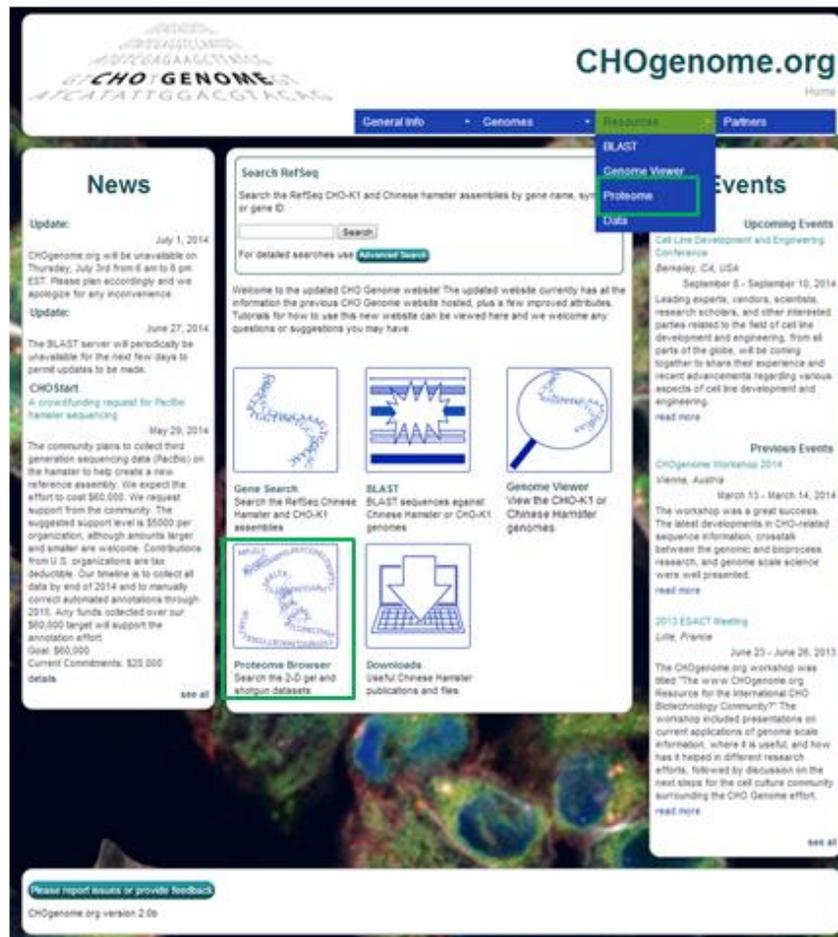


Tutorial 6 – Searching the Proteome Database

The Chinese hamster proteome database can be reached by selecting the “Proteome” resource from the menu bar or by selecting the “Proteome Browser” button from the homepage.



The address for the Chinese hamster proteome database is

<http://www.CHOgenome.org/proteome.php>.

The proteome database provides access to the proteomic data generated from CHO cell lines. This database hosts protein data from 2D polyacrylamide gel electrophoresis (2D PAGE) gels and shotgun proteomics analysis.

To have your data included, please contact us at chogenome@dbi.udel.edu.

2D PAGE Database

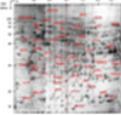
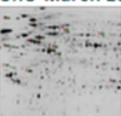
The 2D PAGE database is accessed by selecting the 2D PAGE Results button.



The webpage has the complete list of 2D gels available for public search with a small image of the gel and the publication information, if it has been published.

CHO 2D PAGE Gels

Please select a gel to view experimental details and spot information.

1. CHO-K1 reference map, Electrophoresis (2004) 25, 2545

2. CHO-March 2012 Example (not published)

3. CHO-July 2012 Example (not published)


Selecting an image leads to a much larger image of the gel with a link to the reference (if applicable).

CHO-K1 reference map

Click on a quadrant to view proteins.

ELECTROPHORESIS

Research Article

A two-dimensional electrophoresis map of Chinese hamster ovary cell proteins based on fluorescence staining

Eric J. Hayduk, Leila H. Choe and Kelvin H. Lee*

Article first published online: 2 AUG 2004
DOI: 10.1002/elps.200406010
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Additional Information (Show All)

[How to Cite](#) | [Author Information](#) | [Publication History](#)

ELECTROPHORESIS
Special Issue: Paper
Symposium Imaging and
Detection Technologies in
Electrophoresis
Volume 25, Issue 15, pages
2545-2556, No. 15 August
2004

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Experimental Details

CHO-K1 cells were grown in Ham's F12 medium supplemented with 10% fetal bovine serum.

Samples were separated on a 3-10 linear pH gradient and 12%T polyacrylamide gel. Gels were stained with SYPRO Ruby and MALDI-TOF/TOF was used to identify spots.

Reference

Electrophoresis (2004) 25, 2545

Selecting a quadrant (if the total number of identified proteins is large) leads to a table of the identified proteins, a labeled 2D gel, and links to the NCBI protein and the CHO Genome gene pages.

CHO-K1 reference map - Quadrant 2 Proteins

Spots information

Symbol	Identification	NCBI Protein Accession
act	Actin (Beta Or Gamma)	g095951
act	Actin (Beta Or Gamma)	s02902621
act	Actin (Beta Or Gamma)	gi17620
adprh	ADP-Ribosylarginine Hydrolase	g039055
arbp	Acidic Ribosomal Protein P0	gi12054503
arbp	Acidic Ribosomal Protein P0	gi17158
arbp	Acidic Ribosomal Protein P0	gi11803170
atp5b	ATP Synthase Beta Subunit	gi1374715

ATP synthase beta subunit, partial [Rattus norvegicus]

GenBank: AAB02288.1

FASTA [Statistics](#)

Seq. Id. [Seq. Id.](#)

LOCUS AAB02288 675 aa linear ROD 12-020-1594

DEFINITION ATP synthase beta subunit, partial [Rattus norvegicus].

ACCESSION AAB02288

VERSION AAB02288.1 gi1374715

DBSOURCE locus: AAB02288 accession: K02316.1

Advanced Search Page

Search Term:

Search at least one

- Symbol: CHO-K1 (RefSeq Assembly GCF_000223151.1.2May2014 - Release 101)
- Gene Name: Chinese Hamster (RefSeq Assembly GCF_000113561.1.2May2014 - Release 101)
- Gene ID: CHO-K1 (RefSeq Assembly GCF_000223151.1.1May2012 - Release 1)

Search Results for atp5b

2 Results Found

#	Assembly	Type	Symbol	GeneID	Product Description
1	CHO-K1 (2014)	mRNA	Atp5b	100783024	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide, transcript variant X1
2	Chinese Hamster (2014)	mRNA	Atp5b	100783024	ATP synthase, H+ transporting, mitochondrial F1 complex, beta polypeptide, transcript variant X2

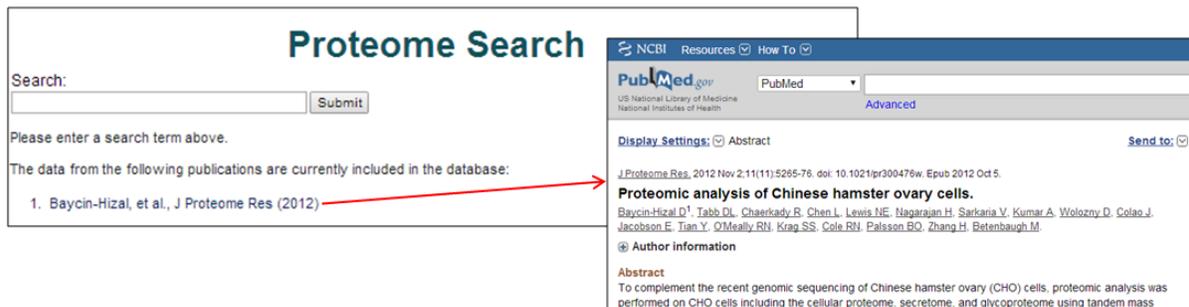
No Results Found for CHO-K1 (2012)

Shotgun Proteomics Database

The shotgun proteomics database is accessed by selecting the Shotgun Results button.



The shotgun proteomics database consists of the protein sets submitted to the CHO genome website. The publication for each dataset (if applicable) is listed following the description of each dataset. The link connects to the Publications page on the CHO genome website, which contains the links for the relevant publications.



The shotgun proteome database is searchable by protein name. The results page consists of all matches from the selected datasets. The protein name and accession identification are provided for each result.

Selection of the accession identification yields the specific details from the identification. These details can consist of the protein name, accession ID, the peptide sequences that were identified, the number of identified sequences, coverage, FDR, and other experiment specific details of possible relevance, including the cluster ID, group ID, SwissProt Annotation Homology, GO annotation, and Sequence ID.

Proteome Search

Search:

2 matches found.

Protein Name	Accession
PREDICTED: cofilin-1-like [Croceolus griseus]	gi 354479736 ref XP_003502065.1
PREDICTED: cofilin-1-like [Croceolus griseus]	gi 354501786 ref XP_003512909.1

The data from the following publications are currently included in the database:

1. Baycin-Hizal, et al., J Proteome Res (2012)

View Proteome Details

Protein Name	PREDICTED: cofilin-1-like [Croceolus griseus]
Accession ID	gi 354479736 ref XP_003502065.1
Identified Peptide Sequences	M11YASSKDAIQK(1+15.9949); MIYASSKDAIQK
Num. Identified Sequences	3
Num. Identified Spectra	48
FDR	0.01902346
Coverage	10
Cluster ID	267
Group ID	2241
SwissProt Annotation/Homology with Highest Percentage	COF1_HUMAN Cofilin-1 OS=Homo sapiens GN=CFL1 PE=1 SV=3
GO Annotation	GO:0003779; actin binding; Molecular Function:
KEGG Annotation	similar to Cofilin-1 (Cofilin, non-muscle isoform) (18 kDa phosphoprotein) (p18) ; K05765 cofilin
Sequence ID	1