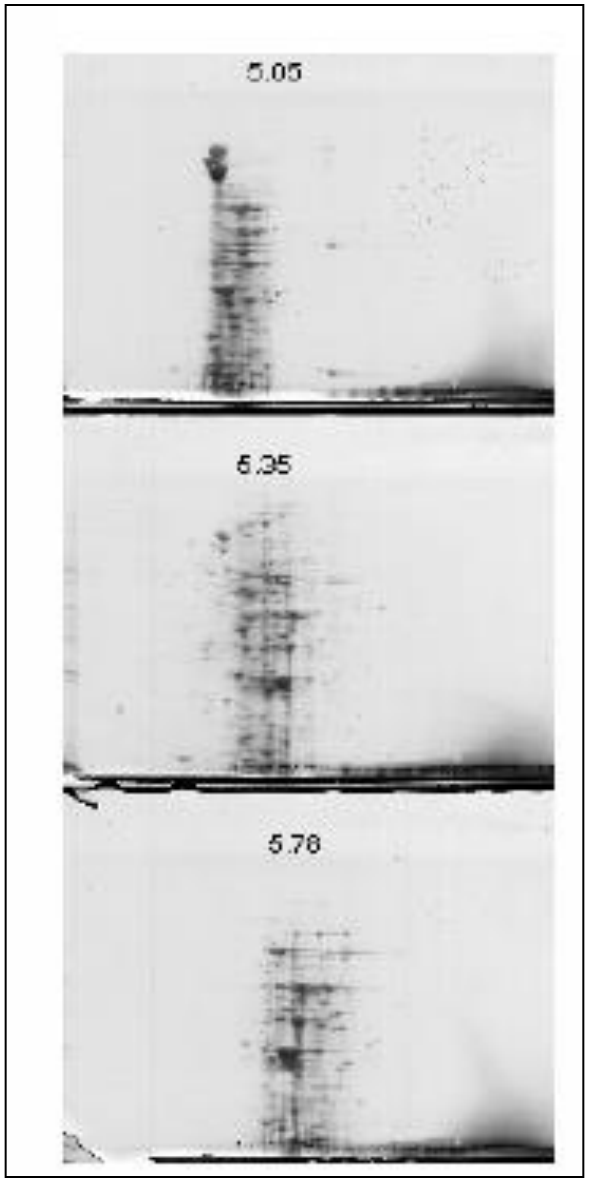


Kasap M, 2005)

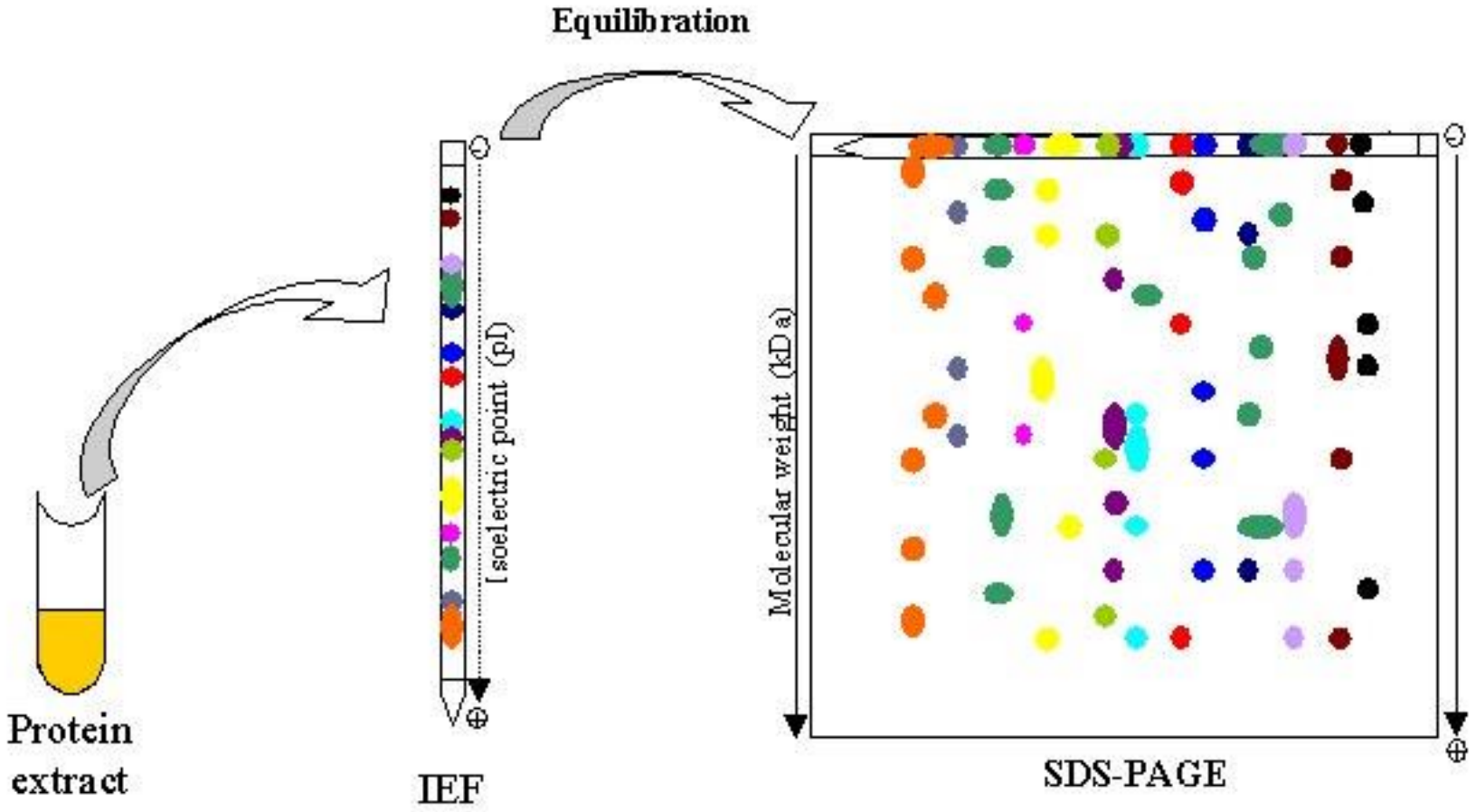
Rotofor- Preparative IEF system



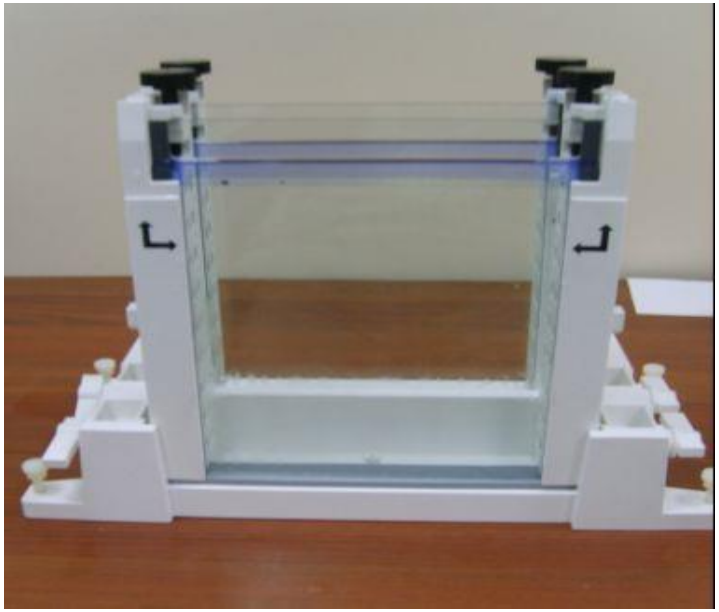




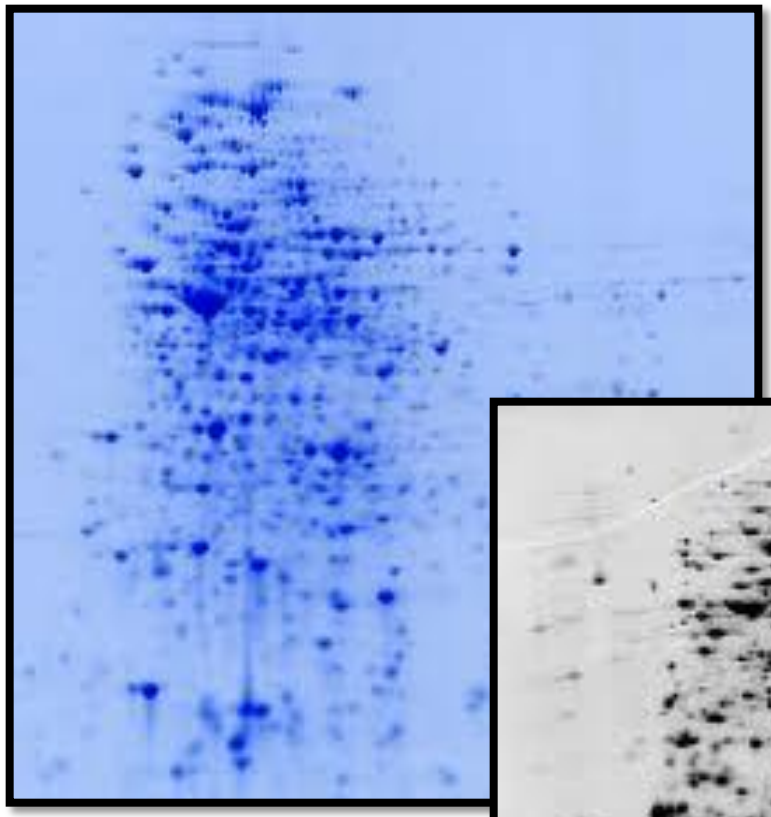
ADIM 2. Proteinlerin Ayrıştırılması



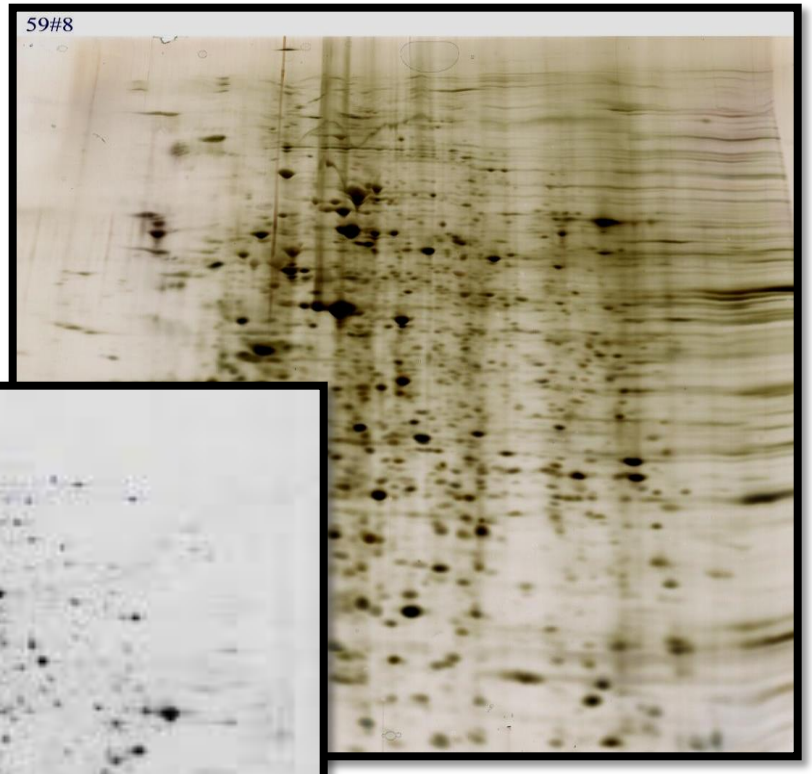

BIO-RAD
PROTEAN IEF Cell



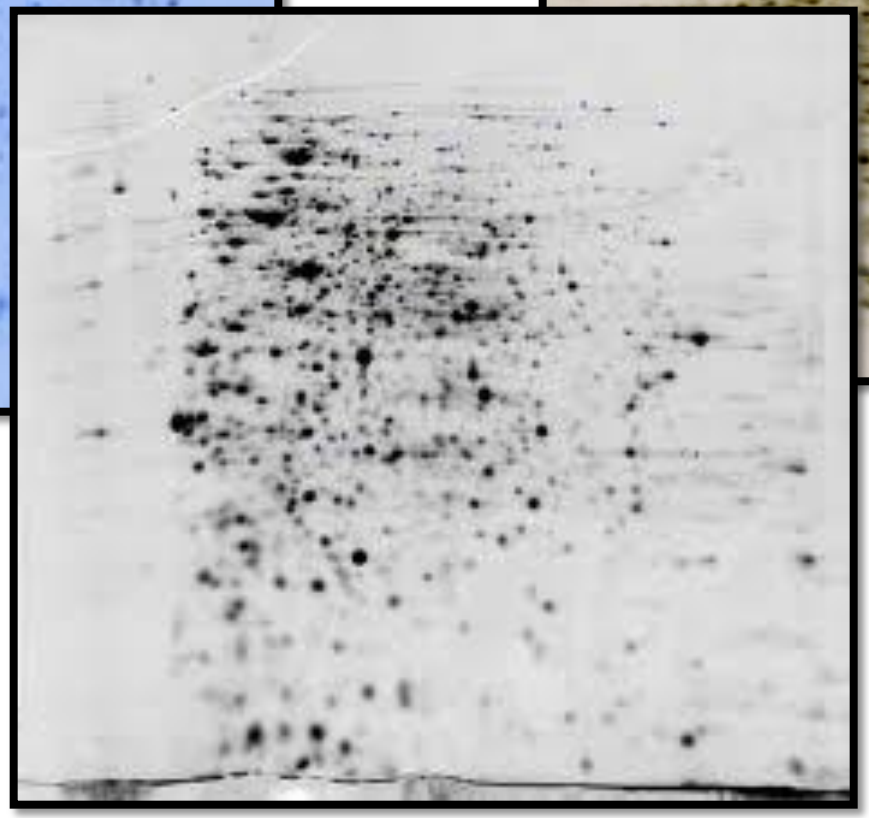
ADIM 3. Jellerin Boyanması



Colloidal
Coomassie Mavisi

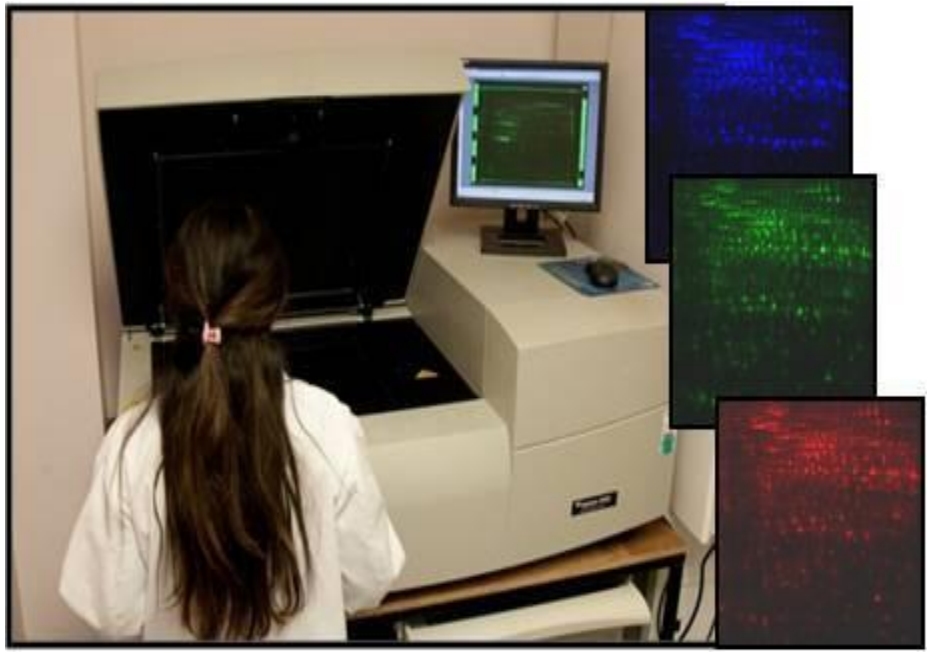


Gümüş Boyama



Sypro Ruby

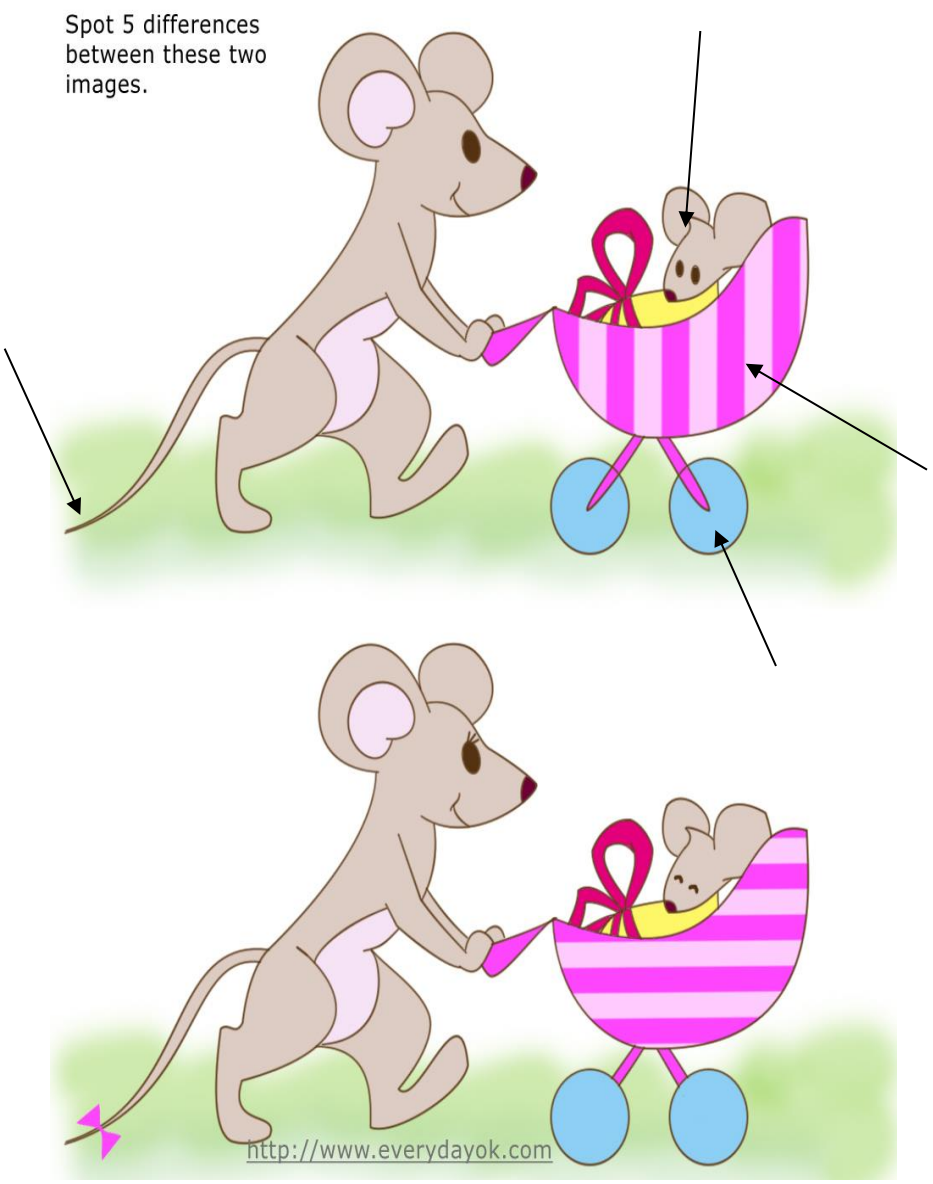
ADIM 4. Jellerin Görüntülenmesi

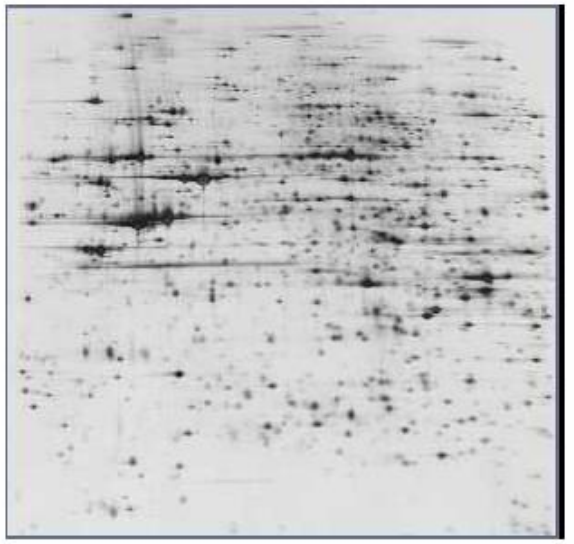


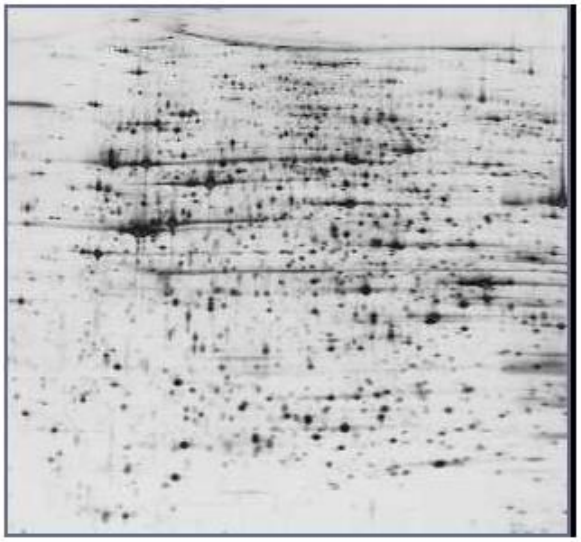
Scanner Tipi İmagerlar

Kameralı Sistemler

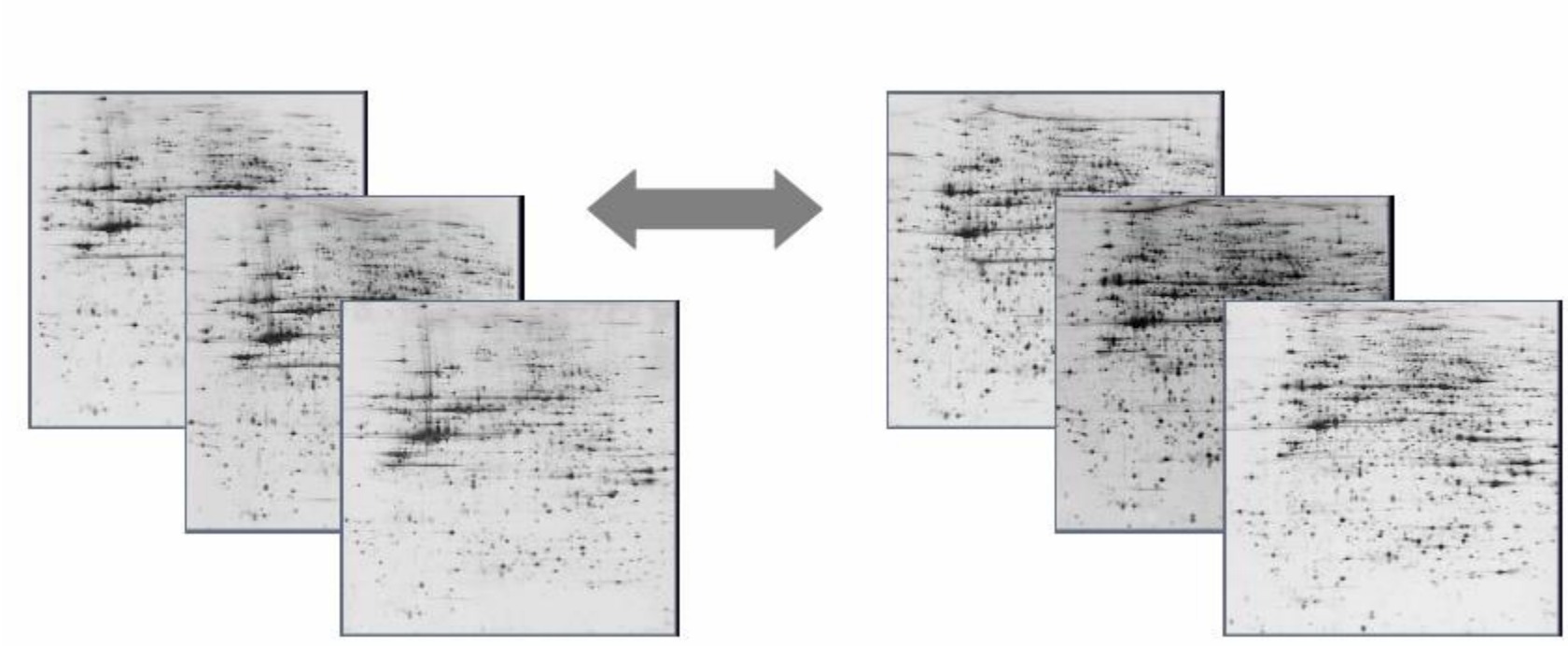
ADIM 5. JELLERİN ANALİZLERİNİN YAPILMASI



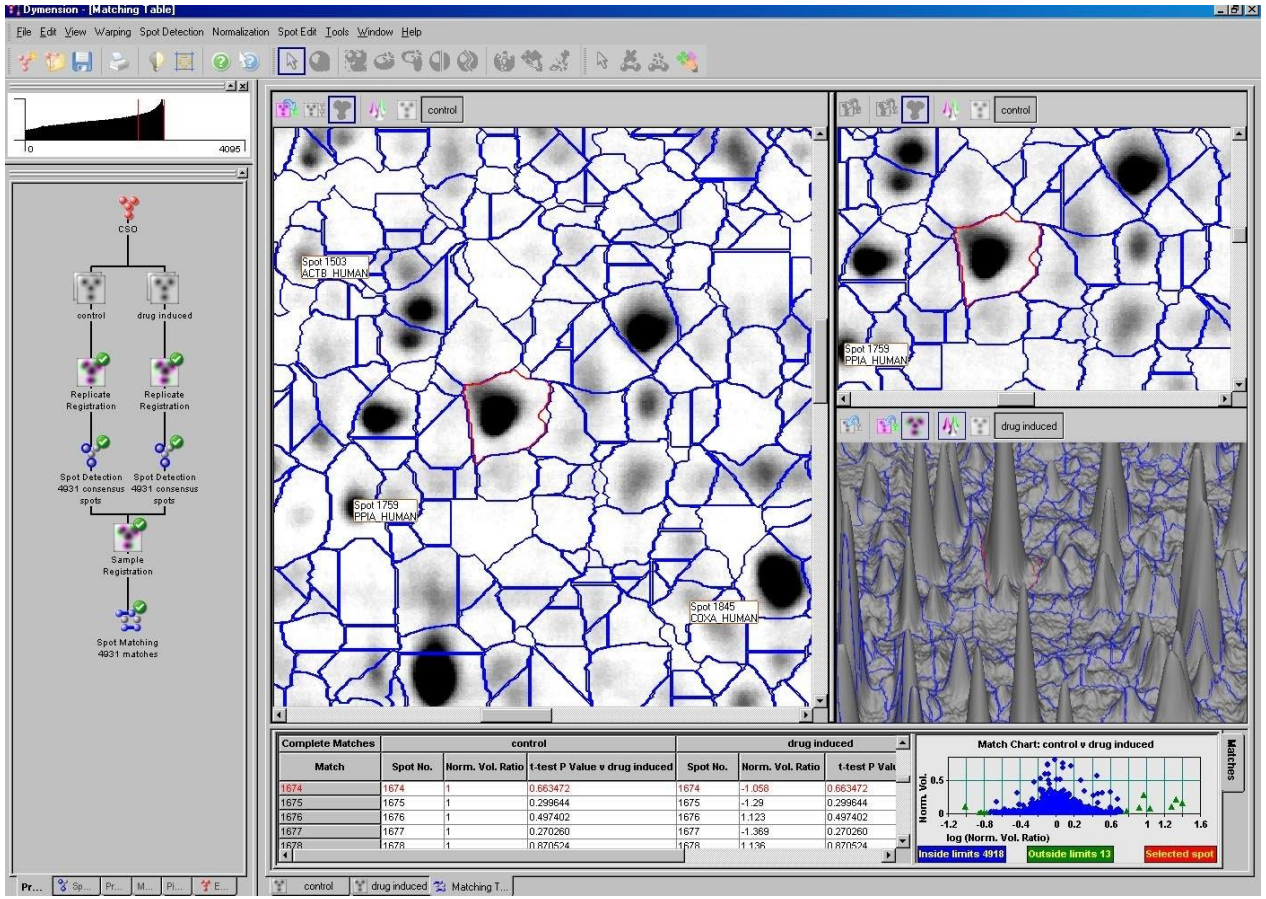




Analiz edilecek jel sayısı artacak olursa durum daha da karmaşık olacaktır.



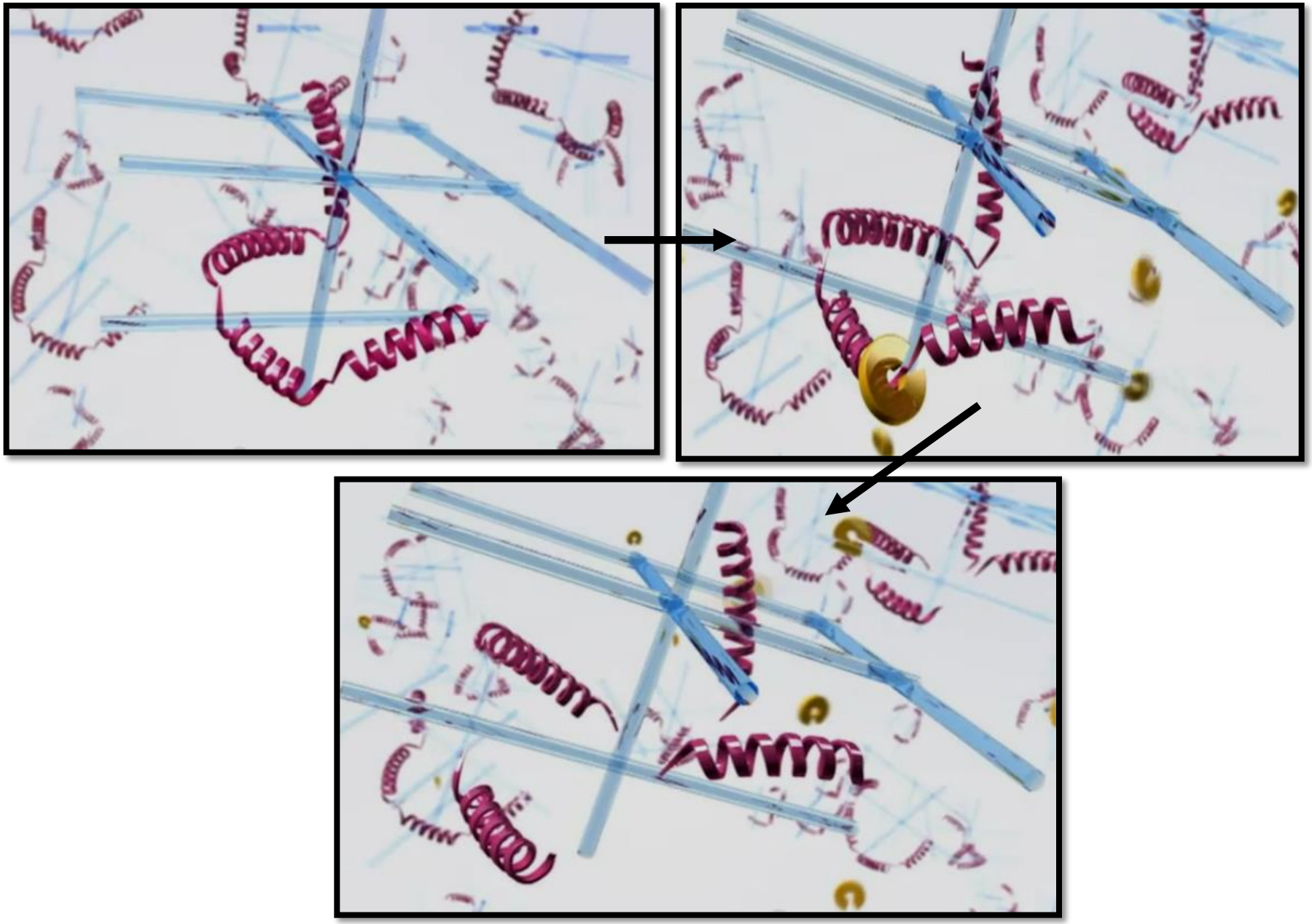
Görüntü analiz yazılımı



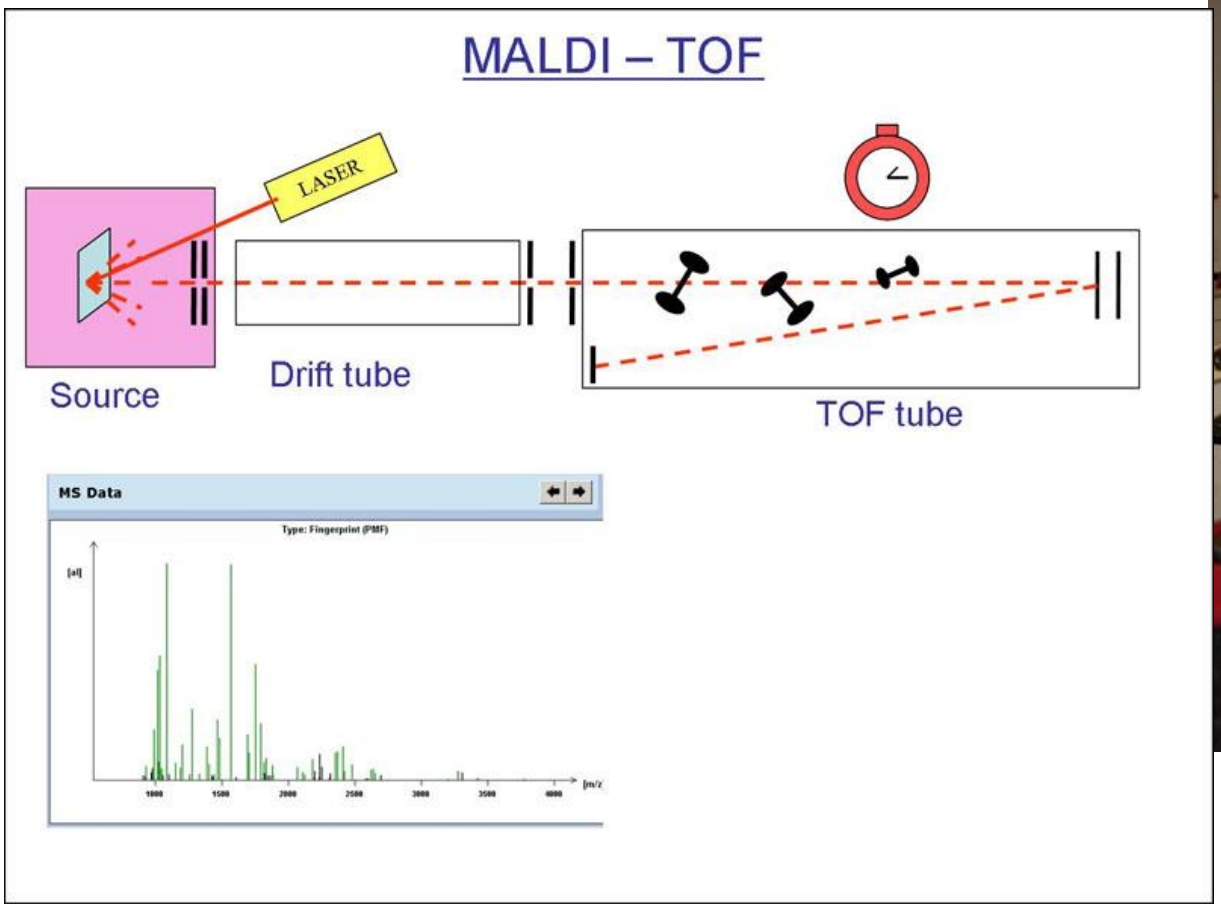
PD-Quest Advance
Melanie
Same Spot
DeCyder
……

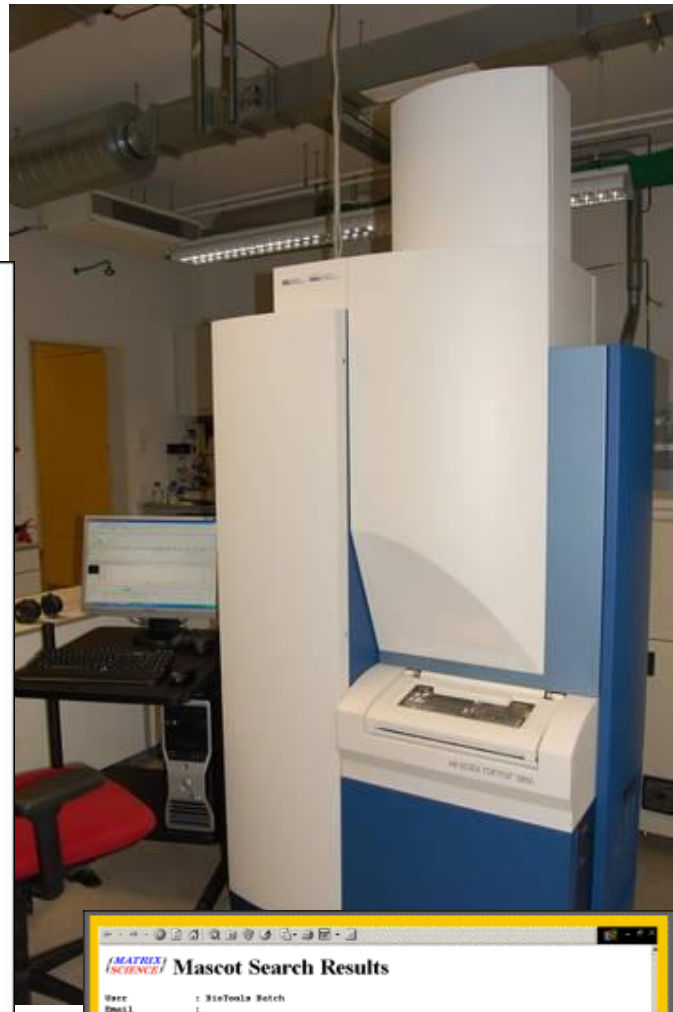
ADIM 6. SPOTLARI KESMEK

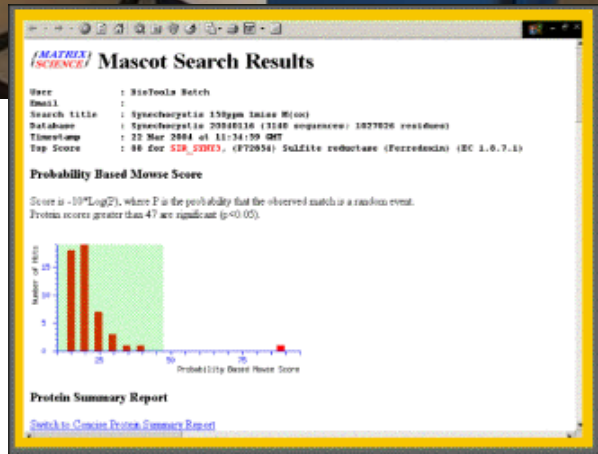
ADIM 7. In-Gel Trypsin Kesimi



ADIM 8. MASS SPEC/MALDI/SELDI vb. ve DATA analizi

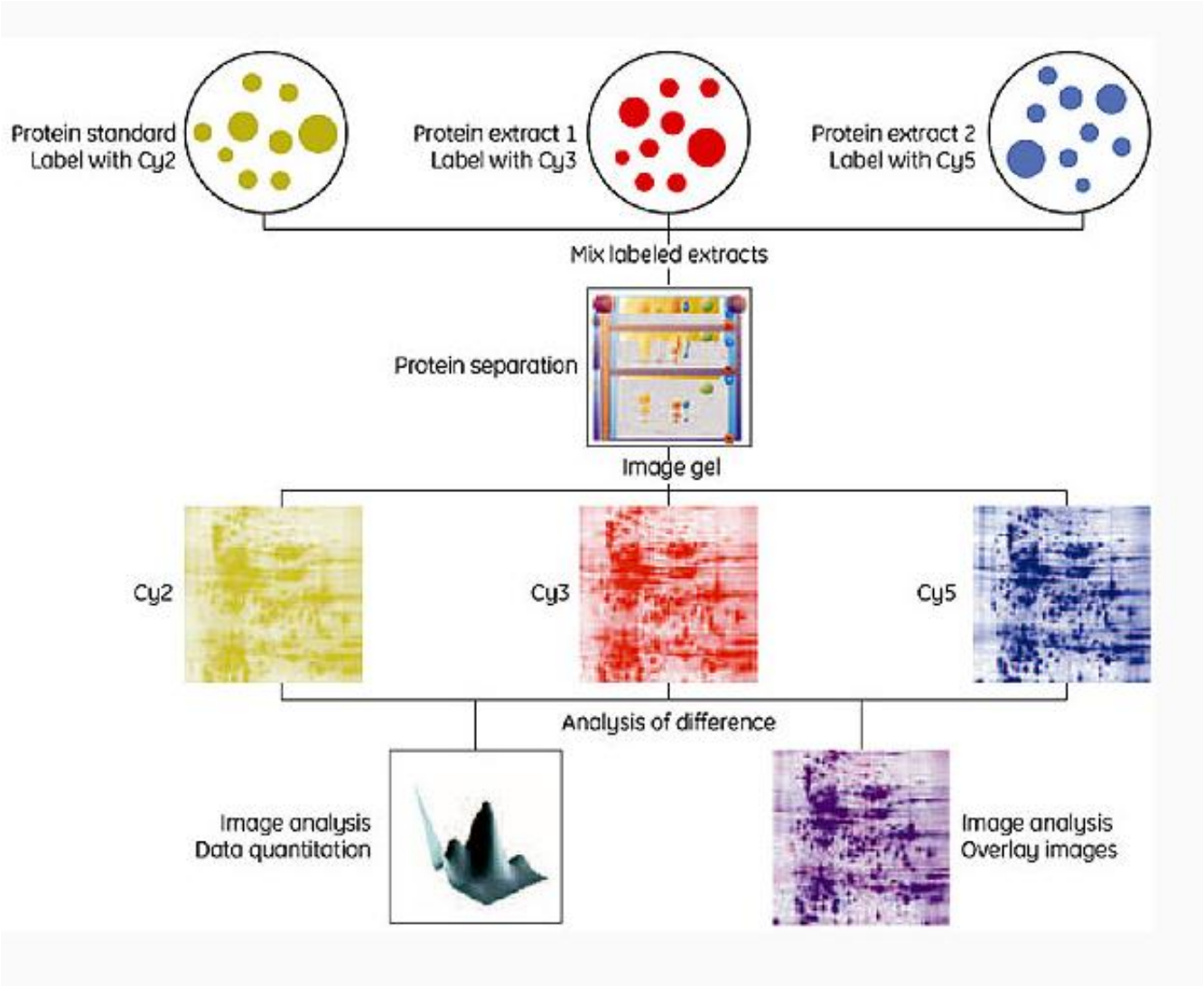






DIGE çalışması için yapılan Deneysel Kurulum

DIGE (Difference Gel Electrophoresis) sistemi



Örnek Çalışma 1

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Linking a compound-heterozygous Parkin mutant (Q311R and A371T) to Parkinson's disease by using proteomic and molecular approaches

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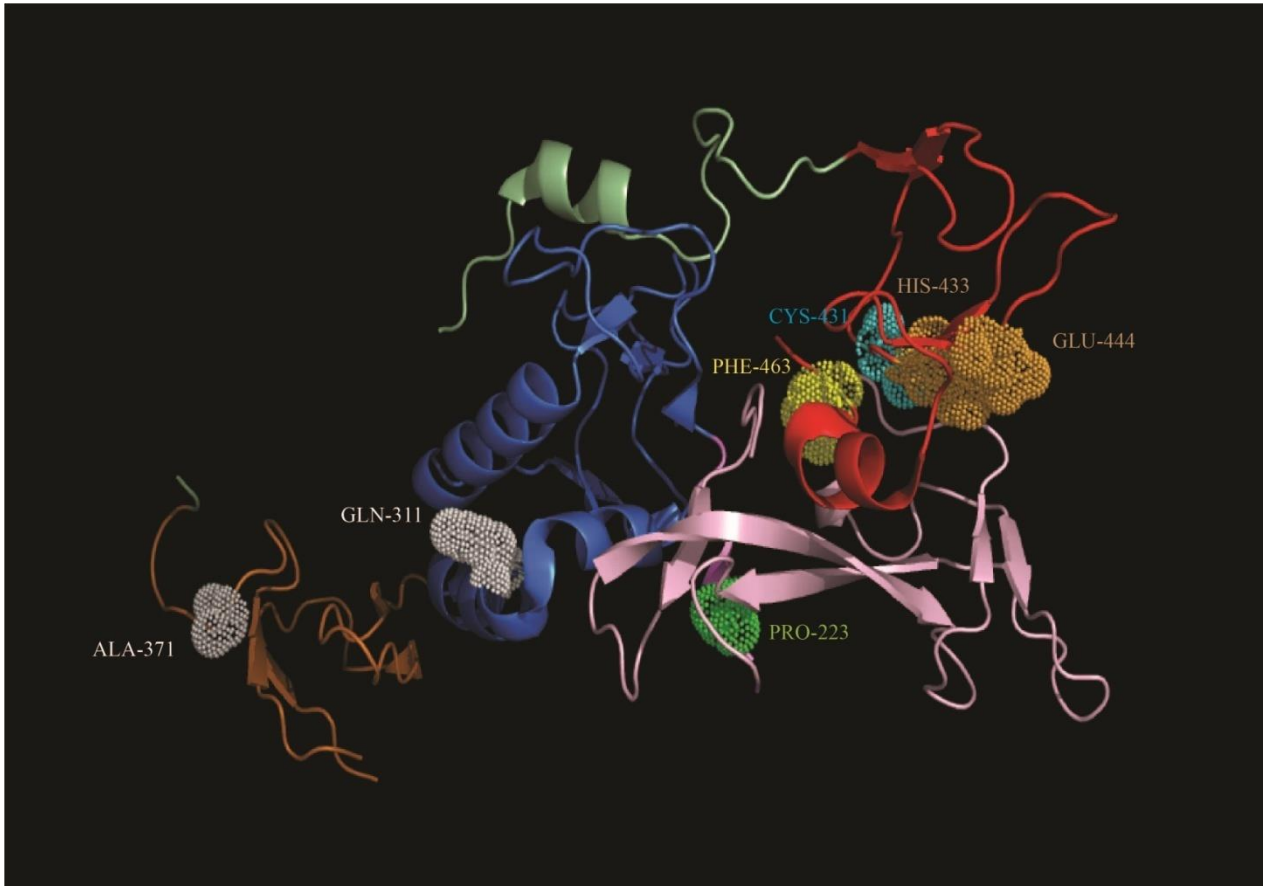
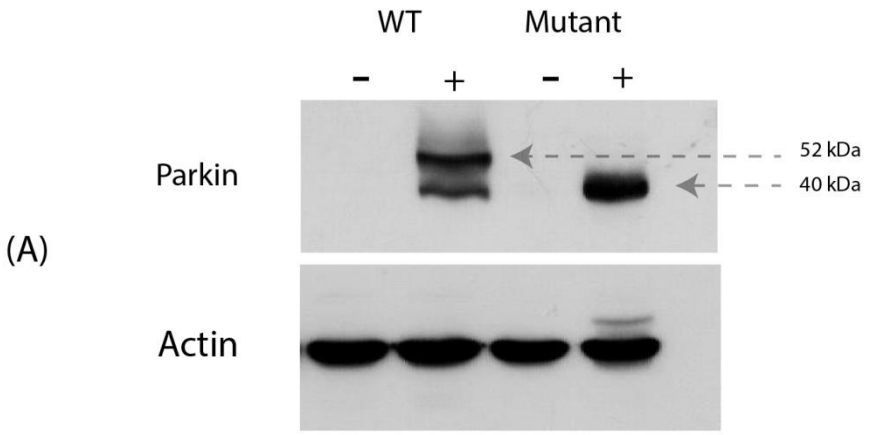
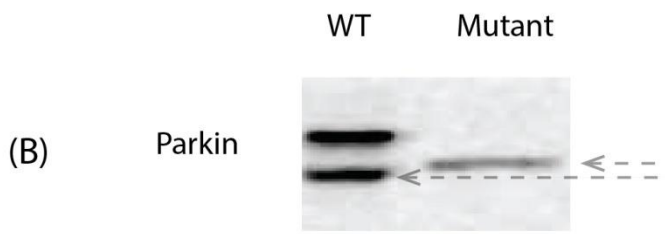
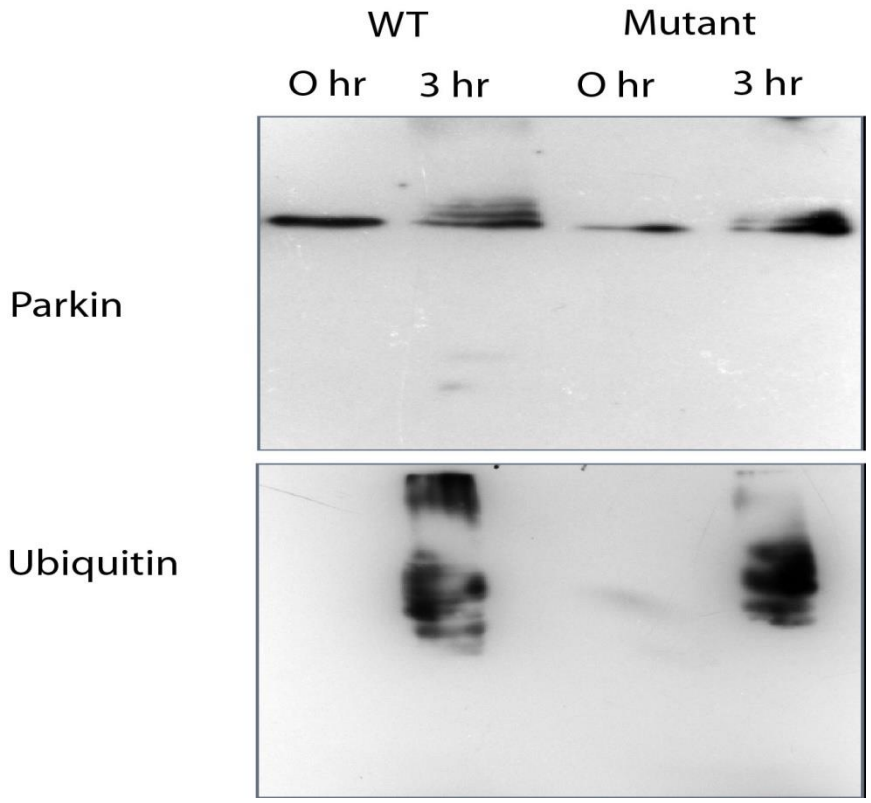
ABSTRACT

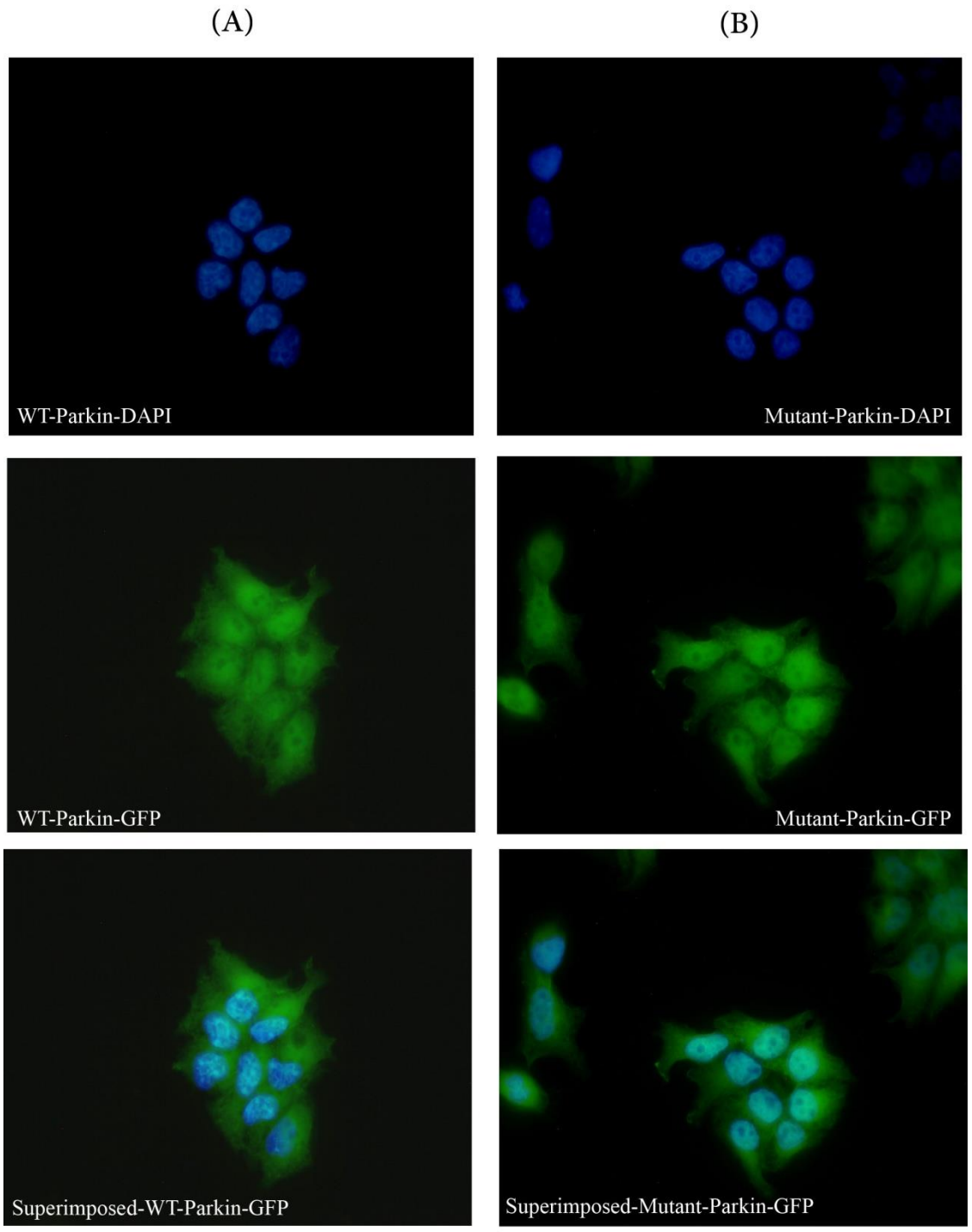
Parkin is an E3-protein ubiquitin ligase, which plays an important role as a scavenger in cell metabolism. Since the discovery of the link between Parkin and Parkinson's disease, Parkin was placed in the center of Parkinson's disease research. Previously, we isolated a mutant form of the Parkin protein (Q311R

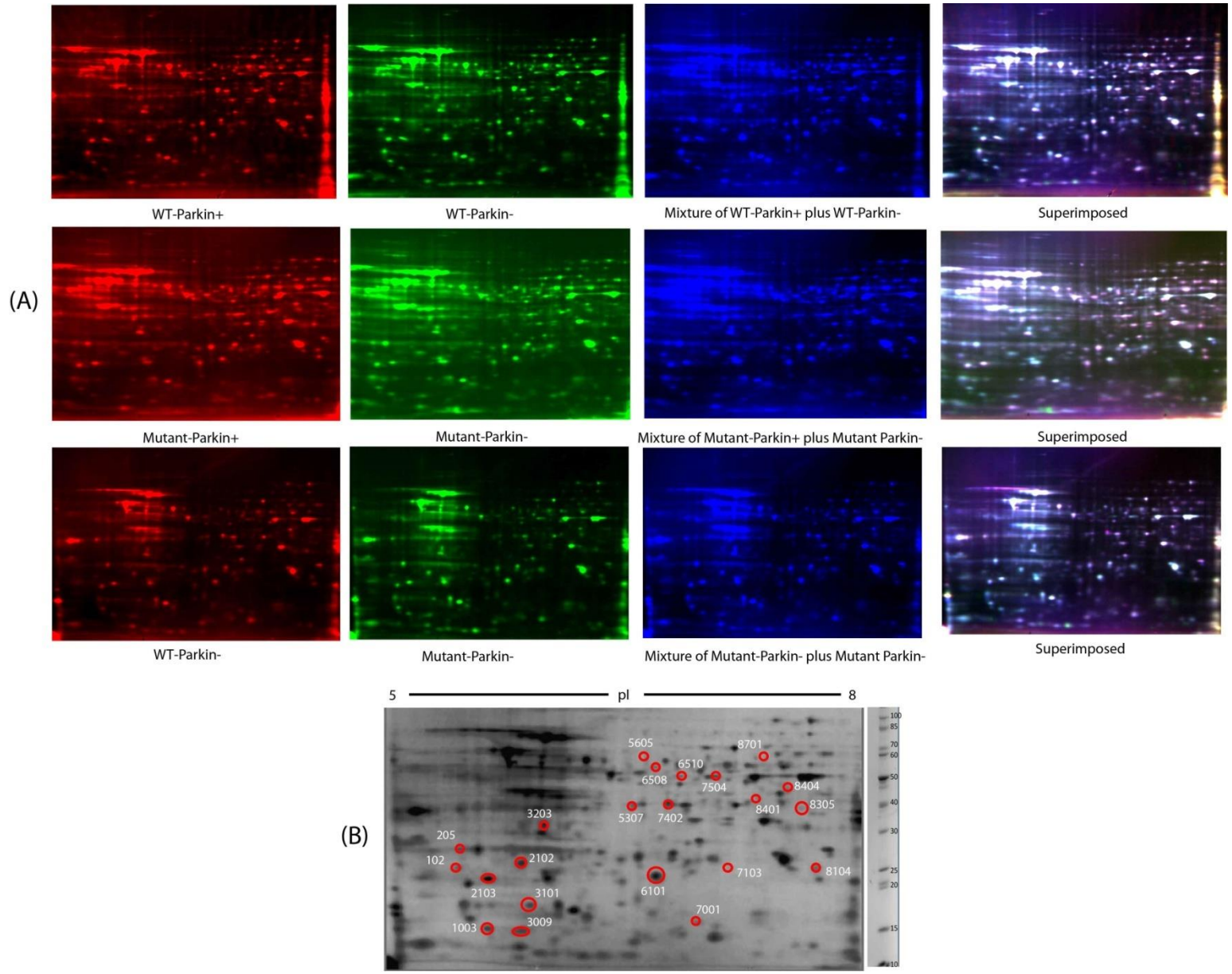

HIS-433
CYS-431
GLU-444
PHE-463
GLN-311
PRO-223
ALA-371


WT
Mutant
-
+
-
+
Parkin
52 kDa
40 kDa
(A)
Actin


WT
Mutant
(B)
Parkin


WT
Mutant
O hr
3 hr
O hr
3 hr
Parkin
Ubiquitin


(A)
(B)
WT-Parkin-DAPI
Mutant-Parkin-DAPI
WT-Parkin-GFP
Mutant-Parkin-GFP
Superimposed-WT-Parkin-GFP
Superimposed-Mutant-Parkin-GFP


(A)
WT-Parkin+
WT-Parkin-
Mixture of WT-Parkin+ plus WT-Parkin-
Superimposed
Mutant-Parkin+
Mutant-Parkin-
Mixture of Mutant-Parkin+ plus Mutant Parkin-
Superimposed
WT-Parkin-
Mutant-Parkin-
Mixture of Mutant-Parkin- plus Mutant Parkin-
Superimposed
(B)
5
pI
8
5605
8701
6510
6508
7504
8404
8401
8305
5307
7402
3203
205
102
2102
7103
8104
2103
3101
6101
7001
3009
1003

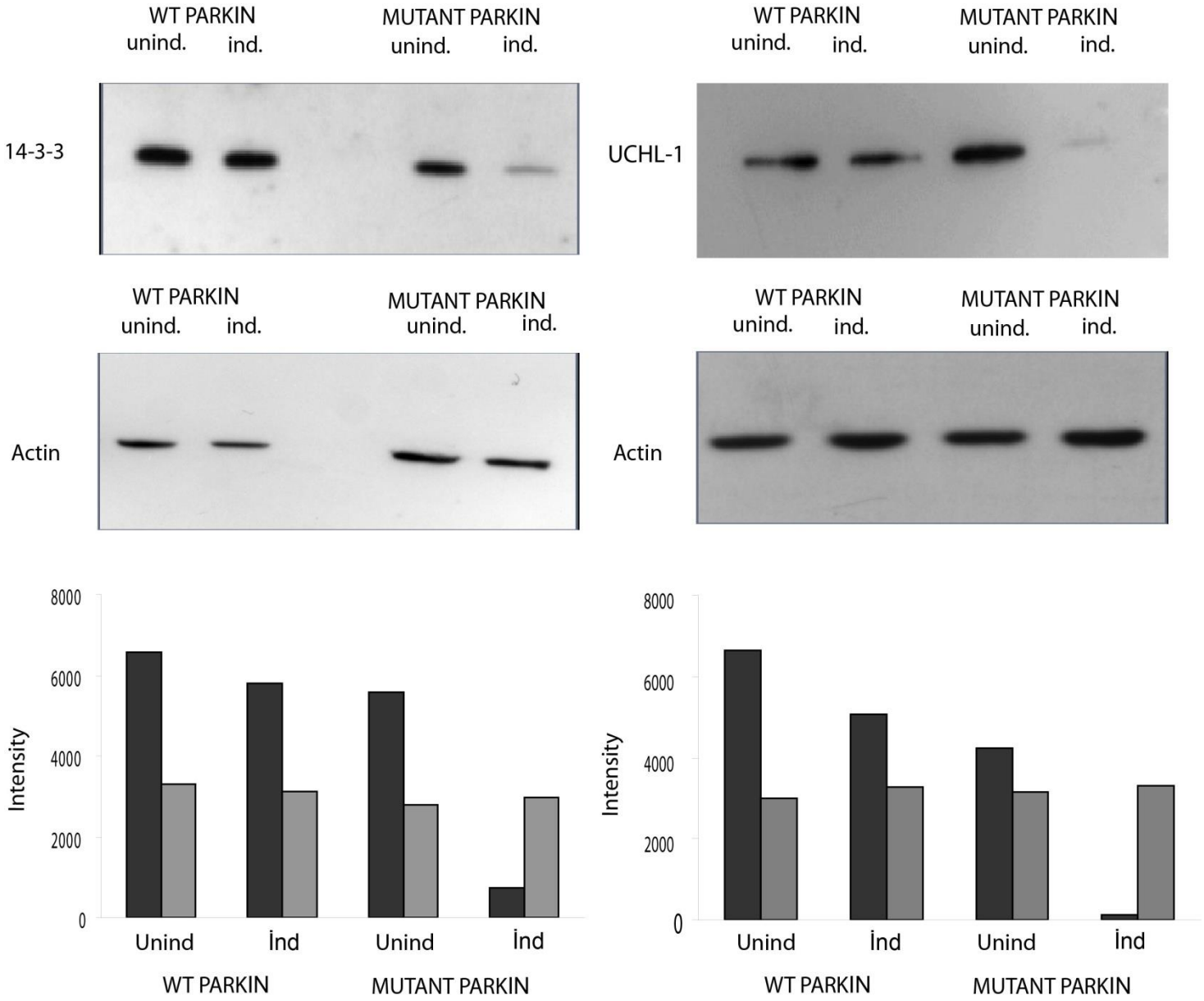
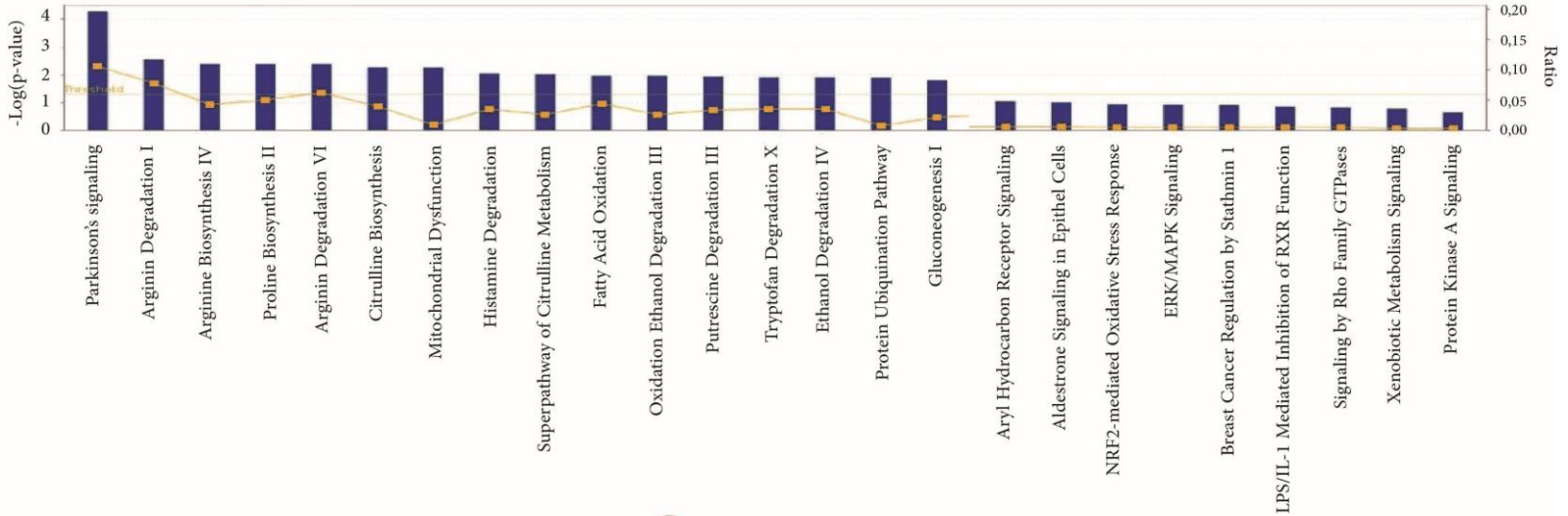

WT PARKIN
unind.
ind.
MUTANT PARKIN
unind.
ind.
14-3-3
UCHL-1
Actin
Actin
8000
6000
4000
2000
0
Intensity
Unind
İnd
Unind
İnd
WT PARKIN
MUTANT PARKIN

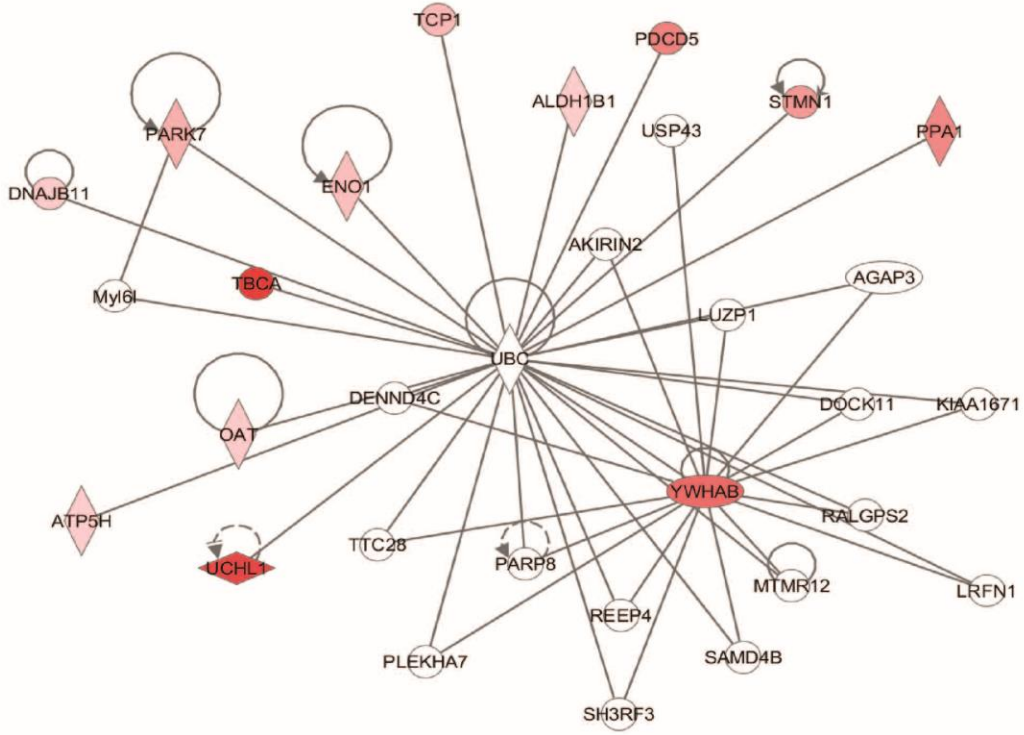
Table 2. Proteins that were differentially expressed in the mutant Parkin expressing SH-SY5Y cells. Classification of the proteins based on molecular function, biological process and cellular localization was performed by using PANTHER (http://www.pantherdb.org/) and Swiss-Prot annotations. (http://www.expasy.org/).

SSP	Gene Name	Protein Name	Swiss-Prot #	Regulated In	Molecular Function	Biological Process	Cellular Localization	Fold of Change	p Value
3009	PDCD5	Programmed cell death protein 5	O14737	Up-regulated in Mutant Parkin + cells	May function in the process of apoptosis	Apoptosis	Cytoplasmic/Nuclear	5.4	0.001
1003	TBCA	Tubulin-Specific chaperon A	O75347	Up-regulated in Mutant Parkin + cells	Involved in early step of the tubulin folding pathway	Protein folding	Cytoplasmic	9.2	0.050
7504	ENO1	Alpha-enolase	P06733	Up-regulated in Mutant Parkin+ cells	Plays a part in various processes including glycolysis, growth control, hypoxia tolerance and allergic responses	Energy metabolism	Cytoplasm Nuclear	2.7	0.015
2102	UCHL1	Ubiquitin carboxyl-terminal hydrolase isozyme L1	P09936	Down-regulated in Mutant Parkin+ cells	Involves in the processing of ubiquitin precursors and ubiquitinated proteins	Protein degradation	Cytoplasm ER-membrane	8.5	0.013

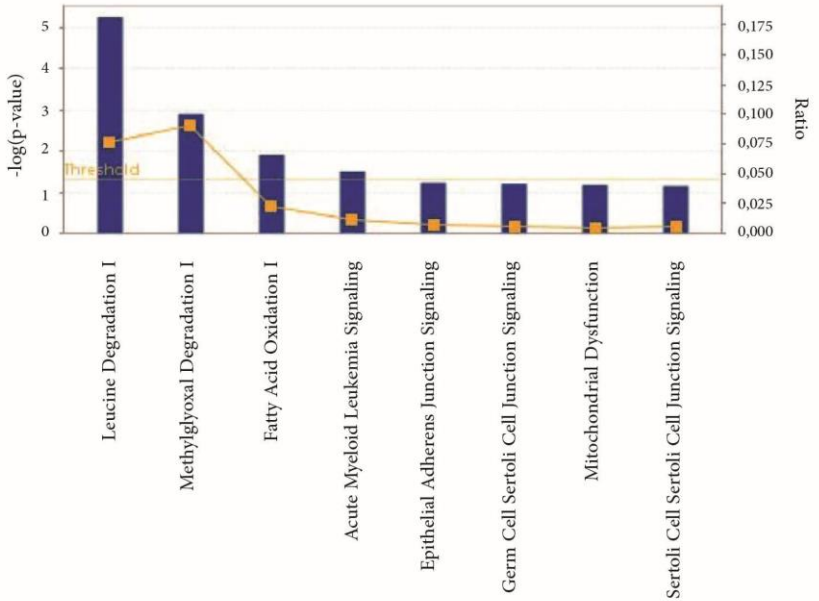
(A)


-Log(p-value)
Ratio
Parkinson's signaling
Arginin Degradation I
Arginine Biosynthesis IV
Proline Biosynthesis II
Arginin Degradation VI
Citrulline Biosynthesis
Mitochondrial Dysfunction
Histamine Degradation
Superpathway of Citrulline Metabolism
Fatty Acid Oxidation
Oxidation Ethanol Degradation III
Putrescine Degradation III
Tryptofan Degradation X
Ethanol Degradation IV
Protein Ubiquination Pathway
Gluconeogenesis I
Aryl Hydrocarbon Receptor Signaling
Aldestrone Signaling in Epithel Cells
NRF2-mediated Oxidative Stress Response
ERK/MAPK Signaling
Breast Cancer Regulation by Stathmin 1
LPS/IL-1 Mediated Inhibition of RXR Function
Signaling by Rho Family GTPases
Xenobiotic Metabolism Signaling
Protein Kinase A Signaling

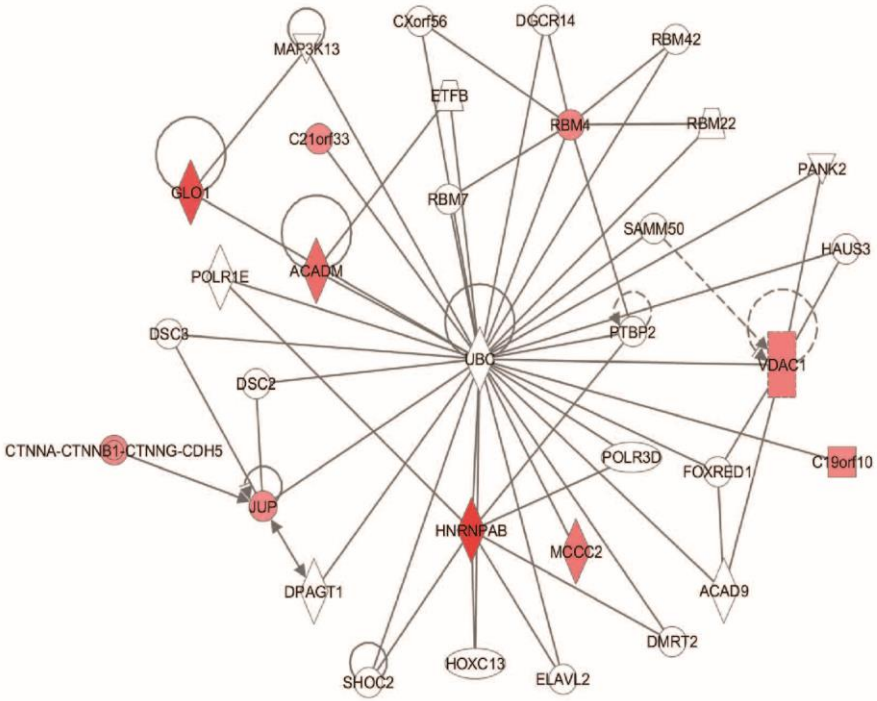
(B)


TCP1
PDCD5
ALDH1B1
STMN1
PARK7
USP43
PPA1
ENO1
DNAJB11
AKIRIN2
AGAP3
TBCA
Myl6l
LUZP1
UBC
DENND4C
DOCK11
KIAA1671
OAT
YWHAB
ATP5H
RALGPS2
TTC28
UCHL1
PARP8
MTMR12
LRFN1
REEP4
PLEKHA7
SAMD4B
SH3RF3

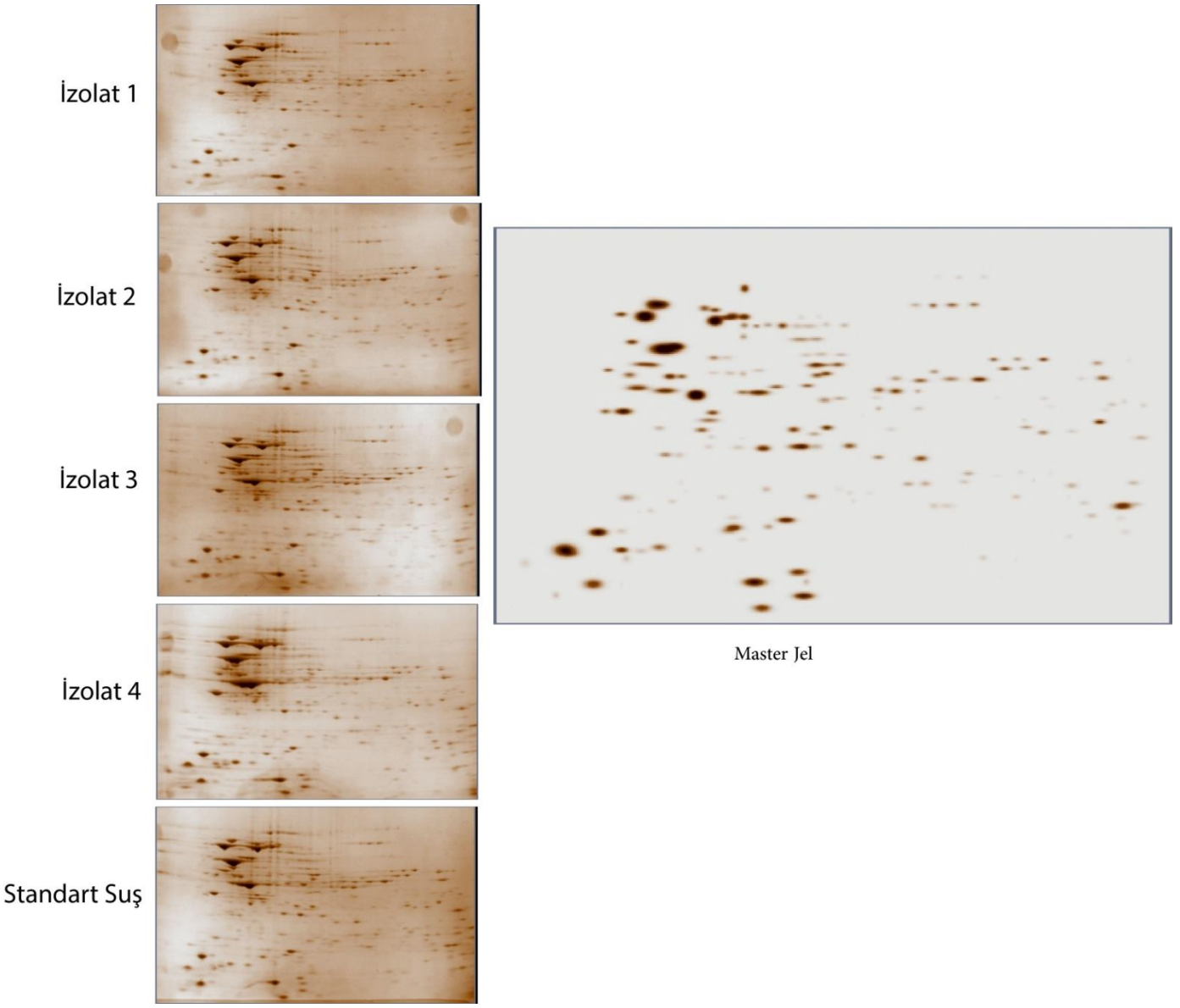
(A)


-log(p-value)
Ratio
Threshold
0
1
2
3
4
5
0,000
0,025
0,050
0,075
0,100
0,125
0,150
0,175
Leucine Degradation I
Methylglyoxal Degradation I
Fatty Acid Oxidation I
Acute Myeloid Leukemia Signaling
Epithelial Adherens Junction Signaling
Germ Cell Sertoli Cell Junction Signaling
Mitochondrial Dysfunction
Sertoli Cell Sertoli Cell Junction Signaling

(B)


MAP3K13
CXorf56
DGCR14
RBM42
ETFB
RBM4
RBM22
C21orf33
GLO1
RBM7
PANK2
SAMM50
HAUS3
ACADM
POLR1E
PTBP2
DSC3
UBC
VDAC1
DSC2
CTNNA-CTNNB1-CTNNG-CDH5
POLR3D
FOXRED1
C19orf10
JUP
HNRNPAB
MCCC2
DPAGT1
ACAD9
DMRT2
SHOC2
HOXC13
ELAVL2

Örnek Çalışma 2



Regule Olan Proteinlerin Tanımlamalarını Yaptık

Spot ID	Result list no.	AC no.	Best Protein Acc.	Best Protein Mass	Best Protein Score	Expect	Matches	Calc. pI	Seq. Cov. (%)	Best Protein Description
J5 - E5501	1	Q14JD8	SYE_FRAT1	52920	443	1.60E-39	21	5.42	31	Glutamyl-tRNA synthetase OS=Francisella tularensis subsp. tularensis (strain FSC 198)
J6 - E8302	1	Q14FQ1	RECA_FRAT1	38809	84	0.0012	15	5.97	26	Protein recA OS=Francisella tularensis subsp. tularensis (strain FSC 198)
J7 - F0801	1	Q6D0B7	DNAK_ERWCT	68907	96	7.90E-05	5	4.83	6	Chaperone protein dnaK OS=Erwinia carotovora subsp. atroseptica
J8 - F4502	1		WP_003018129.1	48817	278	2.90E-24	19	5.29	34	UDP-N-acetyl-D-galactosamine dehydrogenase [Francisella tularensis]
	8		WP_003014275.1	52974	177	3.70E-14	13	5.36	26	glutamate--tRNA ligase [Francisella tularensis]
	11		WP_003035331.1	52867	177	3.70E-14	13	5.49	26	glutaminyl-tRNA synthetase [Francisella tularensis]
J9 - F7212	1	A7NAH6	GCST_FRATF	39491	537	6.40E-49	29	5.73	57	Aminomethyltransferase OS=Francisella tularensis subsp. holarctica (strain FTNF002-00 / FTA)
J10 - NCTC0012	1		WP_003014087.1	13720	140	1.80E-10	13	8.67	53	membrane protein [Francisella tularensis]
	4		WP_003016883.1	10353	135	5.80E-10	8	10.13	59	30S ribosomal protein S15 [Francisella tularensis]
	10		YP_170667.1	13732	118	2.90E-08	11	8.67	43	hypothetical protein FTT_1778c [Francisella tularensis subsp. tularensis SCHU S4]
J11 - NCTC0105	1		WP_003014194.1	20890	185	5.80E-15	11	4.82	35	elongation factor P [Francisella tularensis]
	4		WP_003021600.1	22539	104	7.30E-07	7	9.67	17	50S ribosomal protein L4 [Francisella tularensis]
J12 - NCTC4203	1	Q14JD1	EFTS_FRAT1	30968	104	1.30E-05	4	5.57	14	Elongation factor Ts OS=Francisella tularensis subsp. tularensis (strain FSC 198)
J13 - NCTC5501	1	A7N9Q8	SYE_FRATF	52974	262	2.00E-21	18	5.36	32	Glutamyl-tRNA synthetase OS=Francisella tularensis subsp. holarctica (strain FTNF002-00 / FTA)
J14 - NCTC8201	1	Q5LLT1	RS15_SILPO	10247	54	2.5	8	10.05	78	30S ribosomal protein S15 OS=Silicibacter pomeroyi
	2	Q14JD2	RS2_FRAT1	26453	48	5.6	13	8.48	42	30S ribosomal protein S2 OS=Francisella tularensis subsp. tularensis (strain FSC 198)
	4	B3E3X0	Y658_GEOLS	16890	47	6	10	5.39	57	UPF0178 protein Glov_0658 OS=Geobacter lovleyi (strain ATCC BAA-1151 / DSM 17278 / SZ)

Örnek Çalışma 3

Research Article

Phenotypic and Proteomic Characteristics of Human Dental Pulp Derived Mesenchymal Stem Cells from a Natal, an Exfoliated Deciduous, and an Impacted Third Molar Tooth

Gurler Akpinar,[1] Murat Kasap,[1,2] Ayca Aksoy,[3] Gokhan Duruksu,[3] Gulcin Gacar,[3] and Erdal Karaoz[3,4]

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[3] *Department of Stem Cell, Center for Stem Cell and Gene Therapies Research and Practice, Institute of Health Sciences, Umuttepe, 41380 Kocaeli, Turkey*
[4] *Liv Hospital, Center for Regenerative Medicine and Stem Cell Research & Manufacturing (Liv MedCell), Besiktas, 34340 Istanbul, Turkey*

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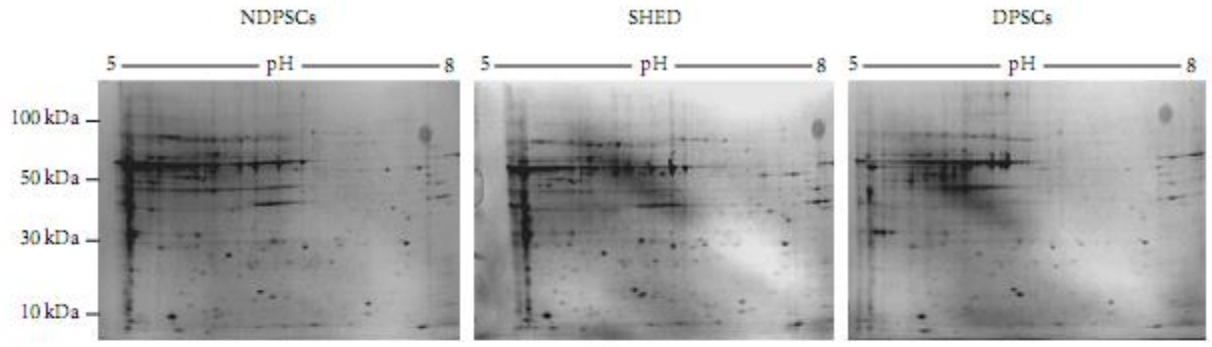
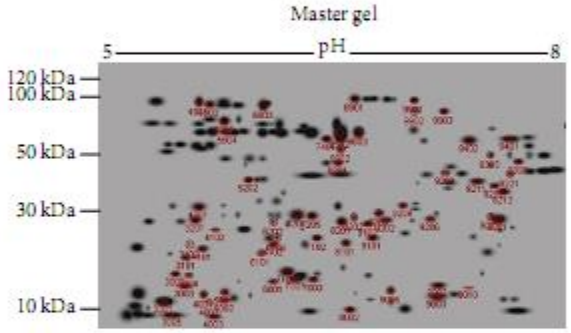
Academic Editor: Pavla Jendelova

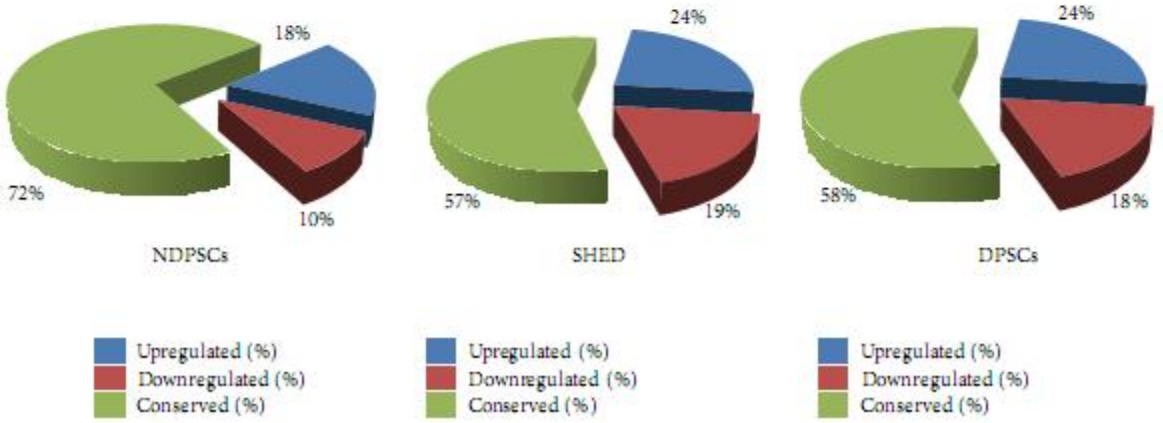
The level of heterogeneity among the isolated stem cells makes them less valuable for clinical use. The purpose of this study was to understand the level of heterogeneity among human dental pulp derived mesenchymal stem cells by using basic cell biology and proteomic approaches. The cells were isolated from a natal (NDPSCs), an exfoliated deciduous (stem cells from human exfoliated deciduous (SHED)), and an impacted third molar (DPSCs) tooth of three different donors. All three stem cells displayed similar features related to morphology, proliferation rates, expression of various cell surface markers, and differentiation potentials into adipocytes, osteocytes, and chondrocytes. Furthermore, using 2DE approach coupled with MALDI-TOF/TOF, we have generated a common 2DE profile for all three stem cells. We found that 62.3 ± 7% of the protein spots were conserved among the three mesenchymal stem cell lines. Sixty-one of these conserved spots were identified by MALDI-TOF/TOF analysis. Classification of the identified proteins based on biological function revealed that structurally important proteins and proteins that are involved in protein folding machinery are predominantly expressed by all three stem cell lines. Some of these proteins may hold importance in understanding specific properties of human dental pulp derived mesenchymal stem cells.


NDPSCs
SHED
DPSCs
5
pH
8
100 kDa
50 kDa
30 kDa
10 kDa

(a)


Master gel
5
pH
8
120 kDa
100 kDa
50 kDa
30 kDa
10 kDa

(b)


18%
72%
10%
24%
57%
19%
24%
58%
18%
NDPSCs
SHED
DPSCs
Upregulated (%)
Downregulated (%)
Conserved (%)

(c)

Teşekkürler

Tıbbi Biyoloji AD

Yard. Doç. Dr. Gürler Akpınar

Yard. Doç. Dr. Aylin Kanlı

Kübra Karaosmanoğlu

Nil Güzel