



M1 SM THORAX ED TG: Recherche in silico.

Gilles Toumaniantz

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Team IIA

L'unité de recherche de l'institut du thorax
Inserm UMR 1087 / CNRS UMR 6291
Nantes, France

1. Les analyses bibliographiques

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Homologous genes sets for selected organisms

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Sequence sets from phylogenetic and population studies

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Protein sequences, 3-D structures, and tools for the study of functional protein domains and active sites

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Conserved protein domains

Identical Protein Groups

Protein sequences grouped by identity

Protein

Protein sequences

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Sequence similarity-based protein clusters

Protein Family Models

Models representing homologous proteins with a common function

Structure

Experimentally-determined biomolecular structures

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Genome sequence assemblies, large-scale functional genomics data, and source biological samples

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Genome assembly information

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Biological projects providing data to NCBI

BioSample

Descriptions of biological source materials

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Genome sequencing projects by organism

Nucleotide

DNA and RNA sequences

SRA

High-throughput sequence reads

Taxonomy

Taxonomic classification and nomenclature

BLAST

A tool to find regions of similarity between biological sequences

blastn

Search nucleotide sequence databases

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Search protein sequence databases

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Search protein databases using a translated nucleotide query

tblastn

Search translated nucleotide databases using a protein query

Primer-BLAST

Find primers specific to your PCR template

Clinical

Heritable DNA variations, associations with human pathologies, and clinical diagnostics and treatments

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Privately and publicly funded clinical studies conducted around the world

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Human variations of clinical significance

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Medical genetics literature and links

OMIM

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Molecular pathways with links to genes, proteins and chemicals

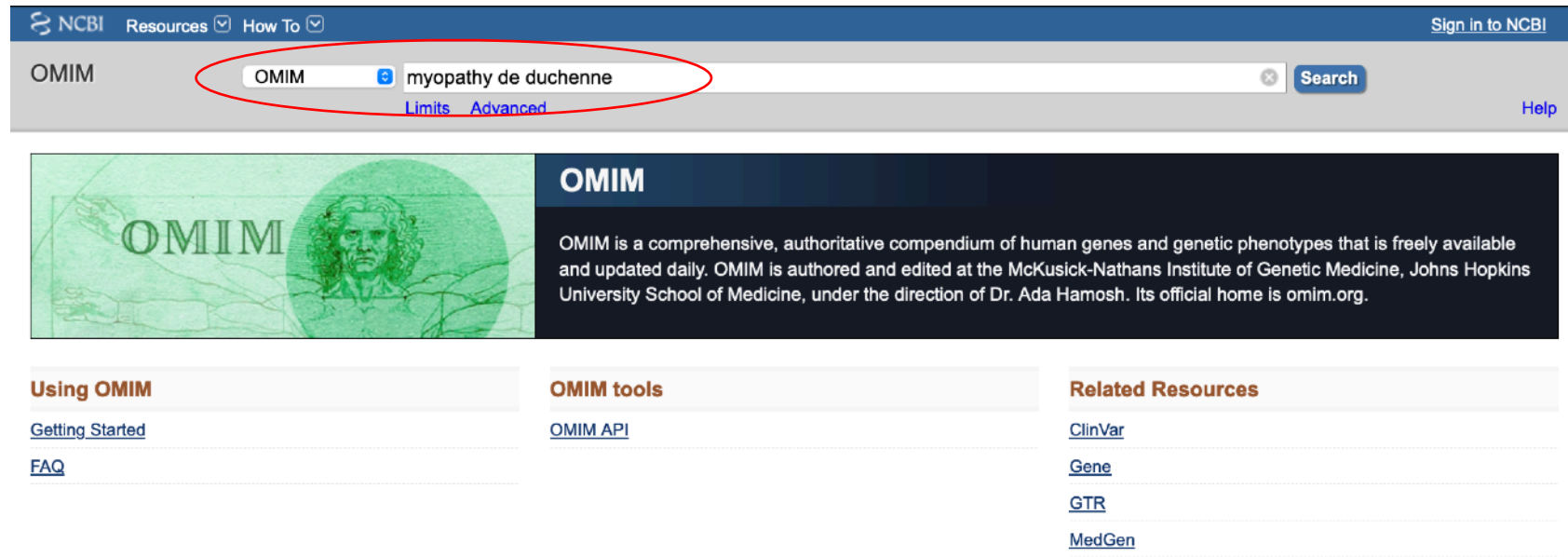
Substances

Deposited substance and chemical information

Le NCBI abrite une série de bases de données pertinentes pour la biotechnologie et la biomédecine et constitue une ressource importante pour les outils et services de bioinformatique.

OMIM : Le projet Héritage mendélien chez l'humain (en anglais : Mendelian Inheritance in Man) est une base de données originellement compilée par Victor A. McKusick et qui dresse un catalogue de toutes les maladies connues qui relèvent de l'un ou l'autre composant génétique et — si possible — les relie aux gènes adéquats au sein du génome humain. Cette base de données est disponible sous forme d'un livre appelé Mendelian Inheritance in Man (MIM), qui en est à sa 13e édition.

La version en ligne est appelée Online Mendelian Inheritance in Man, OMIM, et peut être consultée à partir de la base de données Entrez1 de la National Library of Medicine2.



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OMIM

OMIM is a comprehensive, authoritative compendium of human genes and genetic phenotypes that is freely available and updated daily. OMIM is authored and edited at the McKusick-Nathans Institute of Genetic Medicine, Johns Hopkins University School of Medicine, under the direction of Dr. Ada Hamosh. Its official home is omim.org.

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[#253700 - MUSCULAR DYSTROPHY, LIMB-GIRDLE, AUTOSOMAL RECESSIVE 5; LGMDR5](#)

1. Cytogenetic locations: 13q12.12

OMIM: 253700

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[#608099 - MUSCULAR DYSTROPHY, LIMB-GIRDLE, AUTOSOMAL RECESSIVE 3; LGMDR3](#)

2. Cytogenetic locations: 17q21.33

OMIM: 608099

[Gene summaries](#) [Genetic tests](#) [Medical literature](#)

[#310200 - MUSCULAR DYSTROPHY, DUCHENNE TYPE; DMD](#)

3. Cytogenetic locations: Xp21.2-p21.1

OMIM: 310200

[Gene summaries](#) [Genetic tests](#) [Medical literature](#)

[#158810 - BETHLEM MYOPATHY 1; BTHLM1](#)

4. Cytogenetic locations: 21q22.3, 1p36, 21q22.3

OMIM: 158810

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[#310400 - MYOPATHY, CENTRONUCLEAR, X-LINKED; CNMX](#)

5. Cytogenetic locations: Xq28

OMIM: 310400

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[#254130 - MIYOSHI MUSCULAR DYSTROPHY 1; MMD1](#)

6. Cytogenetic locations: 2p13.2

OMIM: 254130

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[#310440 - MYOPATHY, X-LINKED, WITH EXCESSIVE AUTOPHAGY; MEAX](#)

7. Cytogenetic locations: Xq28

OMIM: 310440

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[#300257 - DANON DISEASE](#)

8. Cytogenetic locations: Xq24

OMIM: 300257

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Database: Select

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myopathy[All Fields] AND de[All Fields] AND duchenne[All Fields]

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myopathy de duchenne (26)

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MUSCULAR DYSTROPHY, DUCHENNE TYPE; DMD

Alternative titles; symbols

DUCHENNE MUSCULAR DYSTROPHY

MUSCULAR DYSTROPHY, PSEUDOHYPERTROPHIC PROGRESSIVE, DUCHENNE TYPE

Phenotype-Gene Relationships

Location	Phenotype	Phenotype MIM number	Inheritance	Phenotype mapping key	Gene/Locus	Gene/Locus MIM number
Xp21.2-p21.1	Duchenne muscular dystrophy	310200	XLR	3	DMD	300377

Clinical Synopsis ▾

PheneGene Graphics ▾



▼ TEXT

A number sign (#) is used with this entry because Duchenne muscular dystrophy is caused by mutation in the gene encoding dystrophin (DMD; [300377](#)).

▼ Description

Dystrophin-associated muscular dystrophies range from the severe Duchenne muscular dystrophy (DMD) to the milder Becker muscular dystrophy (BMD; [300376](#)). Mapping and molecular genetic

ICD+

▼ External Links

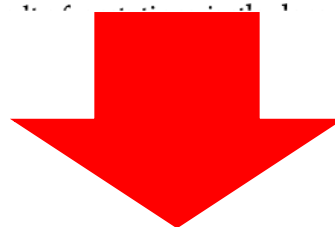
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▼ Description

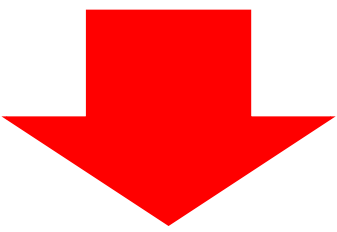
Dystrophin-associated muscular dystrophies range from the severe Duchenne muscular dystrophy (DMD) to the milder Becker muscular dystrophy (BMD; 300376). Mapping and molecular genetic studies indicate that both are the result of mutations in the huge gene that encodes dystrophin, also symbolized DMD. Approximately two-thirds of the mutations in both forms are deletions of one or many exons in the dystrophin gene. Although there is no clear correlation found between the extent of the deletion and the severity of the disorder, DMD deletions usually result in frameshift. Boland et al. (1996) studied a retrospective cohort of 33 male patients born between 1953 and 1983. The mean age at DMD diagnosis was 4.6 years; wheelchair dependency had a median age of 10 years; cardiac muscle failure developed in 15% of patients with a median age of 21.5 years; smooth muscle dysfunction in the digestive or urinary tract occurred in 21% and 6% of the patients, respectively, at a median age of 15 years. In this cohort, death occurred at a median age of 17 years. The authors commented that the diagnosis of DMD is being made at an earlier age but survival has not changed.



▼ Clinical Features

Skeletal Muscle

The most distinctive feature of Duchenne muscular dystrophy is a progressive proximal muscular dystrophy with characteristic pseudohypertrophy of the calves. The bulbar (extraocular) muscles are spared but the myocardium is affected. There is massive elevation of creatine kinase levels in the blood, myopathic changes by electromyography, and myofiber degeneration with fibrosis and fatty infiltration on muscle biopsy. The onset of Duchenne muscular dystrophy usually occurs before age 3 years, and the victim is chairridden by age 12 and dead by age 20. The onset of Becker muscular dystrophy is often in the 20s and 30s and survival to a relatively advanced age is frequent.



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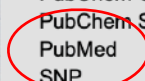
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1 [The relationship among fear and anxiety of COVID-19, pregnancy experience, and mental health disorder in pregnant women: A structural equation model.](#)

Cite Salehi L, Rahimzadeh M, Molaei E, Zaheri H, Esmaelzadeh-Saeieh S.

Brain Behav. 2020 Sep 23:e01835. doi: 10.1002/brb3.1835. Online ahead of print.

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The eligible individuals entered the study through convenience sampling, and data were collected using five questionnaires including the Fear of COVID-19 Scale, the Anxiety of COVID-19 Scale, the pregnancy experiences Scales, Depression Anxiety Stress ...

2 [How to restart the interventional activity in the COVID-19 era. The experience of a private Pain Unit in Spain.](#)

Cite Abejón González D, Monzón EM, Deer T, Hagedorn JM, Araujo R, Abad C, Rios A, Zamora A, Vallejo R.

Share Pain Pract. 2020 Sep 23. doi: 10.1111/papr.12951. Online ahead of print.

PMID: 32969188 Review.

The situation generated in the health system by the COVID-19 pandemic has provoked a crisis involving the necessity to cancel non-urgent and oncologic activity in the operating room and in day-to-day practice. ...We describe procedures to implement these recommendat ...

3 [Experiences of breastfeeding during COVID-19: Lessons for future practical and emotional support.](#)

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- 1 Occurrence and transmission potential of asymptomatic and presymptomatic SARS-CoV-2 infections: A living systematic review and meta-analysis.

Cite Buitrago-Garcia D, Egli-Gany D, Counotte MJ, Hossmann S, Imeri H, Ipekci AM, Salanti G, Low N. PLoS Med. 2020 Sep 22;17(9):e1003346. doi: 10.1371/journal.pmed.1003346. eCollection 2020 Sep.

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BACKGROUND: There is disagreement about the level of asymptomatic severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection. ... (2) Amongst people with SARS-CoV-2 infection who ...

- 2 Interaction between age and vitamin D deficiency in severe COVID-19 infection.

Cite Macaya F, Espejo Paeres C, Valls A, Fernández-Ortiz A, González Del Castillo J, Martín-Sánchez J, Runkle I, Rubio Herrera MÁ.

Share Nutr Hosp. 2020 Sep 22. doi: 10.20960/nh.03193. Online ahead of print.

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BACKGROUND: coronavirus disease 2019 (COVID-19) can induce an exaggerated inflammatory response. Vitamin D is a key modulator of the immune system. ... VDD tended to predict an increased risk of developing severe COVID-19 after adju ...

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eCollection 2020 Sep.

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Diana Buitrago-Garcia ^{1 2}, Dianne Egli-Gany ¹, Michel J Counotte ¹, Stefanie Hossmann ¹, Hira Imeri ¹, Aziz Mert Ipekci ¹, Georgia Salanti ¹, Nicola Low ¹

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Abstract

Background: There is disagreement about the level of asymptomatic severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection. We conducted a living systematic review and meta-analysis to address three questions: (1) Amongst people who become infected with SARS-CoV-2, what proportion does not experience symptoms at all during their infection? (2) Amongst people with SARS-CoV-2 infection who are asymptomatic when diagnosed, what proportion will

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Occurrence and transmission potential of asymptomatic and presymptomatic SARS-CoV-2 infections: A living systematic review and meta-analysis

Diana Buitrago-Garcia , Dianne Egli-Gany , Michel J. Counotte , Stefanie Hossmann, Hira Imeri, Aziz Mert Ipekci, Georgia Salanti, Nicola Low 

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- Abstract
- Author summary
- Introduction
- Methods
- Results

Abstract

Background

There is disagreement about the level of asymptomatic severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection. We conducted a living systematic review and meta-analysis to address three questions: (1) Amongst people who become infected with SARS-CoV-2, what proportion does not experience symptoms at all during their infection? (2)

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RESEARCH ARTICLE

Occurrence and transmission potential of asymptomatic and presymptomatic SARS-CoV-2 infections: A living systematic review and meta-analysis

Diana Buitrago-Garcia^{1,2,6}, Dianne Egli-Gany^{1,6}, Michel J. Counotte^{1,6}, Stefanie Hossmann¹, Hira Imeri¹, Aziz Mert Ipekci¹, Georgia Salanti¹, Nicola Low^{1*}

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Data Availability Statement: The file listing all included studies and files used for all analyses are available from the Harvard Dataverse database.

Abstract

Background

There is disagreement about the level of asymptomatic severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) infection. We conducted a living systematic review and meta-analysis to address three questions: (1) Amongst people who become infected with SARS-CoV-2, what proportion does not experience symptoms at all during their infection? (2) Amongst people with SARS-CoV-2 infection who are asymptomatic when diagnosed, what proportion will develop symptoms later? (3) What proportion of SARS-CoV-2 transmission is accounted for by people who are either asymptomatic throughout infection or presymptomatic?

Methods and findings

We searched PubMed, Embase, bioRxiv, and medRxiv using a database of SARS-CoV-2 literature that is updated daily, on 25 March 2020, 20 April 2020, and 10 June 2020. Studies of people with SARS-CoV-2 diagnosed by reverse transcriptase PCR (RT-PCR) that documented follow-up and symptom status at the beginning and end of follow-up or modelling studies were included. One reviewer extracted data and a second verified the extraction, with disagreement resolved by discussion or a third reviewer. Risk of bias in empirical studies was assessed with an adapted checklist for case series, and the relevance and credibility of modelling studies were assessed using a published checklist. We included a total of 94 studies. The overall estimate of the proportion of people who become infected with SARS-CoV-2 and remain asymptomatic throughout infection was 20% (95% confidence interval [CI] 17–25) with a prediction interval of 3%–67% in 79 studies that addressed this review question. There was some evidence that biases in the selection of participants influence the estimate. In seven studies of defined populations screened for SARS-CoV-2 and then

Table 1. Characteristics of studies reporting on proportion of asymptomatic SARS-CoV-2 infections.

Author	Country, location	Total SARS-CoV-2, n	Asymptomatic SARS-CoV-2, n	Sex of asymptomatic people	Age of asymptomatic people, years, median	Follow-up method ^a
Contact investigation, single						
Tong, ZD [44]	China, Zhejiang	5	3	2 F, 3 M	28 IQR 13–41	1, 3
Huang, R [74]	China, Saqian	2	1	1 F, 0 M	54	3
Jiang, XL [26]	China, Shandong	8	3	3 F, 0 M	35 IQR 0–53	3
Jiang, X [75]	China, Chongqing	3	1	1 F, 0 M	8	2
Liao, J [22]	China, Chongqing	12	3	NR	NR	1, 2
Hu, Z [21]	China, Nanjing	4	1	0 F, 1 M	64	2, 3
Luo, SH [23]	China, Anhui	4	1	1 F, 0 M	50	1, 2, 3
Chan, JF [18]	China, Guangdong	5	1	0 F, 1 M	10	1
Ye, F [40]	China, Sichuan	5	1	0 F, 1 M	28	1, 2
Bai, Y [17]	China, Anyang	6	1	1 F, 0 M	20	1
Luo, Y [85]	China, Wuhan	6	5	NR	37 IQR 7–62	1
Zhang, J [50]	China, Wuhan and Beijing	5	2	1 F, 1 M	NR	2
Zhang, B [110]	China, Guangdong	7	2	0 F, 2 M	13.5 IQR 13–14	3
Huang, L [73]	China, Gansu	7	2	2 F, 0 M	44 IQR 38.5–49.5	2
Qian, G [26]	China, Zhejiang	8	2	1 F, 1 M	30.5 IQR 1–60	1, 2
Gao, Y [70]	China, Wuxi	15	6	3 F, 3 M	50 IQR 48–51	1, 2
Contact investigation, aggregated						
Hijnen, D [72]	Germany	11	1	0 F, 1 M	49	1
Brandstetter, S [62]	Germany	36	2	NR	NR	2
Zhang, W2 [111]	China, Guiyang	12	4	NR	NR	1, 2, 3
Cheng, HY [66]	Taiwan	22	4	NR	NR	1
Wang, Z [17]	China, Wuhan	47	4	NR	NR	1
Wu, J [105]	China, Zhuhai	83	8	NR	NR	1, 2
Luo, L [16]	China, Guangzhou	129	8	NR	NR	1, 2, 3
Ri, Q [50]	China, Shenzhen	87	17	NR	NR	2, 3
Yang, R [108]	China, Wuhan	78	33	22 F, 11 M	37 IQR 26–45	3
Outbreak investigation						
Danis, K [32]	France	13	1	NR	NR	1, 2
Böhmer, MM [61]	Germany	16	1	NR	NR	1
Bozby, AC [94]	USA	6	3	NR	NR	1
Yang, N [48]	China, Xiaoshan	10	2	1 F, 1 M	NR	1, 2
Schwierzeck, V [95]	Germany	12	2	NR	NR	2
Arons, MM [58]	USA	47	3	NR	NR	2
Park, SY [90]	South Korea	19	4	NR	NR	2
Dora, AV [68]	USA	97	6	0 F, 6 M	75 IQR 72–75	3
Tian, S [43]	China, Shandong	24	7	NR	NR	3
Solbach, W [97]	Germany	97	10	NR	NR	2
Graham, N [21]	United Kingdom	126	46	NR	NR	2

(Continued)

Notion de sources et citations...

S7 Fig. Assessment of credibility of mathematical modelling studies. (PDF)

S1 Table. Types of study included in successive versions of the living systematic review, as of 10 June 2020. (DOCX)

S2 Table. Location of studies contributing data to review questions 1 and 2. (DOCX)

Author Contributions

Conceptualization: Diana Buitrago-Garcia, Dianne Egli-Gany, Nicola Low.

Data curation: Diana Buitrago-Garcia, Dianne Egli-Gany, Michel J. Counotte, Stefanie Hossmann, Hira Imeri, Nicola Low.

Formal analysis: Michel J. Counotte, Georgia Salanti.

Investigation: Aziz Mert Ipekci.

Methodology: Diana Buitrago-Garcia, Dianne Egli-Gany, Michel J. Counotte, Georgia Salanti, Nicola Low.

Project administration: Diana Buitrago-Garcia, Dianne Egli-Gany.

Supervision: Nicola Low.

Validation: Diana Buitrago-Garcia, Dianne Egli-Gany, Michel J. Counotte, Stefanie Hossmann, Hira Imeri, Aziz Mert Ipekci, Nicola Low.

Writing – original draft: Diana Buitrago-Garcia, Nicola Low.

Writing – review & editing: Diana Buitrago-Garcia, Dianne Egli-Gany, Michel J. Counotte, Stefanie Hossmann, Hira Imeri, Aziz Mert Ipekci, Georgia Salanti, Nicola Low.

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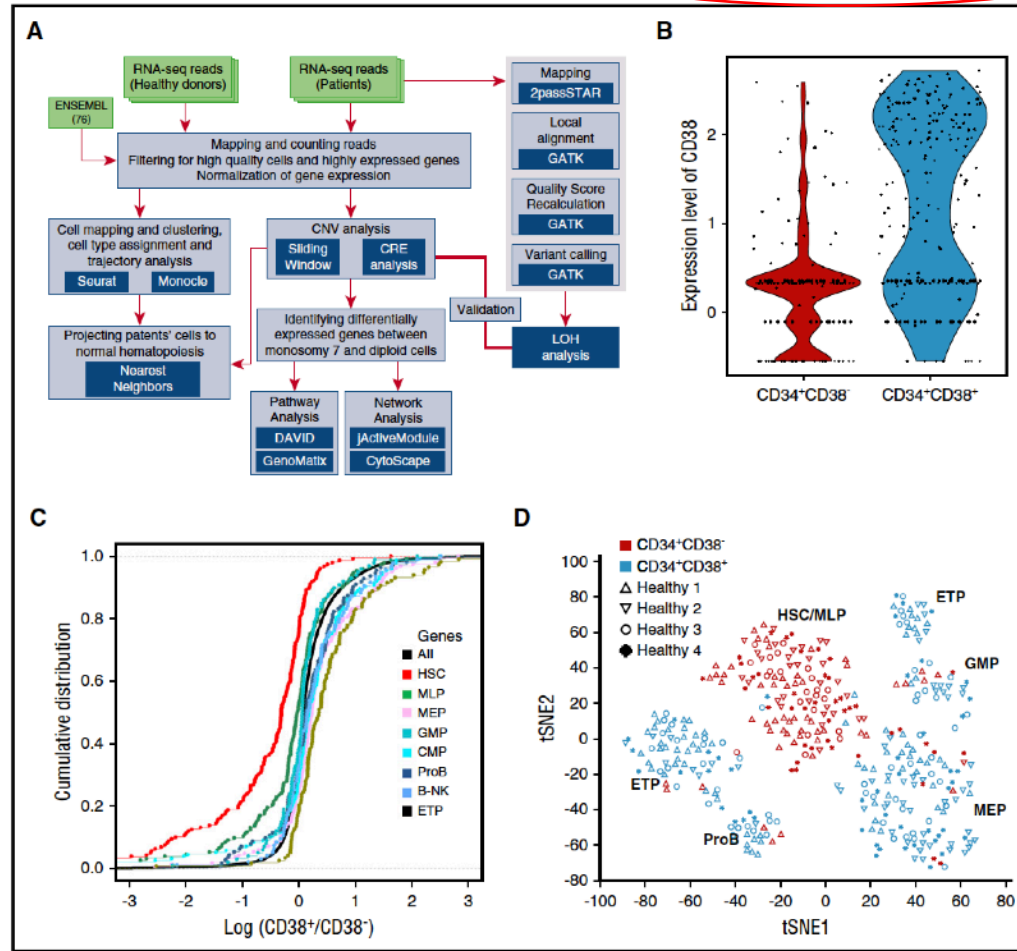


Figure 1. Hematopoietic heterogeneity in healthy donors quantified by scRNA-seq. CD34⁺CD38⁻ and CD34⁺CD38⁺ cells from 4 healthy donors (healthy 1-4) were sorted by surface-membrane markers and subjected to analyses. (A) The schematic pipeline consisting of 3 major analytic components: differentiation analysis with cells from healthy donors, identification and characterization of monosomy 7 cells with gene expression, and validation of monosomy identification with loss of heterozygosity (LOH). CNV, copy-number variation; CRE, chromosome relative expression; GATK, Genome Analysis Toolkit. (B) CD38 expression levels in CD34⁺CD38⁻ and CD34⁺CD38⁺ cells. Each dot represents a single cell. y-axis, batch-corrected gene expression levels. (C) Cumulative distribution of fold changes of expression of hematopoietic cell type signature genes between CD34⁺CD38⁻ and CD34⁺CD38⁺ cells. Each dot represents a gene. B-NK, B cell–natural killer cell precursor; CMP, common myeloid progenitor; ETP, earliest thymic progenitor; GMP, granulocyte-monocyte progenitor; MEP, megakaryocytic-erythroid progenitor; MLP, multi-lymphoid progenitor; ProB, pro-B cell. y-axis, cumulative distribution; x-axis, log (marker gene expression levels in CD34⁺CD38⁻ cells/markers expression levels in CD34⁺CD38⁺ cells). (D) t-distributed stochastic neighbor embedding (tSNE) plot of single-cell gene expression data. Single cells from 4 healthy donors (healthy 1-4) are represented by different symbols. Highly variable genes (1024) across all healthy donors were used in tSNE analysis.

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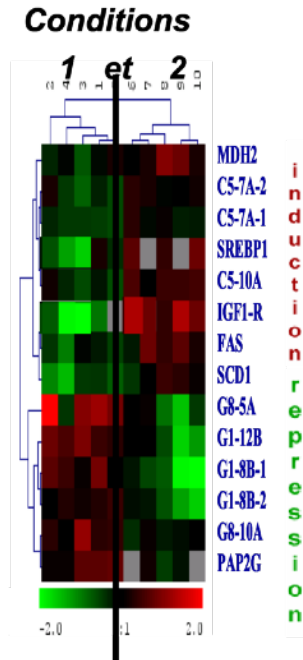
The screenshot shows the website of the University of Nantes library. At the top, there is a navigation bar with a home icon, the text 'UNIVERSITÉ DE NANTES', and links for 'RECHERCHER' (with a magnifying glass icon), 'INTRANET' (with a lock icon), and 'MENU' (with a hamburger icon). Below this is a banner image of a library interior with the text 'Bibliothèque universitaire'. On the left is a vertical navigation menu with items: 'Accueil', 'COVID19', 'Découvrir la BU' (+), 'Les départements' (+), 'Les bibliothèques' (+), 'La documentation' (-), 'La documentation imprimée', 'La documentation numérique' (highlighted with a blue bar), 'La documentation patrimoniale', 'Les services' (+), and 'Les formations' (+). The main content area features a section titled 'Comment accéder aux ressources numériques' with a sub-header 'Vous souhaitez consulter une revue en ligne ou des bases de données qui correspondent à votre thématique de recherche ? C'est simple, il suffit de faire une recherche dans le catalogue des bibliothèques de l'Université, Nantilus !'. Below this is a lightbulb icon and text explaining that members of the University of Nantes can access these resources using their university identifiers. A 'Foire aux questions' section follows, with a highlighted question 'Comment trouver des ressources numériques dans Nantilus ?' and two answers: 'Indiquer un titre (de revue, de livre, de base) ou un sujet dans la barre de recherche' and 'lancer la recherche en cliquant sur la loupe'. On the right side, there is a 'Sélection thématique de vos BU' graphic and a chat window from 'Ubib' with the text 'Besoin d'aide ? Un.e bibliothécaire est en ligne pour vous aider' and buttons for 'Démarrer un chat' and 'Non merci'. A speech bubble icon is also visible at the bottom right.

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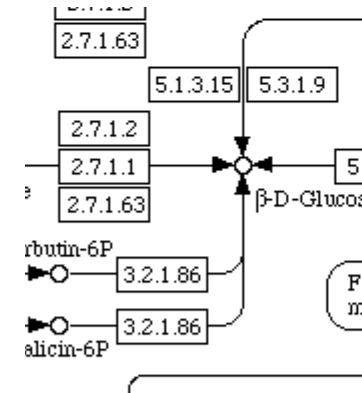
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→ Construire un modèle intégré de connaissance

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Building the human genome
The Human Genome Reference DNA Sequence was completed in April 2003. The current version is listed as a build number on the [Genome View](#) page and includes an accompanying set of [statistics](#) and [release notes](#).

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Hits: 1 2 3 4 5 6 7 8 9 10 11 12 13
10 30 14 2 10

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109 13

The chromosomal locations of several genes believed to be associated with the human BRCA1 gene implicated in breast cancer, highlighted using the Map Viewer query "BRCA1" (build [36](#)).

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BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. [Learn more](#)


NEWS

[Using BLAST Well, How to Maximize Your Search Efforts: Webinar on October 3, 2018](#)


In this webinar, the NCBI BLAST team lead will show you how to be more effective with BLAST.

Thu, 27 Sep 2018 11:00:00 EST [More BLAST news...](#)


Web BLAST



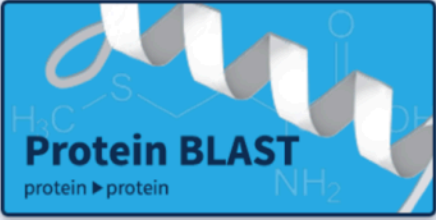
Nucleotide BLAST
nucleotide ▶ nucleotide



blastx
translated nucleotide ▶ protein



tblastn
protein ▶ translated nucleotide



Protein BLAST
protein ▶ protein

BLAST Genomes

Enter organism common name, scientific name, or tax id

Use up and down arrows to choose an item from the autocomplete.

Human Mouse Rat Microbes

2. Les analyses nucléotidiques

BLAST Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

NCBI/ BLAST/ blastn suite

blastn blastp blastx tblastn tblastx

BLASTN programs search nucleotide databases using a nucleotide query sequence.

Enter Query Sequence

Enter accession number, gi, or FASTA sequence [Clear](#)

tcgctgctgctccagccagcgaggctcagcgccgctgtcgcagcagtggaaccgaggatgggcctac

Query subrange

From

To

Or, upload file [Parcourir...](#)

Job Title

Enter a descriptive title for your BLAST search

Blast 2 sequences

Choose Search Set

Database

Human genomic + transcript Mouse genomic + transcript Others (nr etc.):

Nucleotide collection (nr/nt)

Organism Optional

Enter organism name or id--completions will be suggested

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Entrez Query Optional

Enter an Entrez query to limit search

Program Selection

Optimize for

Highly similar sequences (megablast)

More dissimilar sequences (discontiguous megablast)

Somewhat similar sequences (blastn)

Choose a BLAST algorithm

2. Les analyses nucléotidiques

CCGCCTGCCTCCAGCCAGCGAGGCGCCAGCGCCGCTGCTGGCAGCAGCGGACCCGCGGCTACGCGCCAC

From

To

Or, upload file

Job Title
Enter a descriptive title for your BLAST search

Blast 2 sequences

Choose Search Set

Database Human genomic + transcript Mouse genomic + transcript Others (nr etc.):

Organism Optional

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Entrez Query Optional

Program Selection

Optimize for Highly similar sequences (megablast)
 More dissimilar sequences (discontiguous megablast)
 Somewhat similar sequences (blastn)
Choose a BLAST algorithm

Search **database nr** using **Megablast (Optimize for highly similar sequences)**

Show results in a new window

2. Les analyses nucléotidiques

BLAST Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

My NCBI [Sign In] [Register]

NCBI/ BLAST/ blastn suite/ Formatting Results - HRDEGBVV01R

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Nucleotide Sequence (716 letters)

Query ID	lc 27220	Database Name	nr
Description	None	Description	All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
Molecule type	nucleic acid	Program	BLASTN 2.2.18+ Citation
Query Length	716		

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#)

▼ Graphic Summary

Distribution of 45 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments

Color key for alignment scores

<40	40-50	50-80	80-200	>=200
-----	-------	-------	--------	-------

Query

0 100 200 300 400 500 600 700

2. Les analyses nucléotidiques

▼ Descriptions

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer

Sequences producing significant alignments:
(Click headers to sort columns)

Accession	Description	Max score	Total score	Query coverage	E value	Max ident	Links
NM_012701.1	Rattus norvegicus adrenergic, beta-1-, receptor (Adrb1), mRNA	1317	1317	100%	0.0	99%	U E G
J05901.1	R.norvegicus beta-1-adrenergic receptor gene, complete cds	1317	1317	100%	0.0	99%	U
D00634.1	Rattus norvegicus gene for beta-1 adrenergic receptor, complete cds	1299	1299	100%	0.0	99%	E G
BC147435.1	Mus musculus adrenergic receptor, beta 1, mRNA (cDNA clone MGC:182135 IMAC	1157	1157	100%	0.0	95%	U G
NM_007419.2	Mus musculus adrenergic receptor, beta 1 (Adrb1), mRNA	1157	1157	100%	0.0	95%	U E G
AC158549.8	Mus musculus chromosome 19, clone RP24-216K4, complete sequence	1157	1157	100%	0.0	95%	
L10084.1	Mus musculus beta-1 adrenergic receptor gene, complete cds	1157	1157	100%	0.0	95%	E G
X75540.1	M.mullata beta 1 adrenergic receptor gene	1057	1057	100%	0.0	93%	
AK018378.1	Mus musculus 16 days embryo lung cDNA, RIKEN full-length enriched library, clon	1037	1037	91%	0.0	95%	U E G
AF169006.1	Homo sapiens beta-1-adrenergic receptor (ADRB1) gene, complete cds	1029	1029	100%	0.0	92%	G
NM_001009375.1	Felis catus adrenergic, beta-1-, receptor (ADRB1), mRNA >gb AF192344.1 AF192	1029	1029	100%	0.0	92%	G
EU332832.1	Homo sapiens adrenergic, beta-1-, receptor (ADRB1) gene, complete cds	1024	1024	100%	0.0	92%	
XM_521608.2	PREDICTED: Pan troglodytes beta-1-adrenergic receptor (ADRB1), mRNA	1024	1024	100%	0.0	92%	G
NM_000684.2	Homo sapiens adrenergic, beta-1-, receptor (ADRB1), mRNA	1024	1024	100%	0.0	92%	U E G
AY567837.1	Homo sapiens adrenergic, beta-1-, receptor (ADRB1) gene, complete cds	1024	1024	100%	0.0	92%	
AF169007.1	Homo sapiens beta-1-adrenergic receptor (ADRB1) gene, complete cds	1024	1024	100%	0.0	92%	G
AL355543.13	Human DNA sequence from clone RP11-86E10 on chromosome 10 Contains the A	1024	1024	100%	0.0	92%	
J03019.1	Human beta-1-adrenergic receptor mRNA, complete cds	1024	1024	100%	0.0	92%	U E G
AC005886.2	b240g16, complete sequence	1018	1018	100%	0.0	92%	
AB334518.1	Sus scrofa ADRB1 gene for beta-1 adrenergic receptor, complete cds, breed: Lanc	1013	1013	100%	0.0	92%	G
AB334517.1	Sus scrofa ADRB1 gene for beta-1 adrenergic receptor, complete cds, breed: Jinh	1009	1009	100%	0.0	92%	G
NM_001123074.1	Sus scrofa adrenergic, beta-1-, receptor (ADRB1), mRNA	1003	1003	100%	0.0	92%	U G
AF042454.1	Sus scrofa beta-1 adrenergic receptor gene, complete cds	1003	1003	100%	0.0	92%	G
NM_001008713.1	Canis lupus familiaris adrenergic, beta-1-, receptor (ADRB1), mRNA	979	979	100%	0.0	91%	U G
U73207.1	Canis familiaris beta1 adrenergic receptor (dogbeta1) gene, complete cds	979	979	100%	0.0	91%	E G
EU332753.1	Cavia porcellus beta-1 adrenergic receptor (ADRB1) gene, complete cds	935	935	99%	0.0	90%	
DQ538524.1	Bos taurus beta 1 adrenergic receptor gene, complete cds	907	907	100%	0.0	89%	G

2. Les analyses nucléotidiques

M14379.1	Turkey beta-adrenergic receptor mRNA, complete cds	501	501	89%	2e-138	81%	U
AF055349.1	Meriones unguiculatus beta-1-adrenergic receptor mRNA, partial cds	364	364	30%	2e-97	96%	
BC169226.1	Homo sapiens cDNA clone IMAGE:9093418, partial cds	261	261	24%	3e-66	93%	
AF041457.1	Cervus dama beta 1 adrenergic receptor mRNA, partial cds	228	228	20%	3e-56	95%	
U51098.1	Cavia porcellus beta3-adrenergic receptor mRNA, partial cds	132	132	52%	3e-27	74%	G

Alignments Select All [Get selected sequences](#) [Distance tree of results](#)

[ref|NM_012701.1](#) [U](#) [G](#) Rattus norvegicus adrenergic, beta-1-, receptor (Adrb1), mRNA
Length=1401

GENE ID: 24925 Adrb1 | adrenergic, beta-1-, receptor [Rattus norvegicus]
(Over 10 PubMed links)

Score = 1317 bits (713), Expect = 0.0
Identities = 715/716 (99%), Gaps = 0/716 (0%)
Strand=Plus/Plus

```
Query 1 TCGCTGCTGCCTCCAGCCAGCGAGGGCTCAGCGCCGCTGTCGCAGCAGTGGACCCGGGT 60
Sbjct 121 TCGCTGCTGCCTCCAGCCAGCGAGGGCTCAGCGCCGCTGTCGCAGCAGTGGACCCGGGT 180
Query 61 ATGGGCCTACTCCTGGCGCTCATCGTCTGCTCATCGTAGTGGGCAACGTGTTGGTGATC 120
Sbjct 181 ATGGGCCTACTCCTGGCGCTCATCGTCTGCTCATCGTAGTGGGCAACGTGTTGGTGATC 240
Query 121 GTGGCCATCGCCAAGACCCCGGGCTGCAGACGCTCACCAACCTCTTCATCATGTCCCTG 180
Sbjct 241 GTGGCCATCGCCAAGACCCCGGGCTGCAGACGCTCACCAACCTCTTCATCATGTCCCTG 300
Query 181 GCCAGCGCCGATCTGGTCA TGGGACTGCTGGTGGTGCCTTTCGGGGCCACCATTTGGTGTG 240
Sbjct 301 GCCAGCGCCGATCTGGTCA TGGGACTGCTGGTGGTGCCTTTCGGGGCCACCATTTGGTGTG 360
Query 241 TGGGGCCGCTGGGAGTACGGCTCCTTCTTCTGTGAGCTCTGGACTTCGGTAGACGTGCTA 300
Sbjct 361 TGGGGCCGCTGGGAGTACGGCTCCTTCTTCTGTGAGCTCTGGACTTCGGTAGACGTGCTA 420
Query 301 TGTGTGACGGCCAGCATCGAGACCCCTGTGTGTCATCGCCCTGGAGCGCTTCCTCGGCATC 360
Sbjct 421 TGTGTGACGGCCAGCATCGAGACCCCTGTGTGTCATCGCCCTGGAGCGCTTCCTCGGCATC 480
Query 361 ACGCTGCCCTTTCGCTACCAGACCTGCTGACGCGCGCGGAGCGCGGGCCCTCGTGTGC 420
```

Position 470/début séquence référencée

2. Les analyses nucléotidiques

NCBI Nucleotide

Search Nucleotide for [] Go Clear

Display GenBank Show 20 Send to Hide: sequence all but gene, CDS and mRNA feat

Range: from begin to end Reverse complemented strand Features: STS Refresh

1: [NM_012701](#). Reports Rattus norvegicus...[gi:6978458]

[Comment](#) [features](#) [Sequence](#)

LOCUS NM_012701 1401 bp mRNA linear ROD 10-OCT-2008

DEFINITION Rattus norvegicus adrenergic, beta-1-, receptor (Adrb1), mRNA.

ACCESSION NM_012701 XM_001063787

VERSION NM_012701.1 GI:6978458

KEYWORDS .

SOURCE Rattus norvegicus (Norway rat)

ORGANISM [Rattus norvegicus](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 1401)

AUTHORS Bidasee,K.R., Zheng,H., Shao,C.H., Parbhu,S.K., Rozanski,G.J. and Patel,K.P.

TITLE Exercise training initiated after the onset of diabetes preserves myocardial function: effects on expression of beta-adrenoceptors

JOURNAL J. Appl. Physiol. 105 (3), 907-914 (2008)

PUBMED [18583384](#)

REMARK GeneRIF: Myocardial Adrb1 reduction in type 1 diabetes is prevented using exercise training.

REFERENCE 2 (bases 1 to 1401)

AUTHORS Fu,A., Li,X. and Zhao,B.

TITLE Role of beta1-adrenoceptor in the basolateral amygdala of rats with anxiety-like behavior

JOURNAL Brain Res. 1211, 85-92 (2008)

PUBMED [18423428](#)

REMARK GeneRIF: results suggested that the beta1-AR played an important role in anxiety-like behavior

REFERENCE 3 (bases 1 to 1401)

AUTHORS Abraham,P.A., Xing,G., Zhang,L., Yu,E.Z., Post,R., Gamble,E.H. and Li,H.

TITLE beta1- and beta2-adrenoceptor induced synaptic facilitation in rat basolateral amygdala

JOURNAL Brain Res. 1209, 65-73 (2008)

PUBMED [18396264](#)

REMARK GeneRIF: These data suggest that beta-adrenoceptor mediated synaptic facilitation in the amygdala is mediated by both beta1 and beta2-adrenoceptor activation.

REFERENCE 4 (bases 1 to 1401)

AUTHORS Plante,E., Lachance,D., Champetier,S., Drolet,M.C., Roussel,E., Arsenault,M. and Couet,J.

TITLE Benefits of long-term beta-blockade in experimental chronic aortic regurgitation

JOURNAL Am. J. Physiol. Heart Circ. Physiol. 294 (4), H1888-H1895 (2008)

PUBMED [18296565](#)

REMARK GeneRIF: Long-term beta-blockade in chronic aortic regurgitation improved heart function and restored beta1/2 adrenergic receptor

Identité

Bibliographie

2. Les analyses nucléotidiques

```

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                        /db_xref="RATMAP:34960"
                        /db_xref="RGD:2059"
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                        /gene_synonym="RATBlAR"
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                        /gene_synonym="RATBlAR"
                        /standard_name="Adrb1"
                        /db_xref="UniSTS:256461"
     STS                1252..1351
                        /gene="Adrb1"
                        /gene_synonym="BlAR"
                        /gene_synonym="RATBlAR"
                        /standard_name="Adrb1"
                        /db_xref="UniSTS:141043"
ORIGIN
1 atggggcggcgg gggcgcctgc cctgggcgcc tccgaacct gcaacctgtc gtcggcggcg
61 ccgctgcccc acggcgcggc caccgcggca cgactgctg tctcgcgctc gcctcccggc
121 tcgctgctgc ctccagccag cgaggcctca gcgcgcctgt cgcagcagtg gaccgcgggt
181 atgggcctac tctggcgcct catcgtgctg ctcactgtag tgggcaactg gttggtgatc
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301 gccagcgcgg atctgtgcat gggactgctg gtggtgcctt tcggggccac cattgtgggtg
361 tggggccgct gggagtacgg ctctctcttc tgtgagctct ggacttcggt agacgtgcta
421 tgtgtgacgg ccagcatcga gacctgtgt gtcactgccc tggaccgcta cctcggccatc
481 acgctgccc ttcgctacca gaccctgctg acgcgcgcgc gagcgcgggc cctcgtgtgc
541 acagtgctgg ccatctccgc gctggtgtcc ttctgcccc tctcatgca cttggtggcg

```

Défaut en position
470/début
séquence
référencée

Phase ouverte de lecture

Protéine

Séquence nucléotidique

2. Les analyses nucléotidiques

Question à étudier:

Mutation silencieuse, faux-sens ou non-sens chez mon patient ?

2. Les analyses nucléotidiques

Question à étudier:

Mutation silencieuse, faux-sens ou non-sens chez mon patient ?

Basic BLAST

Choose a BLAST program to run.

nucleotide blast	Search a nucleotide database using a nucleotide query <i>Algorithms: blastn, megablast, discontinuous megablast</i>
protein blast	Search protein database using a protein query <i>Algorithms: blastp, psi-blast, phi-blast</i>
blastx	Search protein database using a translated nucleotide query
tblastn	Search translated nucleotide database using a protein query
tblastx	Search translated nucleotide database using a translated nucleotide query

2. Les analyses nucléotidiques

BLAST Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

NCBI/ BLAST/ tblastx

blastn blastp blastx **tblastx**

tblastx TBLASTX search translated nucleotide database using a translated nucleotide query

Enter Query Sequence

Enter accession number, gi, or FASTA sequence [Clear](#)

tcgctgctgcctccagccagcagggctcagcgcgcgtgctgcagcagtgaccgcgggtatgggctac

Query subrange

From

To

Or, upload file [Parcourir...](#)

Genetic code

Job Title

Enter a descriptive title for your BLAST search

Blast 2 sequences

Choose Search Set

Database

Organism Optional

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Entrez Query Optional

BLAST Search database nr using Tblastx (Search translated nucleotide database using a translated nucleotide query)

Show results in a new window

2. Les analyses nucléotidiques

BLAST Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

My NCBI [Sign In] [Register]

NCBI/BLAST/tblastx/ Formatting Results - HRFE3ZC7015

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Nucleotide Sequence (716 letters)

Query ID	lc 22459	Database Name	nr
Description	None	Description	All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences)
Molecule type	nucleic acid	Program	TBLASTX 2.2.18+ Citation
Query Length	716		

Other reports: [Search Summary](#) [Taxonomy reports](#)

Graphic Summary

Distribution of 1000 Blast Hits on the Query Sequence

Mouse-over to show define and scores, click to show alignments

Color key for alignment scores

<40	40-50	50-80	80-200	>=200
-----	-------	-------	--------	-------

2. Les analyses nucléotidiques

▼ **Alignments** Select All [Get selected sequences](#) [Distance tree of results](#)

> [gb|J05561.1|RATB1AR](#) **G** R.norvegicus beta-1-adrenergic receptor gene, complete cds
Length=1645

[GENE ID: 24925 Adrb1](#) | adrenergic, beta-1-, receptor [Rattus norvegicus]
([Over 10 PubMed links](#))

Score = 439 bits (952), Expect = 6e-154
Identities = 177/178 (99%), Positives = 177/178 (99%), Gaps = 0/178 (0%)
Frame = -3/-3

Query	534	EIAALGVVVAARFVALGPPPVHEDGQEGHQRGDGP	355
		PHCAHEGPRSRARQQALVAKGQRDG	
Sbjct	722	EIAALGVVVAARFVALGPPPVHEDGQEGHQRGDGP	543
		PHCAHEGPRSRARQQALVAKGQRDG	
Query	354	EEAVQGGDTQGLDAGRHT*HVVYRSP	175
		ELTEEGAVLPAAPHHNGGPERHHQQSHDQIGAGQG	
Sbjct	542	EEAVQGGDTQGLDAGRHT*HVVYRSP	363
		ELTEEGAVLPAAPHHNGGPERHHQQSHDQIGAGQG	
Query	174	HDEEVGERLQPRGLGDGHDHQHVAHYDEQHDERQE*AHTRG	1
		PLLRRQR*ALAGWRQQR	
Sbjct	362	HDEEVGERLQPRGLGDGHDHQHVAHYDEQHDERQE*AHTRG	189
		PLLRRQR*ALAGWRQQR	

2. *Les analyses nucléotidiques*

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer

Position sur le génome ???

2. Les analyses nucléotidiques

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer

Position sur le génome ???

1: ADRB1 adrenergic, beta-1-, receptor [*Rattus norvegicus*]
GeneID: 24925 updated 15-Oct-2008

Summary

Official Symbol ADRB1

Official Full Name adrenergic, beta-1-, receptor

Primary source [RGD:2059](#)

See related [Ensembl:ENSRNOG00000017002](#); [RATMAP:34960](#)

Gene type protein coding

RefSeq status PROVISIONAL

Organism [Rattus norvegicus](#)

Lineage *Eukaryota*; *Metazoa*; *Chordata*; *Craniata*; *Vertebrata*; *Euteleostomi*; *Mammalia*; *Eutheria*; *Euarchontoglires*; *Glires*; *Rodentia*; *Sciurognathi*; *Muroidea*; *Muridae*; *Murinae*; *Rattus*

Also known as B1AR; RATB1AR; ADRB1

Summary binds beta-adrenergic receptor agonists isoproterenol, norepinephrine, and epinephrine; mediates adenylylcyclase induction; involved in regulation of calcium current [RGD]

Genomic regions, transcripts, and products

Go to [reference sequence details](#)

NC_005100.2

[263925655] 5' [263927959] 3'

[NM_012701.1](#) [NP_036602.1](#)

■ = coding region ■ = untranslated region

Entrez Gene Home

Table Of Contents

- Summary
- Genomic regions, transcripts...
- Genomic context
- Bibliography
- Interactions
- General gene information
- General protein information
- Reference Sequences
- Related Sequences
- Additional Links

Links

- Conserved Domains
- Genome
- GEO Profiles
- HomoloGene
- Map Viewer
- Nucleotide
- PubChem Compound
- PubChem Substance
- Full text in PMC
- Probe
- Protein
- PubMed
- PubMed (GeneRIF)
- Taxonomy
- UniSTS
- Ensembl
- Evidence Viewer
- KEGG
- ModelMaker
- RATMAP
- RGD
- UniGene
- LinkOut

Entrez Gene Info

2. Les analyses nucléotidiques

Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer

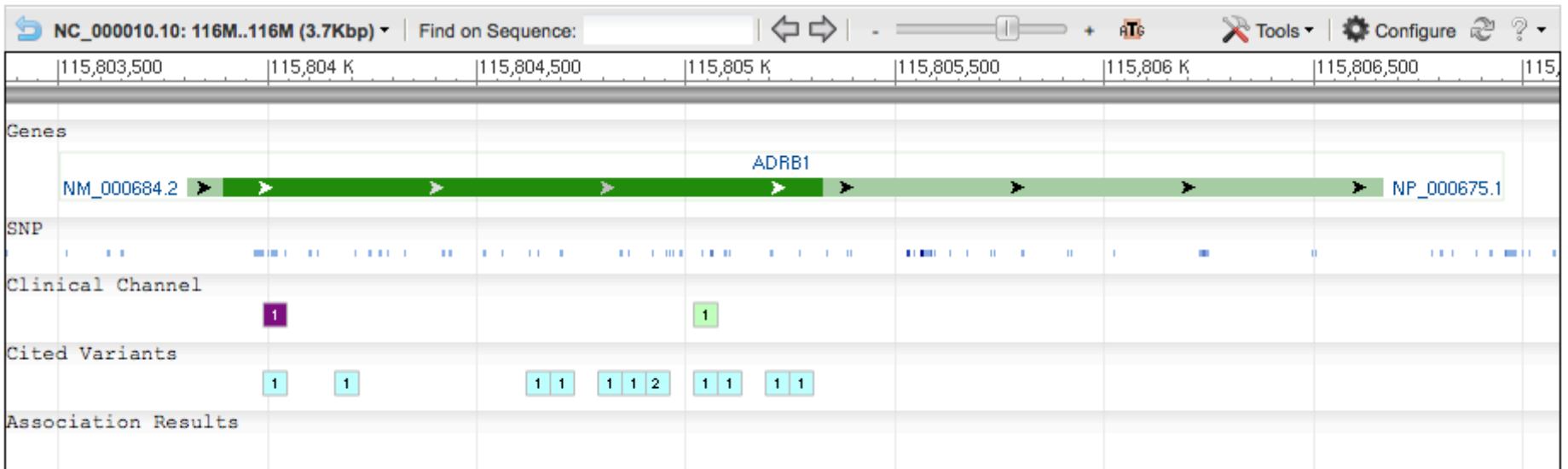
Position sur le génome ???

Genomic regions, transcripts, and products

Genomic Sequence

Go to [reference sequence details](#)

Go to nucleotide [Graphics](#) [FASTA](#) [GenBank](#)



Exons, introns, SNP, etc...

3. Les pathologies héréditaires

3. Les pathologies héréditaires

The screenshot shows the NCBI Entrez Nucleotide search interface. The search term is "beta drenergic receptor". The results page includes a navigation menu on the left, a search bar, and a main content area with a description of the database and a section for the Human Genome.

NCBI Entrez Nucleotide

All Databases PubMed Nucleotide Prot

Search OMIM for beta drenergic receptor Go Clear

Limits Preview/Index History Clipboard Details

About Entrez

Entrez Nucleotide Help | FAQ

Entrez Tools

Check sequence revision history

LinkOut

My NCBI (Cubby)

Related resources BLAST

Reference sequence project

Search for Genes

Submit to GenBank

Search for full length cDNAs

The Entrez Nucleotide database is a collection of sequences from several sources, including GenBank, RefSeq, and PDB. The number of bases in these databases continues to grow at an exponential rate.

Human Genome

Explore [human genome resources](#) or browse the human genome sequence using the [Map Viewer](#).

Building the human genome

The Human Genome Reference DNA Sequence was completed in April 2003. The current version is listed as a build number on the [Genome View](#) page and includes an accompanying set of [statistics](#) and [release notes](#).

[Homo sapiens \(human\) genome view](#) BLAST search the human genome

[Build 36.2 statistics](#) [Switch to previous build](#)

Human genome map showing chromosomes 1-22, X, and Y. Hit counts are displayed below each chromosome:

Chromosome	Hit Count
1	10
2	30
3	14
4	2
5	10
6	10
7	10
8	10
9	10
10	10
11	10
12	10
13	10
14	10
15	10
16	10
17	109
18	10
19	10
20	10
21	10
22	10
X	10
Y	10
III	10
not placed	10

3. Les pathologies héréditaires

The screenshot shows the OMIM website interface. At the top, the NCBI logo is on the left, and the OMIM logo with the text 'Online Mendelian Inheritance in Man' and the Johns Hopkins University logo is on the right. Below the header, there is a search bar with 'OMIM' selected in the dropdown and 'beta drenergic receptor' entered. Buttons for 'Go', 'Clear', and 'Save Search' are visible. Below the search bar, there are tabs for 'Limits', 'Preview/Index', 'History', 'Clipboard', and 'Details'. A message states: 'The following term was not found: drenergic. See [Details](#).' Below this, it says 'Did you mean: [beta adrenergic receptor](#) (99 items)'. There are controls for 'Display' (set to 'Titles'), 'Show' (set to '20'), and 'Send to'. Below these, there are counts: 'All: 1464', 'OMIM UniSTS: 190', and 'OMIM dbSNP: 227'. The results are listed as 'Items 1 - 20 of 1464'. Four items are shown, each with a checkbox, a link to the OMIM ID, and the gene name and map locus.

Entrez

OMIM
Search OMIM
Search Gene Map
Search Morbid Map

Help
OMIM Help
How to Link

FAQ
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Symbols
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Locus-Specific
Model Organisms
MitoMap
Phenotype

All Databases PubMed Nucleotide Protein Genome

Search OMIM for beta drenergic receptor Go Clear Save Search

Limits Preview/Index History Clipboard Details

The following term was not found: drenergic.
See [Details](#).

Did you mean: [beta adrenergic receptor](#) (99 items)

Display Titles Show 20 Send to

All: 1464 OMIM UniSTS: 190 OMIM dbSNP: 227

Items 1 - 20 of 1464

1: [+141900](#)
HEMOGLOBIN--BETA LOCUS; HBB
BETA-THALASSEMIA, INCLUDED
Gene map locus [11p15.5](#)

2: [+109690](#)
BETA-2-ADRENERGIC RECEPTOR; ADRB2
BETA-2-ADRENORECEPTOR AGONIST, REDUCED RESPONSE TO, INCLUDED
Gene map locus [5q32-q34](#)

3: [*608886](#)
PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR-GAMMA, COACTIVATOR 1, BETA; PPARGC1B
Gene map locus [5q33](#)

4: [*104760](#)
AMYLOID BETA A4 PRECURSOR PROTEIN; APP
Gene map locus [21q21](#)

L'onglet OMIM est un outils de synthèse

3. Les pathologies héréditaires

NCBI OMIM Online Mendelian Inheritance in Man Johns Hopkins University

Search OMIM for [] Go Clear

Limits Preview/Index History Clipboard Details

Display Detailed Show 20 Send to

***109691** Links

BETA-3-ADRENERGIC RECEPTOR; ADRB3

Gene map locus [8p12-p11.2](#)

TEXT

CLONING

[Emorine et al. \(1989\)](#) isolated a third beta-adrenergic receptor, beta-3-adrenergic receptor (ADRB3). (See ADRB1 ([109630](#)) and ADRB2 ([109690](#).) Exposure of eukaryotic cells transfected with this gene to adrenaline or noradrenaline promoted the accumulation of adenosine 3-prime,5-prime-monophosphate. The potency of beta-AR agonists and inhibitors was described.

[Van Spronsen et al. \(1993\)](#) demonstrated that the transcription start sites of the mouse and human ADRB3 mRNA are located in a region comprised between 150 and 200 nucleotides 5-prime from the ATG translation start codon. Motifs potentially implicated in heterologous regulation of ADRB3 expression by glucocorticoids and by beta-adrenergic agonists were identified upstream from these cap sites.

GENE STRUCTURE

[Van Spronsen et al. \(1993\)](#) described the exon/intron structure of the mouse and human ADRB3 genes. Their results suggested that utilization of alternate promoters and/or 3-prime untranslated regions may allow tissue-specific regulation of the expression of ADRB3.

MAPPING

[Wilkie et al. \(1993\)](#) presented a list of G protein-coupled receptor genes (their Table 3), indicating that the ADRB3 gene had been mapped to 8p12-p11.2 and the homologous gene to mouse chromosome 8.

MOLECULAR GENETICS

The beta-3-adrenergic receptor, located mainly in adipose tissue, is involved in the regulation of lipolysis and thermogenesis. The potential relevance of this receptor to obesity (see [601665](#)) in humans led [Clement et al. \(1995\)](#) to screen obese patients for the mutation in the ADRB3 gene that results in replacement of tryptophan by arginine at position 64 (W64R; [109691.0001](#)). They studied DNA extracted from leukocytes of 94 normal subjects and 185 unrelated patients with morbid obesity, as defined by a body-mass index (BMI; the weight in kilograms divided by the square of the height in meters) greater than 40. The mutation was detected by analysis of RFLPs with the restriction enzyme BstNI, which discriminates between the normal and mutant sequences. The frequency of the W64R variant was similar in the morbidly obese patients and the normal subjects: 0.08 and 0.10, respectively. However, patients with morbid obesity who were heterozygous for the allele had an increased capacity to gain weight: the mean weight in the 14 heterozygous patients was 140 kg, as compared with 126 kg in the 171 patients without the mutation (P = 0.03). There were no homozygotes in this sample. The cumulative 25-year change in weight (from the age of 20 years) was 67 kg in W64R heterozygotes, as compared with 51 kg in those without the mutation. The maximum weight differential (the maximal lifetime weight minus the weight at 20 years of age) in the heterozygotes was 74 kg, as compared with 59 kg in the patients without the mutation (P = 0.02). [Clement et al. \(1995\)](#) interpreted the findings as indicating that the ADRB3 gene mutation W64R increases the capacity to gain weight.

ANIMAL MODEL

To determine whether the sympathetic nervous system is the efferent arm of diet-induced thermogenesis, [Bachman et al. \(2002\)](#) created mice that lacked the beta-adrenergic receptors ADRB1, ADRB2, and ADRB3. Beta-less mice on a chow

3. Les pathologies héréditaires

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ANIMAL MODEL

To determine whether the sympathetic nervous system is the efferent arm of diet-induced thermogenesis, [Bachman et al. \(2002\)](#) created mice that lacked the beta-adrenergic receptors ADRB1, ADRB2, and ADRB3. Beta-less mice on a chow diet had a reduced metabolic rate and were slightly obese. On a high-fat diet, beta-less mice, in contrast to wildtype mice, developed massive obesity that was due entirely to a failure of diet-induced thermogenesis. [Bachman et al. \(2002\)](#) concluded that the beta-adrenergic receptors are necessary for diet-induced thermogenesis and that this efferent pathway plays a critical role in the body's defense against diet-induced obesity. 🗨️

ALLELIC VARIANTS (selected examples)

.0001 OBESITY, SUSCEPTIBILITY TO [ADRB3, TRP64ARG]

Using a candidate gene approach to study the genetics of obesity ([601665](#)), [Clement et al. \(1995\)](#) found evidence suggesting that the trp64-to-arg (W64R) variant of the ADRB3 gene increases the capacity to gain weight. [Gagnon et al. \(1996\)](#) failed to find an association between W64R and obesity in studies in 2 cohorts: the Quebec Family Study (QFS) and the Swedish Obese Subjects (SOS). 🗨️

[Walston et al. \(1995\)](#) found that Pima Indians homozygous for the W64R ADRB3 mutation had an earlier onset of noninsulin-dependent diabetes mellitus (NIDDM; [125853](#)) and tended to have a lower resting metabolic rate. The authors suggested that the mutation may accelerate the onset of NIDDM by altering the balance of energy metabolism in visceral adipose tissue. 🗨️

[Elbein et al. \(1996\)](#) tested the hypothesis that the beta-3-adrenergic receptor locus affects diabetes susceptibility, obesity as measured by body mass index (BMI), and components of the insulin ([176730](#)) resistance syndrome, by examining ADRB3 allele sharing in families ascertained for 2 or more sibs with NIDDM. They found no evidence for linkage to NIDDM as a dichotomous trait and no evidence for linkage to BMI, waist/hip ratio, insulin levels, or glucose levels as quantitative traits or to reported age of onset among NIDDM individuals. The W64R mutation present in 11% of the population also did not show linkage or association. They concluded that the beta-3-adrenergic receptor locus does not play an important role in NIDDM susceptibility or in the insulin resistance syndrome among members of families with a strong predisposition to NIDDM. 🗨️

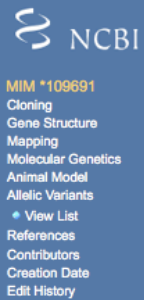
[Kim-Motoyama et al. \(1997\)](#) examined the frequency of the W64R variant in 278 Japanese men in relation to visceral obesity assessed by computerized tomography. They found that the mutation was more frequent in subjects with higher BMI. In subjects with a moderate degree of obesity, the mutation (homozygotes and heterozygotes) was associated with visceral obesity (higher ratio of visceral to subcutaneous fat area). Furthermore, the W64R variant was more frequent in subjects with lower serum triglyceride levels, and homozygotes, but not heterozygotes, exhibited lower triglyceride levels. [Kim-Motoyama et al. \(1997\)](#) suggested that the mutation may describe a subset of subjects characterized by decreased lipolysis in visceral adipose tissue. 🗨️

To examine the effect of W64R on body weight during adult life, the ADRB3 genotypes of 186 unselected Japanese men, most of whom had records of body weight measured yearly from 25 to 53 years of age, were determined by [Nagase et al. \(1997\)](#). Of these subjects, 26 were diagnosed as having noninsulin-dependent diabetes mellitus (NIDDM) and 41 as having impaired glucose tolerance. The results suggested that ADRB3 is not a major contributing factor to obesity or NIDDM in Japanese men. 🗨️

[Buetner et al. \(1998\)](#) examined the prevalence of the 2 ADRB3 alleles in Germany and looked for associations between the ADRB3 genotype and obesity and NIDDM. The frequencies of the different genotypes in the examined cohort were as follows: trp64/trp64, 88.3%; trp64/arg64, 10.8%; and arg64/arg64, 0.8%. The authors found no significant differences between the different genotypes when comparing age, BMI, weight, total and high density lipoprotein, cholesterol, fasting insulin, HbA1c, and blood pressure. They concluded that the NIDDM phenotype did not differ significantly between the different genotype groups in terms of age of diabetes onset or HbA1c. 🗨️

Using hyperinsulinemic/euglycemic clamp methodology, [Garcia-Rubi et al. \(1998\)](#) measured insulin sensitivity in 13 obese women heterozygous for the W64R ADRB3 variant and in 14 women homozygous for the normal gene. Exogenous glucose infusion during the clamp was significantly lower ($P = 0.03$) in W64R heterozygotes (241 ± 135 mg/min) compared with normal homozygotes (379 ± 172 mg/min). They concluded that obese postmenopausal women who are heterozygous for the W64R variant have greater insulin resistance than women homozygous for the normal gene matched for age, body composition, and physical activity. 🗨️

[Mitchell et al. \(1998\)](#) detected an effect of the W64R variant on obesity in a Mexican-American population. They had previously identified a major quantitative trait locus (QTL) influencing the serum concentrations of leptin on 2p in a Mexican-American population in south Texas ([Comuzzie et al., 1997](#)). They studied 45 sib pairs who were concordant (identical by descent) for this locus on chromosome 2, which had been shown previously to be tightly linked to obesity in this population. The W64R variant, detected by PCR-RFLP analysis, was present in 1 sib within each of the 45 sib pairs. Presence of the variant was associated with a significantly higher values in body mass index, fat mass, and waist circumference. The paired-sib design enhanced their ability to detect the effects of this variant by allowing them to account for variation attributable to another obesity susceptibility locus and to background genes. 🗨️



Gene map

Entrez Gene
Nomenclature
RefSeq
GenBank
Protein
UniGene

LinkOut
HGVS
HGMD
GAD
MGI

4. Les analyses génomiques

4. Les analyses génomiques

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Genome

This resource organizes information on genomes including sequences, maps, chromosomes, assemblies, and annotations.

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- [Prokaryotic reference genomes](#)

Genome Annotation and Analysis

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- [Prokaryotic Genome Annotation](#)
- [PASC \(Pairwise Sequence Comparison\)](#)

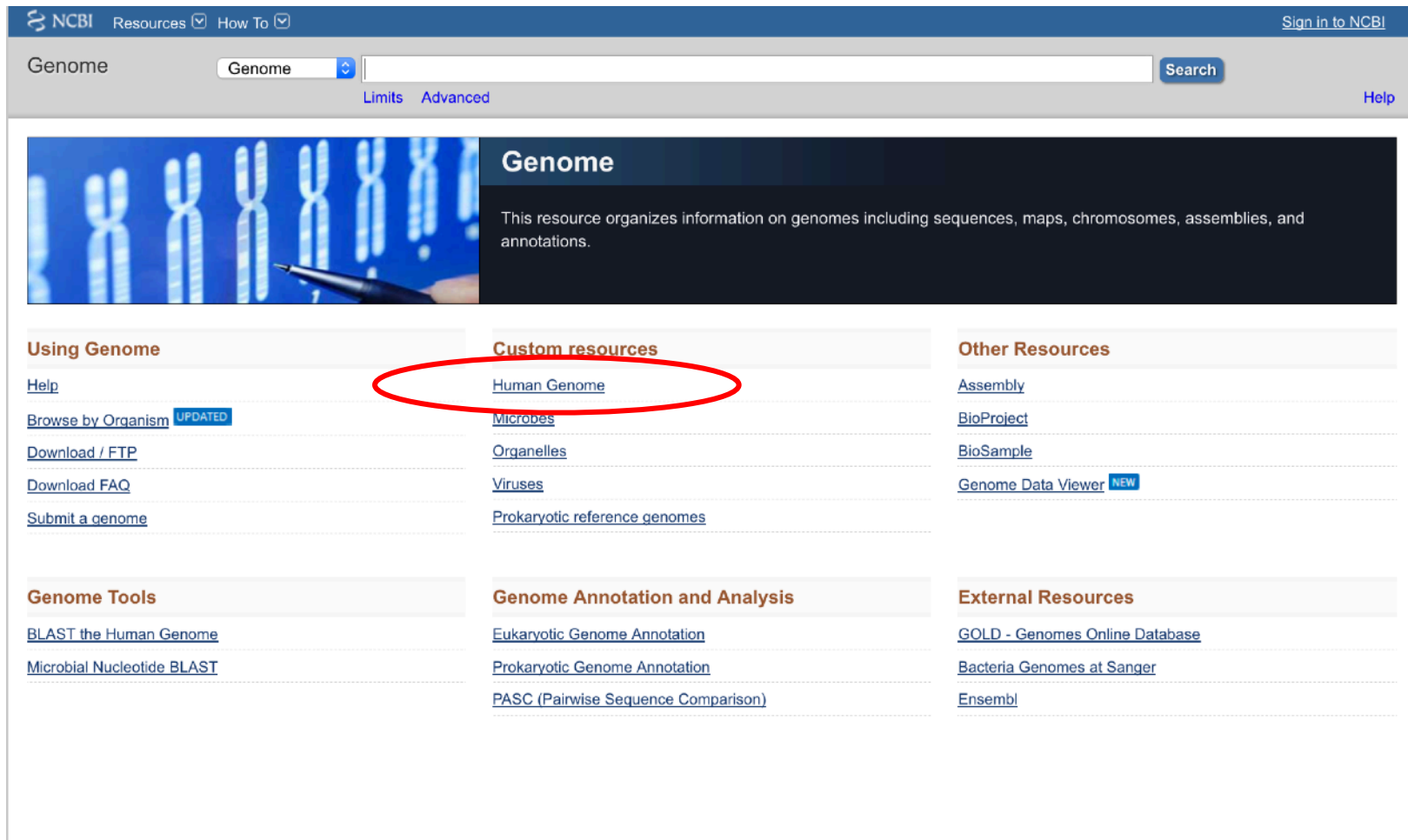
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4. Les analyses génomiques



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4. Les analyses génomiques

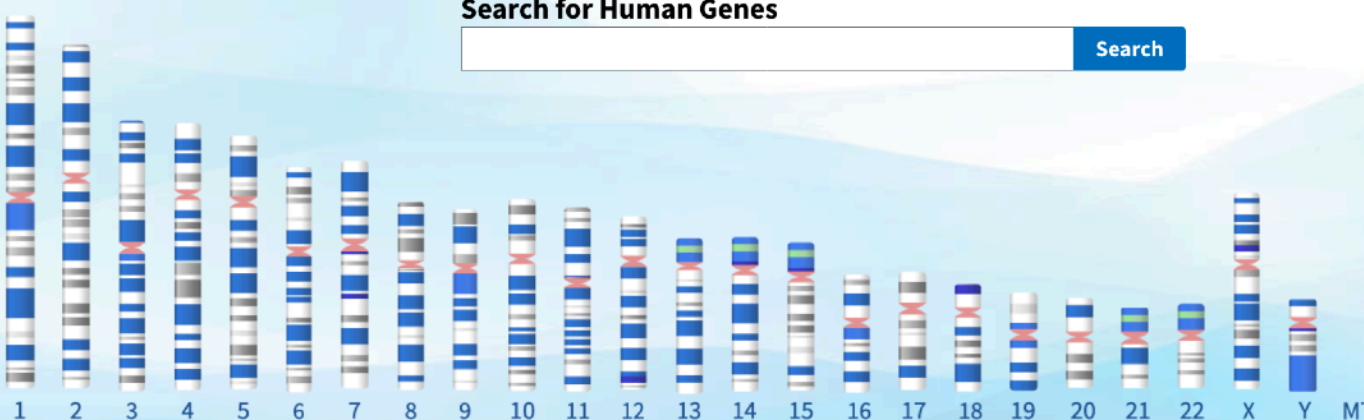
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1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y MT

Select a chromosome to access the [Genome Data Viewer](#)

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	GRCh38	GRCh37
Reference Genome Sequence	Fasta	Fasta
RefSeq Reference Genome Annotation	gff3	gff3

4. Les analyses génomiques

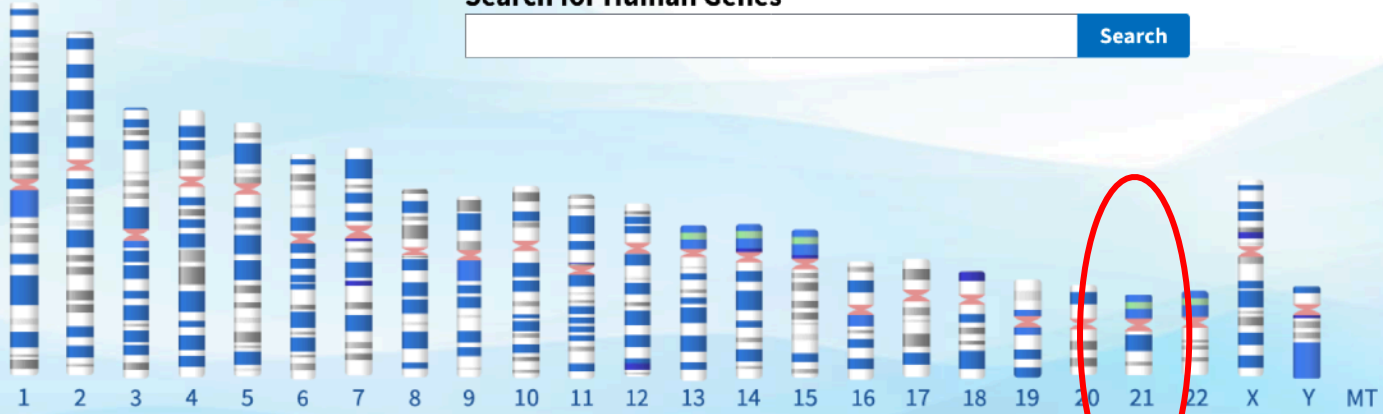
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Download

	GRCh38	GRCh37
Reference Genome Sequence	Fasta	Fasta
RefSeq Reference Genome Annotation	gff3	gff3

4. Les analyses génomiques



J'ai accès à tout ce qui est annoté sur le chromosome 21 ici...

4. Les analyses génomiques

Ici un Map Viewer sur le chromosome Y.

NCBI NCBI Map Viewer

PubMed Entrez BLAST OMIM Taxonomy Structure

Search

Find Find in This View Advanced Search

BLAST The Hu

Human genome overview page (Build 38.3)
Human genome overview page (Build 35.1)
Map Viewer Home

Map Viewer Help
Human Maps Help
FTP
Data As Table View
Maps & Options
Compress Map
Region Shown:
 Go

out
zoom
in

You are here:
Ideogram

default
master

Homo sapiens (human) Build 36.3 (Current)

Chromosome: 1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X [Y] MT

Master Map: Genes On Sequence [Summary of Maps](#) [Download/View Sequ](#)

Region Displayed: 0-58M bp

Symbol	Links	E	Cyto	Description
LOC100132419	sv dl ev mm	protein	Yp11.32	hypothetical protein LOC100132419
SHOX	OMIM HGNC sv pr dl ev mm hm sts CCDS SNP	best RefSeq	Xpter-p22.32;Yp11.3	short stature homeobox
LOC100129445	sv dl ev mm	protein	Yp11.32	hypothetical protein LOC100129445
LOC652827	sv pr dl ev mm	SNP mRNA	Yp11.31	similar to hypothetical gene supported by AK125149
USP12P3	HGNC sv dl ev mm	best RefSeq	Yp11.2	ubiquitin specific peptidase 12 pseudogene 3
TTY7	HGNC sv dl ev mm sts	best RefSeq	Yp11.2	testis-specific transcript, Y-linked 7
TBL1Y	OMIM HGNC sv pr dl ev mm hm CCDS SNP	best RefSeq	Yp11.2	transducin (beta)-like 1Y-linked
TTY15	HGNC sv dl ev mm sts	best RefSeq	Yq11.1	testis-specific transcript, Y-linked 15
CDY4P	HGNC sv dl ev mm	best RefSeq	Yq11.2	chromodomain protein, Y-linked 4 pseudogene
HSFY1	OMIM HGNC sv pr dl ev mm hm sts CCDS SNP	best RefSeq	Yq11.222	heat shock transcription factor, Y-linked 1
USP9Y2	HGNC sv dl ev mm	best RefSeq	Yq11.221-q11.222	USP9Y pseudogene 2
OFDYP7	HGNC sv dl ev mm	best RefSeq	Yq11.222	OFD1 pseudogene Y-linked 7
RBMY1B	HGNC sv pr dl ev mm hm sts CCDS SNP	best RefSeq	Yq11.223	RNA binding motif protein, Y-linked, family 1, member B
OFDYP16	HGNC sv dl ev mm	best RefSeq	Yq11.223	OFD1 pseudogene Y-linked 16
RBMY2WP	HGNC sv dl ev mm	best RefSeq	Yq11.223	RNA binding motif protein, Y-linked, family 2, member W pseudogene
LOC360020	sv dl ev mm	best RefSeq	Yq11.223	protein phosphatase 1, regulatory (inhibitor) subunit 12B pseudogene
CDY1B	HGNC sv pr dl ev mm hm sts CCDS SNP	best RefSeq	Yq11.223	chromodomain protein, Y-linked, 1B
TTY17B	HGNC sv dl ev mm	best RefSeq	Yq11.223	testis-specific transcript, Y-linked 17B
RBMY2DP	HGNC sv pr dl ev mm	best RefSeq	Yq11.23	RNA binding motif protein, Y-linked, family 2, member D pseudogene
IL9R	OMIM HGNC sv pr dl ev mm hm sts CCDS SNP	best RefSeq	Xq28 and Yq12	interleukin 9 receptor

RNA-seq exon coverage, aggregate (filtered), NCBI Homo sapiens Annotation Release 109 - log base 2 scaled

RNA-seq intron-spanning reads, aggregate (filtered), NCBI Homo sapiens Annotation Release 109 - log base 2 scaled

4. Les analyses génomiques

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NCBI Genome Resource Guides

Access to genome resource guides for selected organisms.

Mammals

Organism	Reference Assembly	Current NCBI Build	Map Viewer Release date	Resource Links
human	Build 36.3	36.3	24 Mar 2008	G B M P
mouse	Build 37.1	37.1	5 Jul 2007	G B M P
rat	RGSC v3.4	4.1	6 Jul 2006	G B M P
cow	Btau_4.0	4.1	5 Aug 2008	G B M P
dog	Build 2.1	2.1	8 Sep 2005	G B M P

[Show \(+\)](#)

Birds

Organism	Reference Assembly	Current NCBI Build	Map Viewer Release date	Resource Links
chicken	Build 2.1	2.1	29 Nov 2006	G B M P
zebra finch	na	na	na	G B P

Amphibians

Organism	Reference Assembly	Current NCBI Build	Map Viewer Release date	Resource Links
frog	na	na	na	G B P

Echinoderms

Organism	Reference Assembly	Current NCBI Build	Map Viewer Release date	Resource Links
sea urchin	Build 2.1	2.1	18 Oct 2006	G B M P

Fish

Organism	Reference Assembly	Current NCBI Build	Map Viewer Release date	Resource Links
zebrafish	Zv7	3.1	12 Jul 2008	G B M P
fugu	Truv4.0	na	na	P
pufferfish	Tniv7	na	na	P
stickleback	Broad v1.0	na	na	P

Legend

- [G](#) Genome Resources
- [B](#) BLAST
- [M](#) Map Viewer
- [P](#) Genome Project

NCBI Genome Resource guides provide links, scoped searches, and alerts for a variety of genome-oriented data sources.

Les autres espèces...

5. Les analyses protéiques

5. Les analyses protéiques

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BLAST Home Recent Results Saved Strategies Help

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance. [Learn more](#)


NEWS

[Using BLAST Well, How to Maximize Your Search Efforts: Webinar on October 3, 2018](#)

In this webinar, the NCBI BLAST team lead will show you how to be more effective with BLAST.

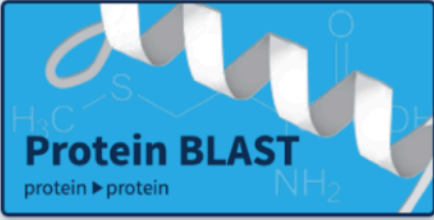
Thu, 27 Sep 2018 11:00:00 EST [More BLAST news...](#)

Web BLAST



blastx
translated nucleotide > protein

tblastn
protein > translated nucleotide



BLAST Genomes

Enter organism common name, scientific name, or tax id Search

Use up and down arrows to choose an item from the autocomplete.

Human Mouse Rat Microbes

Idem sur les protéines...

5. Les analyses protéiques

BLAST Basic Local Alignment Search Tool

Home Recent Results Saved Strategies Help

► NCBI/ BLAST/ blastp suite

blastn blastp blastx tblastn tblastx

BLASTP programs search protein databases using a protein query. [more](#)

Enter Query Sequence

Enter accession number, gi, or FASTA sequence [Clear](#)

AQECHSNPRCCSFASNMPYALLSSSVSFYLP LLVMLFVYARV FVAKRQRRFVRR ELGRFPPEESPRSP

Query subrange

From

To

Or, upload file [Parcourir...](#)

Job Title

Enter a descriptive title for your BLAST search

Blast 2 sequences

Choose Search Set

Database

Organism Optional

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown.

Entrez Query Optional

Program Selection

Algorithm

blastp (protein-protein BLAST)

PSI-BLAST (Position-Specific Iterated BLAST)

PHI-BLAST (Pattern Hit Initiated BLAST)

Choose a BLAST algorithm

BLAST Search database nr using Blastp (protein-protein BLAST)

5. Les analyses protéiques

BLAST Basic Local Alignment Search Tool

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NCBI/BLAST/blastp suite/ Formatting Results - HRGK4VXW013

[Edit and Resubmit](#) [Save Search Strategies](#) [Formatting options](#) [Download](#)

Protein Sequence (138 letters)

Query ID	lcl 7334	Database Name	nr
Description	None	Description	All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Molecule type	amino acid	Program	BLASTP 2.2.18+ Citation
Query Length	138		

Other reports: [Search Summary](#) [Taxonomy reports](#) [Distance tree of results](#)

Graphic Summary

[Show Conserved Domains](#)

Putative conserved domains have been detected, click on the image below for detailed results.

Query seq. Superfamilies

7tm_1 super-family

Distribution of 100 Blast Hits on the Query Sequence

Mouse-over to show defline and scores, click to show alignments

Color key for alignment scores	
Score Range	Color
<40	Black
40-50	Blue
50-80	Green
80-200	Purple
>=200	Red

5. Les analyses protéiques

▼ **Alignments** Select All [Get selected sequences](#) [Distance tree of results](#)

```
> ref|NP\_037240.1 | UG adrenergic, beta-3-, receptor [Rattus norvegicus]
  gb|AAA74470.1 | G beta-adrenergic receptor
  Length=400

  GENE ID: 25645 Adrb3 | adrenergic, beta-3-, receptor [Rattus norvegicus]
  (Over 10 PubMed links)

  Score = 276 bits (706), Expect = 4e-73, Method: Compositional matrix adjust.
  Identities = 138/138 (100%), Positives = 138/138 (100%), Gaps = 0/138 (0%)

  Query 1   AQECHSNPRCCSFASNMPYALLSSSVSFYLLVLMFLVYARVFVVAKRQRRFVRRRELGRF 60
           AQECHSNPRCCSFASNMPYALLSSSVSFYLLVLMFLVYARVFVVAKRQRRFVRRRELGRF
  Sbjct 183 AQECHSNPRCCSFASNMPYALLSSSVSFYLLVLMFLVYARVFVVAKRQRRFVRRRELGRF 242

  Query 61  PPEESPRSPSRSPSPATVGTPTASDGVVPCGRRPARLLPLGEHRALRTLGLIMGIFSLCW 120
           PPEESPRSPSRSPSPATVGTPTASDGVVPCGRRPARLLPLGEHRALRTLGLIMGIFSLCW
  Sbjct 243 PPEESPRSPSRSPSPATVGTPTASDGVVPCGRRPARLLPLGEHRALRTLGLIMGIFSLCW 302

  Query 121 LPFFLANVLRALVGPSLV 138
           LPFFLANVLRALVGPSLV
  Sbjct 303 LPFFLANVLRALVGPSLV 320
```

6. Exemple publication utilisant la bioinfo

OPEN ACCESS Freely available online



A Rapid Screening Assay to Search for Phosphorylated Proteins in Tissue Extracts

Ignazio Garaguso, Juergen Borlak*

Centre for Pharmacology and Toxicology, Hannover Medical School, Hannover, Germany

Abstract

Reversible protein phosphorylation is an essential mechanism in the regulation of diverse biological processes, nonetheless is frequently altered in disease. As most phosphoproteome studies are based on optimized *in-vitro* cell culture studies new methods are in need to improve *de novo* identification and characterization of phosphoproteins in extracts from tissues. Here, we describe a rapid and reliable method for the detection of phosphoproteins in tissue extract based on an experimental strategy that employs 1D and 2D SDS PAGE, Western immunoblotting of phosphoproteins, in-gel protease digestion and enrichment of phosphopeptides using metal oxide affinity chromatography (MOAC). Subsequently, phosphoproteins are identified by MALDI-TOF-MS/MS with the CHCA-TL or DHB ML sample matrix preparation method and further characterized by various bioinformatic software tools to search for candidate kinases and phosphorylation-dependent binding motifs. The method was applied to mouse lung tissue extracts and resulted in an identification of 160 unique phosphoproteins. Notably, TiO₂ enrichment of pulmonary protein extracts resulted in an identification of additional 17 phosphoproteins and 20 phosphorylation sites. By use of MOAC, new phosphorylation sites were identified as evidenced for the advanced glycosylation end product-specific receptor. So far this protein was unknown to be phosphorylated in lung tissue of mice. Overall the developed methodology allowed efficient and rapid screening of phosphorylated proteins and can be employed as a general experimental strategy for an identification of phosphoproteins in tissue extracts.

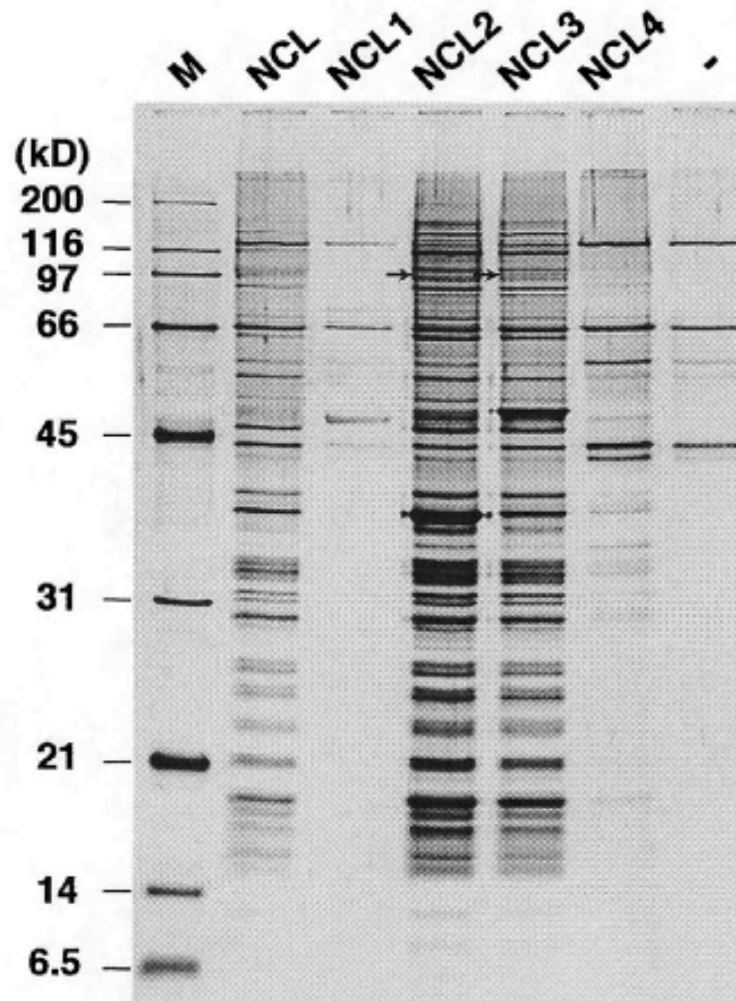
Citation: Garaguso I, Borlak J (2012) A Rapid Screening Assay to Search for Phosphorylated Proteins in Tissue Extracts. PLoS ONE 7(11): e50025. doi:10.1371/journal.pone.0050025

Editor: Christina Lynn Addison, Ottawa Hospital Research Institute, Canada

Received: August 30, 2012; **Accepted:** October 19, 2012; **Published:** November 15, 2012

5. Les analyses protéiques

Migration de protéines: Gel en 1 dimension



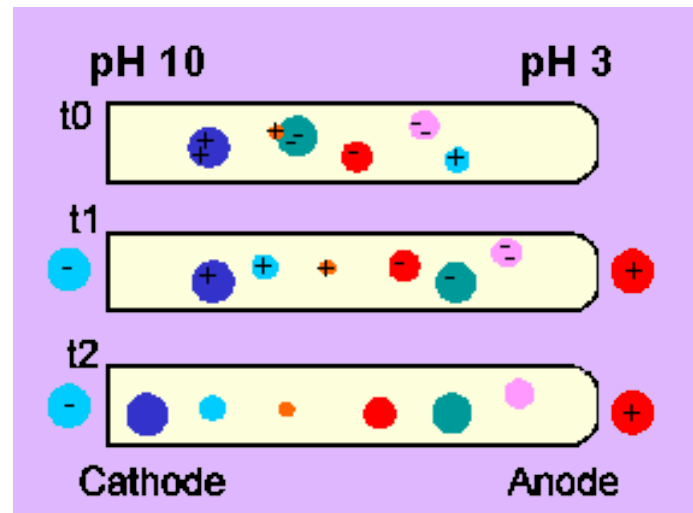
Les protéines migrent selon leur poids moléculaire

5. *Les analyses protéiques*

- **L'électrophorèse bidimensionnelle** consiste à séparer les protéines :
 - dans une première dimension par focalisation isoélectrique (IEF) selon leur pI
 - dans une deuxième direction, perpendiculaire à la première, selon leur poids moléculaire.

5. Les analyses protéiques

- Première dimension : IEF (électrofocalisation)
 - Gradient de pH sous l'effet d'un champ électrique
 - Migration des protéines à travers le gradient de pH jusqu'à une charge nette nulle lorsqu'elles atteignent leur pI



5. Les analyses protéiques

1ère dimension :
Électrofocalisation
(gradient de pH)

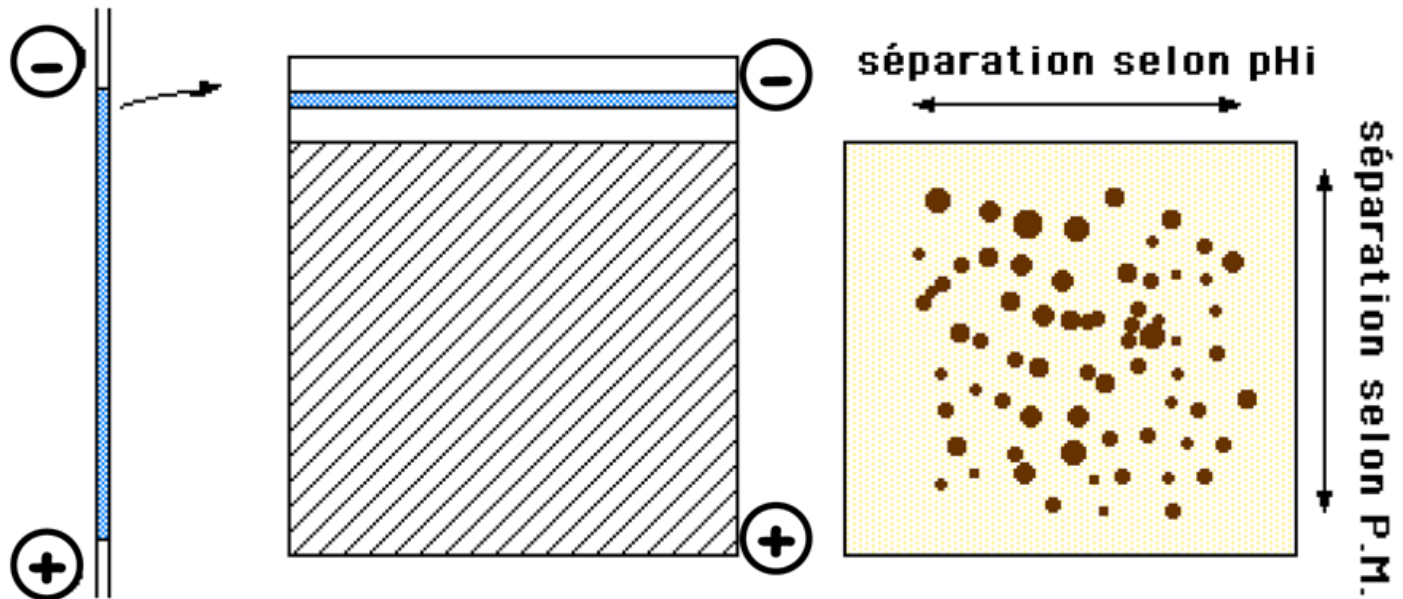


5. Les analyses protéiques

1ère dimension :
Électrofocalisation
(gradient de pH)

2ème dimension :
Gel dénaturant
(SDS-PAGE)

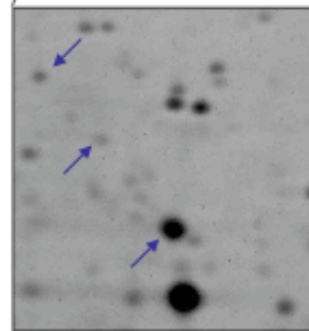
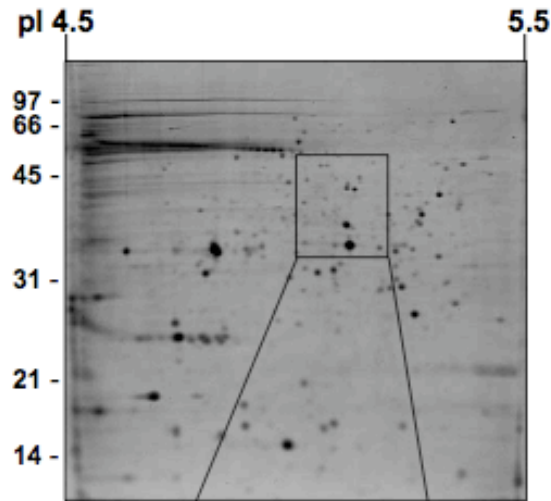
Coloration
(bleu de Coomassie;
 AgNO_3)



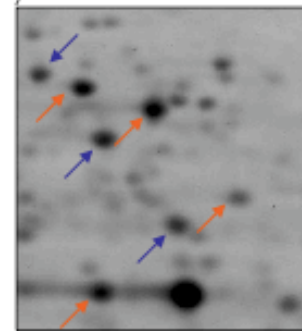
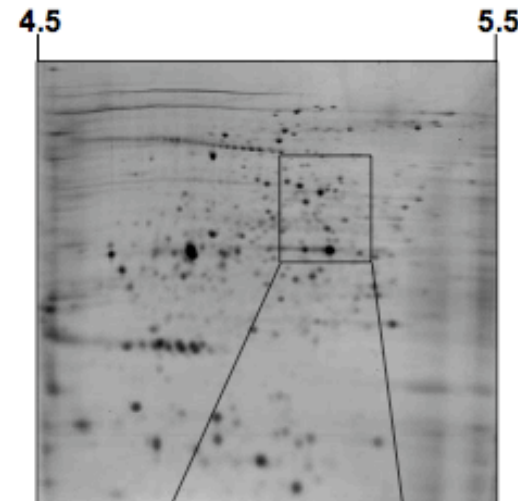
5. Les analyses protéiques



Etudes différentielles

Condition 1



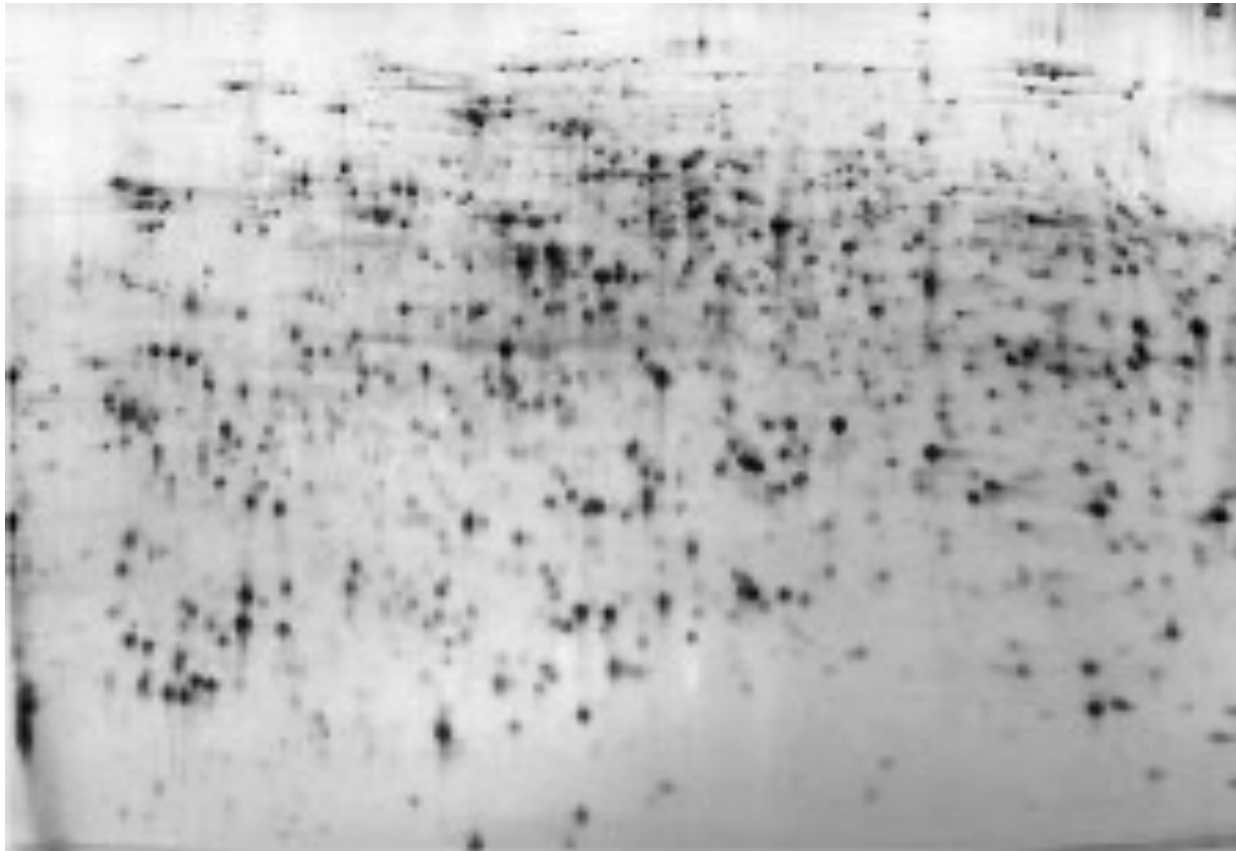
Condition 2



-  stage-specific
-  altered expression level

5. Les analyses protéiques

- Il existe des banques de données de résultats




E. coli


5. Les analyses protéiques

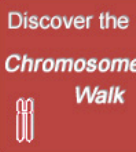
<http://expasy.org/ch2d/>

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 **SWISS-2DPAGE**
Two-dimensional polyacrylamide gel electrophoresis database

 **SIB** 10th Anniversary
Pioneers at the heart of science
2008 - 10th Anniversary

Discover the Chromosome Walk 

SWISS-2DPAGE contains data on proteins identified on various 2-D PAGE and SDS-PAGE reference maps. You can locate these proteins on the 2-D PAGE maps or display the region of a 2-D PAGE map where one might expect to find a protein from UniProtKB/Swiss-Prot [[More details](#) / [References](#) / [Linking to SWISS-2DPAGE](#) / [Commercial users](#) / [Disclaimer](#)].

Release 18.6, September 2006 and updates up to 31-January-2008 (contains 1265 entries in 36 reference maps from human, mouse, *Arabidopsis thaliana*, *Dictyostelium discoideum*, *Escherichia coli*, *Saccharomyces cerevisiae*, and *Staphylococcus aureus* (N315)).

[\[Search\]](#)[\[Documents\]](#)[\[Services\]](#)[\[Software\]](#)[\[Related servers\]](#)[\[Other databases\]](#)[\[Job openings\]](#)

Access to SWISS-2DPAGE

- by description (any word in the DE, OS, GN and ID lines)
- by accession number (AC lines)
- by clicking on a spot: select one of our 2-D PAGE or SDS-PAGE reference maps, click on a spot and then get the corresponding information from the SWISS-2DPAGE database.
- by author (RA lines)
- by spot serial number (2D and 1D lines)
- by experimental pI/Mw range
- by experimental identification methods
- by full text search
- retrieve all the protein entries identified on a given reference map
- complex queries (SRS like)
- compute estimated location on reference maps for a user-entered sequence

SWISS-2DPAGE documents

- User manual
- Release notes (September 26, 2006)
- FAQ (Frequently Asked Questions about SWISS-2DPAGE)
- Protocols:
 - Technical information about 2-D PAGE (IPG's, silver staining, protocols, etc)
 - High performance 2-D gel comparison
- Figure captions of SWISS-2DPAGE maps available from publications:
 - Human CSF, ELC, HEPG2, HEPG2SP, LIVER, LYMPHOMA, PLASMA, PLATELET, RBC, U937, CEC, KIDNEY.
 - *Dictyostelium discoideum*, *Escherichia coli*, *Saccharomyces cerevisiae*.

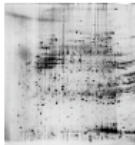
5. Les analyses protéiques

<http://expasy.org/ch2d/>

Homo sapiens (Human)

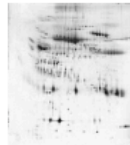
CEC_HUMAN

{ Colorectal epithelia cells }
Tissue: Colon epithelium



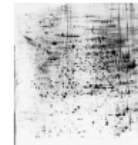
CSF_HUMAN

{ Cerebrospinal Fluid }
Tissue: Cerebrospinal fluid



DLD1_HUMAN

{ Colorectal adenocarcinoma cell line (DL-1) }
Tissue: Colon adenocarcinoma



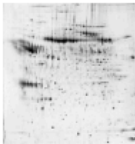
ELC_HUMAN

{ Erythroleukemia Cell }
Tissue: Erythroleukemia



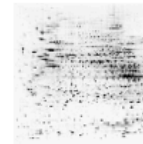
HEPG2SP_HUMAN

{ HepG2 Secreted Proteins }
Tissue: Hepatoblastoma



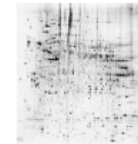
HEPG2_HUMAN

{ HepG2 }
Tissue: Hepatoblastoma



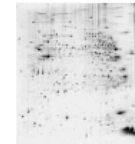
HL60_HUMAN

{ Promyelocytic leukemia cells }
Tissue: Promyelocytic leukemia



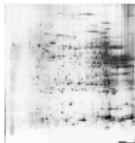
KIDNEY_HUMAN

{ Kidney }
Tissue: Kidney



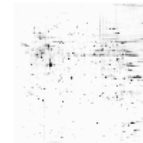
LIVER_HUMAN

{ Liver }
Tissue: Liver



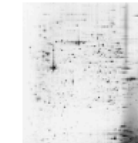
LYMPHOCYTE_HUMAN

{ Lymphocytes }
Tissue: Lymphocyte



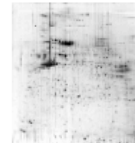
LYMPHOMA_HUMAN

{ Lymphoma }
Tissue: Lymphoma



NUCLEI_LIVER_HUMAN

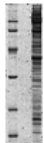
{ Soluble nuclear proteins and matrix from liver tissue }
Tissue: Liver



NUCLEOLI_HELA_1D_HUMAN

{ SDS-PAGE of nucleolar proteins from Human HeLa cells } { 2D-PAGE of nucleolar proteins from Human HeLa cells }

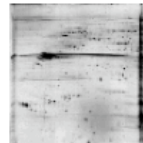
Tissue: Cervix carcinoma



NUCLEOLI_HELA_2D_HUMAN

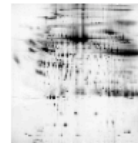
{ 2D-PAGE of nucleolar proteins from Human HeLa cells }

Tissue: Cervix carcinoma



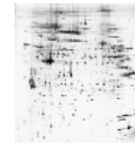
PLASMA_HUMAN

{ Plasma }
Tissue: Plasma



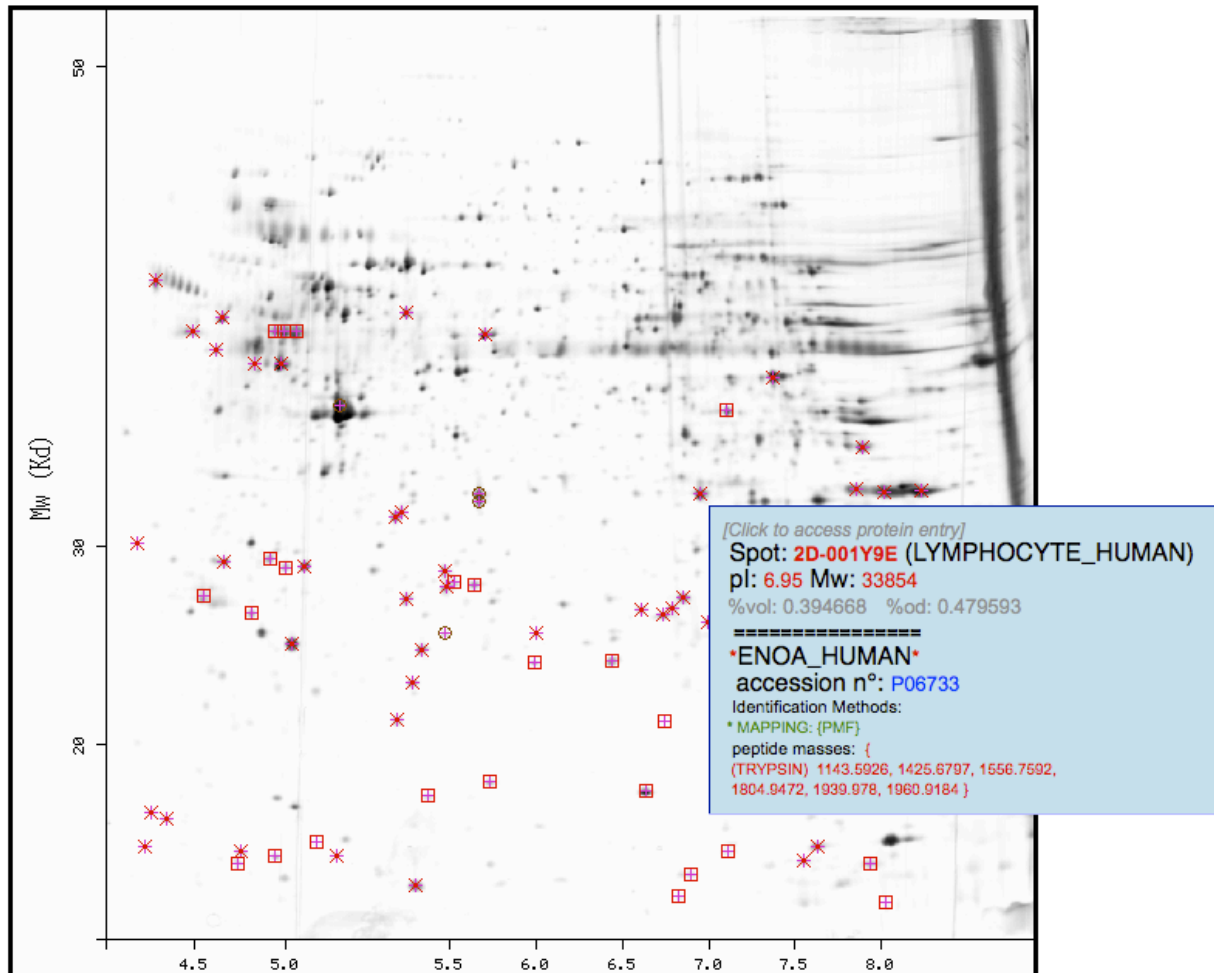
PLATELET_HUMAN

{ Platelet }
Tissue: Platelet

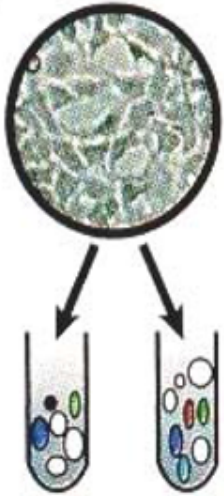


5. Les analyses protéiques

Get more information by dragging your mouse pointer over any spot, or click on a spot to access all its associated protein entries.



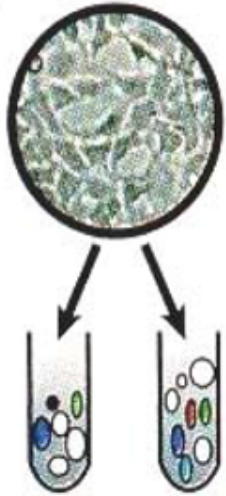
5. Les analyses protéiques



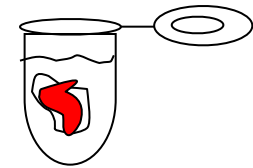
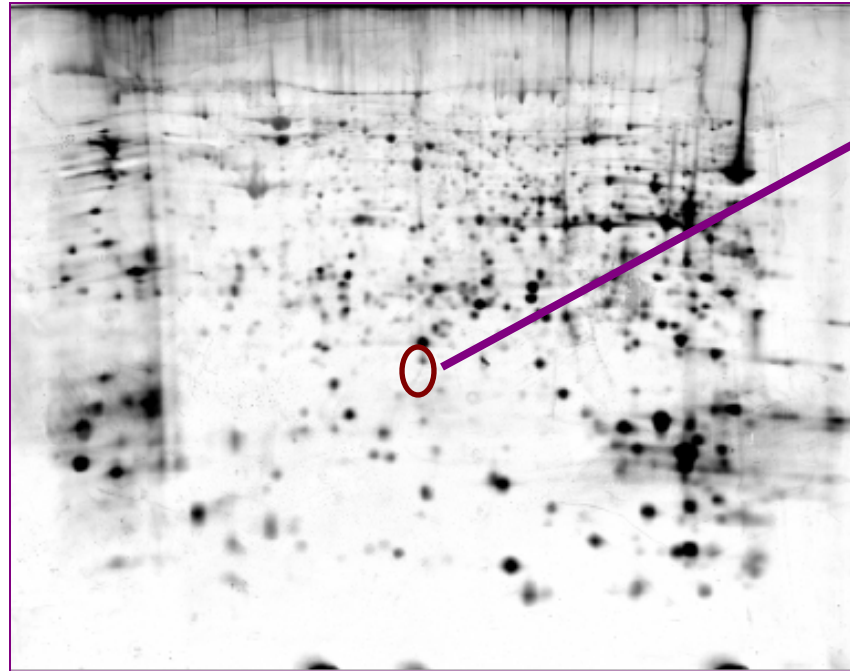
Fractionnement
et extraction
des protéines

5. Les analyses protéiques

Après avoir repéré la protéine d'intérêt sur le gel 2D, on excise le spot



Fractionnement
et extraction
des protéines

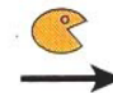


lavage;

déshydratation du
morceau de gel prélevé ;

réhydratation par une
solution contenant de la
trypsine.

Digestion à
la trypsine

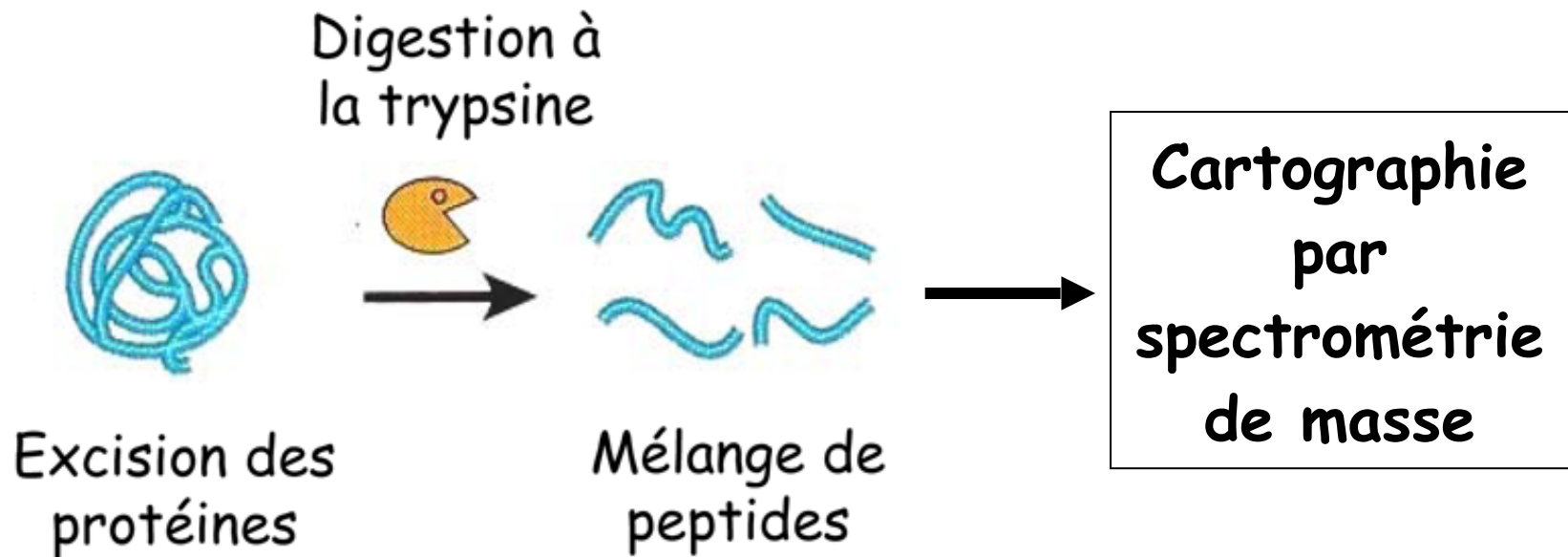


Excision des
protéines

Mélange de
peptides

Une série de peptides résultant de la digestion de la protéine

5. Les analyses protéiques



5. Les analyses protéiques

- **Définition**

La spectrométrie de masse (mass spectrometry ou MS) est une technique physique d'analyse permettant de détecter et d'identifier des molécules d'intérêt par mesure de leur masse mono-isotopique.

De plus, la spectrométrie de masse permet de caractériser la structure chimique des molécules en les fragmentant.

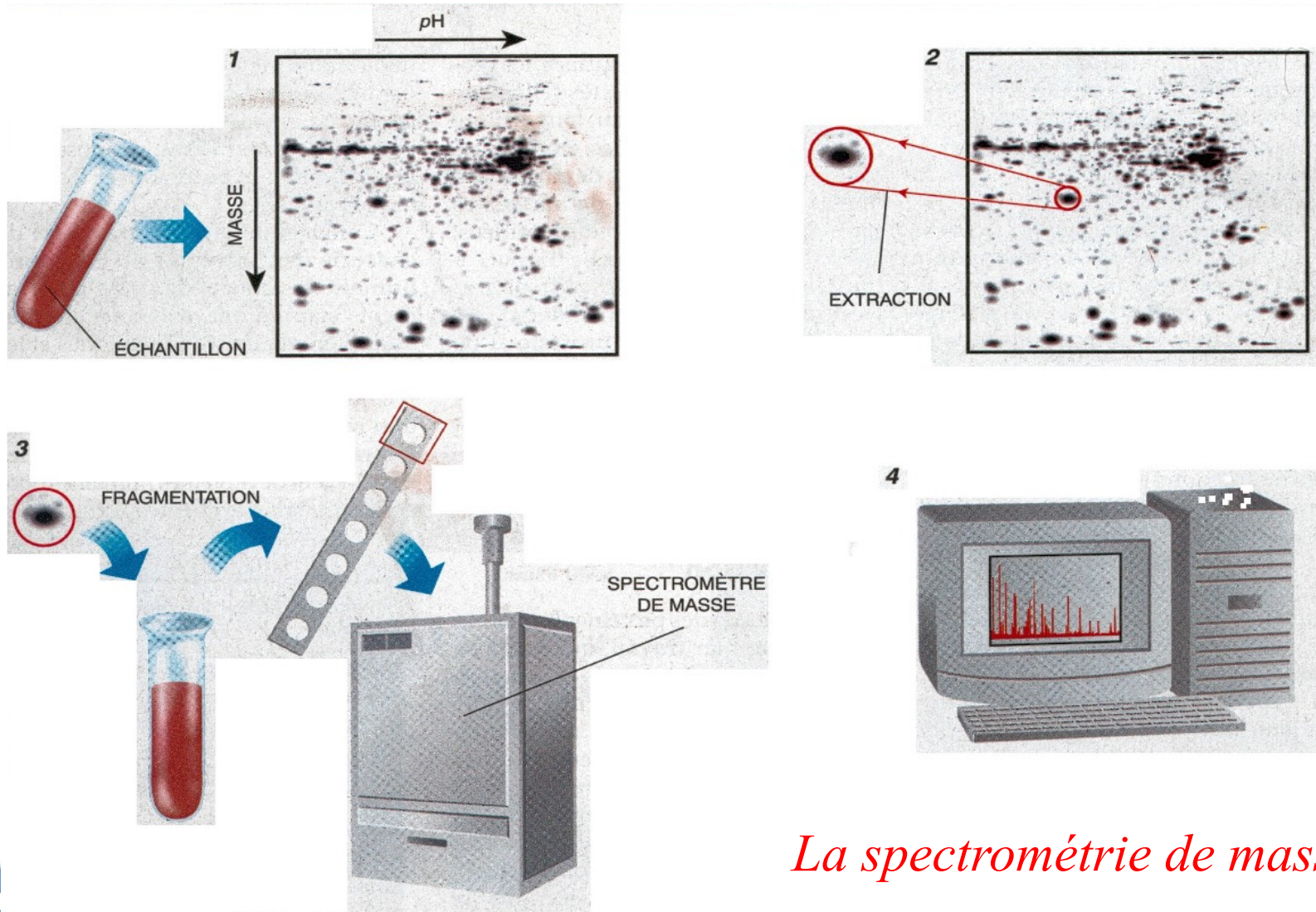
5. Les analyses protéiques

- **La spectrométrie de masse**
 - Utilisée pour identifier une protéine, ou suivre ses modifications,
 - Mesure la masse des peptides issus d'une digestion trypsique,
 - Les bases de données de séquences permettent de prédire la masse théorique des fragments de protéolyse : on peut identifier une protéine d'après le spectre de masse de ses fragments de protéolyse (il faut disposer de la séquence).

5. Les analyses protéiques

- **Principe** : Son principe réside dans la **séparation** en phase gazeuse de **molécules chargées** (ions) en fonction de leur rapport **masse/charge** (m/z). La spectrométrie de masse est utilisée dans pratiquement tous les domaines scientifiques : physique, astrophysique, chimie en phase gazeuse, chimie organique, dosages, biologie, médecine...
 - Substance analysée en phase gazeuse (diff RMN subst condensée)
 - Importance des paramètres de la phase de vaporisation de l'échantillon
 - Mesure du déplacement de particules chargées dans un champs électromagnétique
 - Importance des paramètres définissant l'ionisation de l'échantillon
 - Obtention d'un spectre de masse qui montre la variation d'un courant ionique en fonction de m/z
 - **Attention destruction de l'échantillon analysé !**

5. Les analyses protéiques



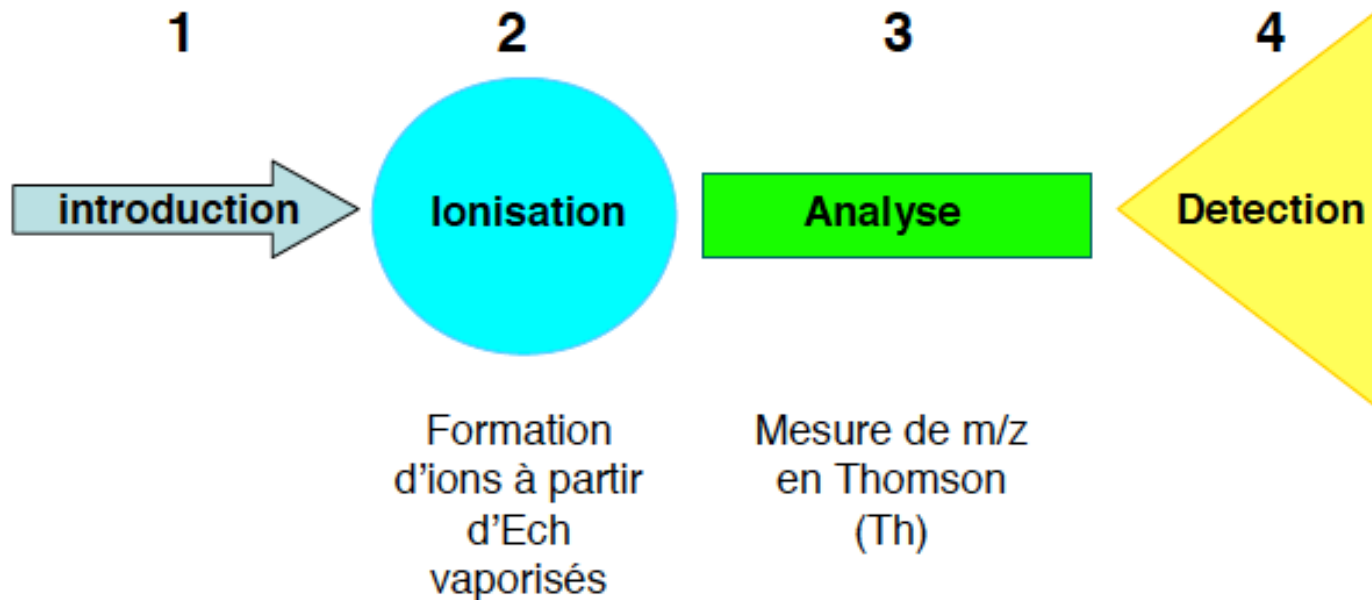
La spectrométrie de masse

5. Les analyses protéiques

La spectrométrie de masse

Le spectromètre de masse se compose donc de quatre parties :

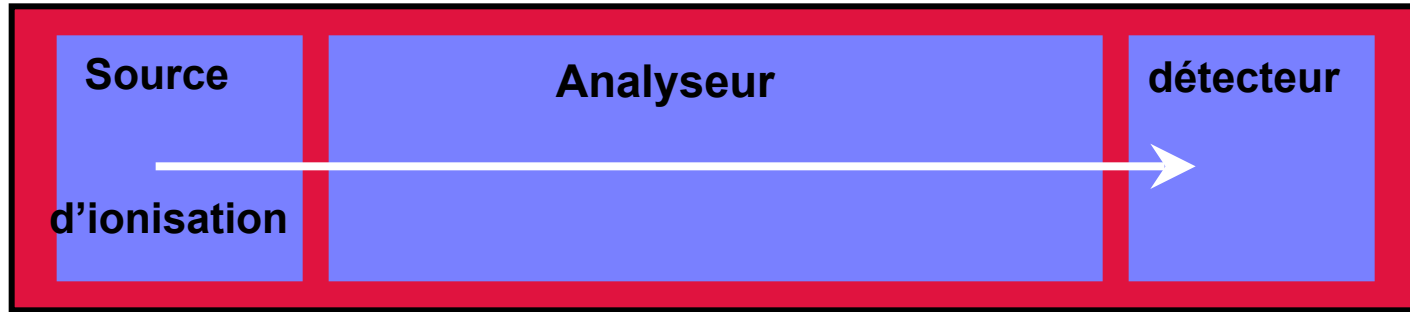
- 1- Le système d'introduction de l'échantillon
- 2- La source d'ionisation: elle consiste à vaporiser les molécules et à les ioniser.
- 3- L'analyseur
- 4- Le détecteur et système de traitement



5. Les analyses protéiques

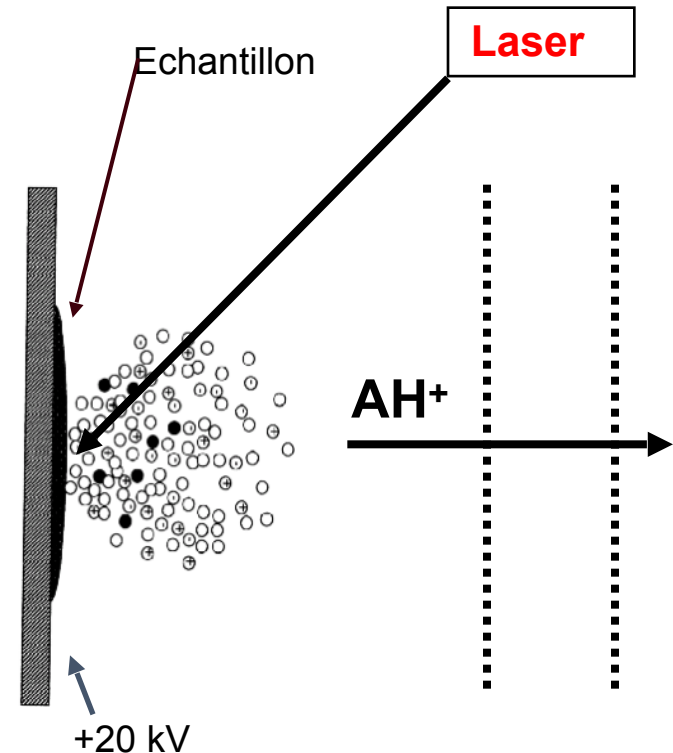
La spectrométrie de masse

1/2



Source d'ionisation :

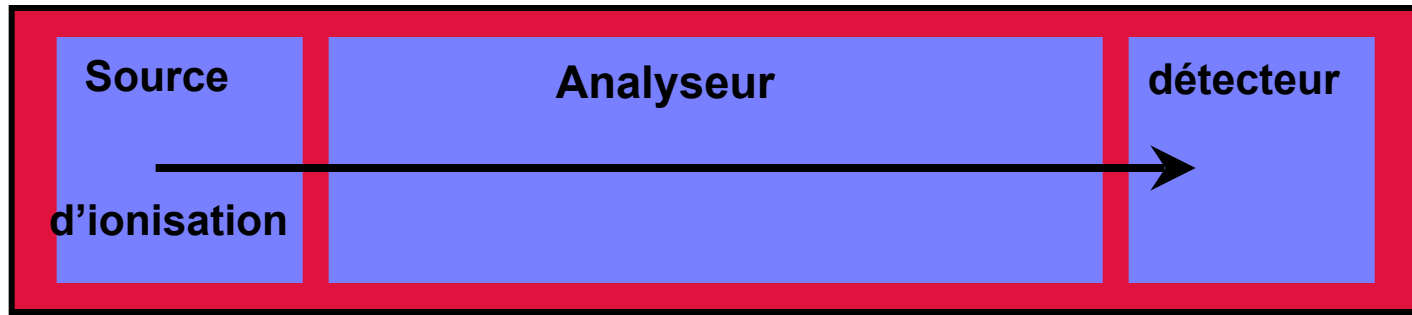
Les molécules doivent passer en phase gazeuse et s'ioniser



5. Les analyses protéiques

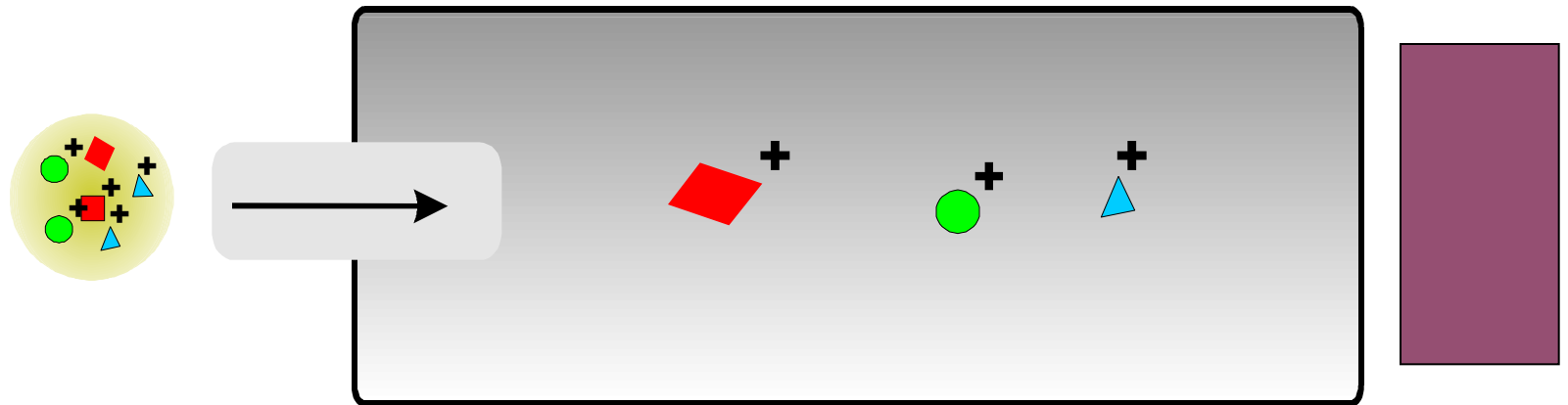
3

La spectrométrie de masse



L'analyseur de masse

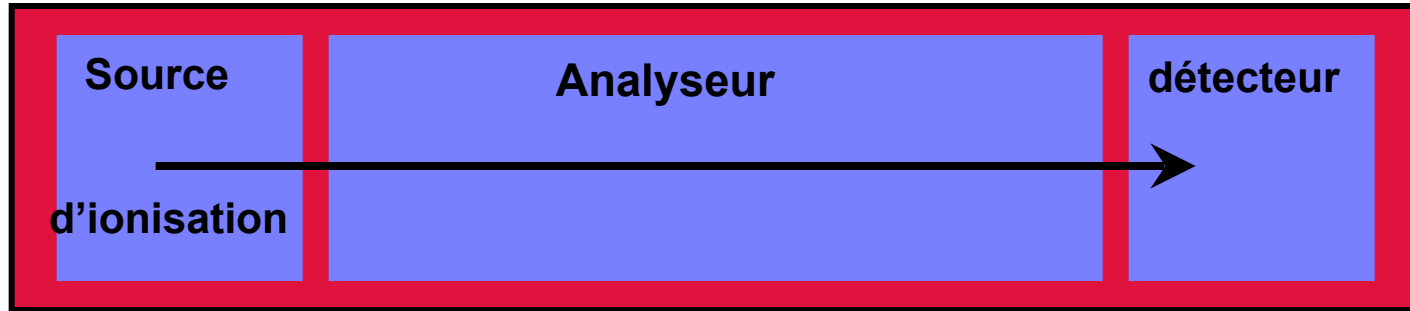
Détecteur



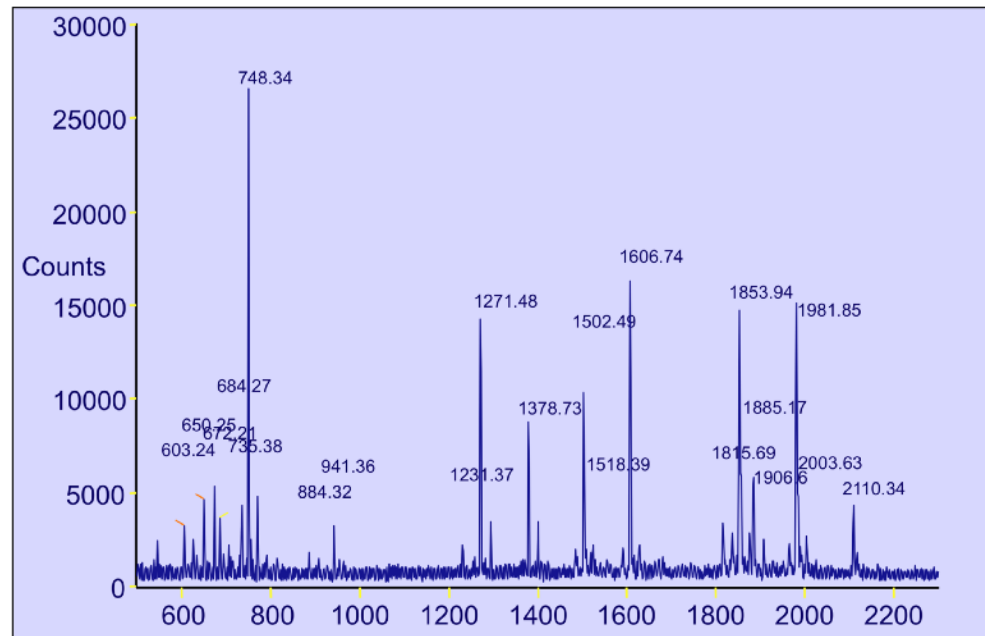
5. Les analyses protéiques

4

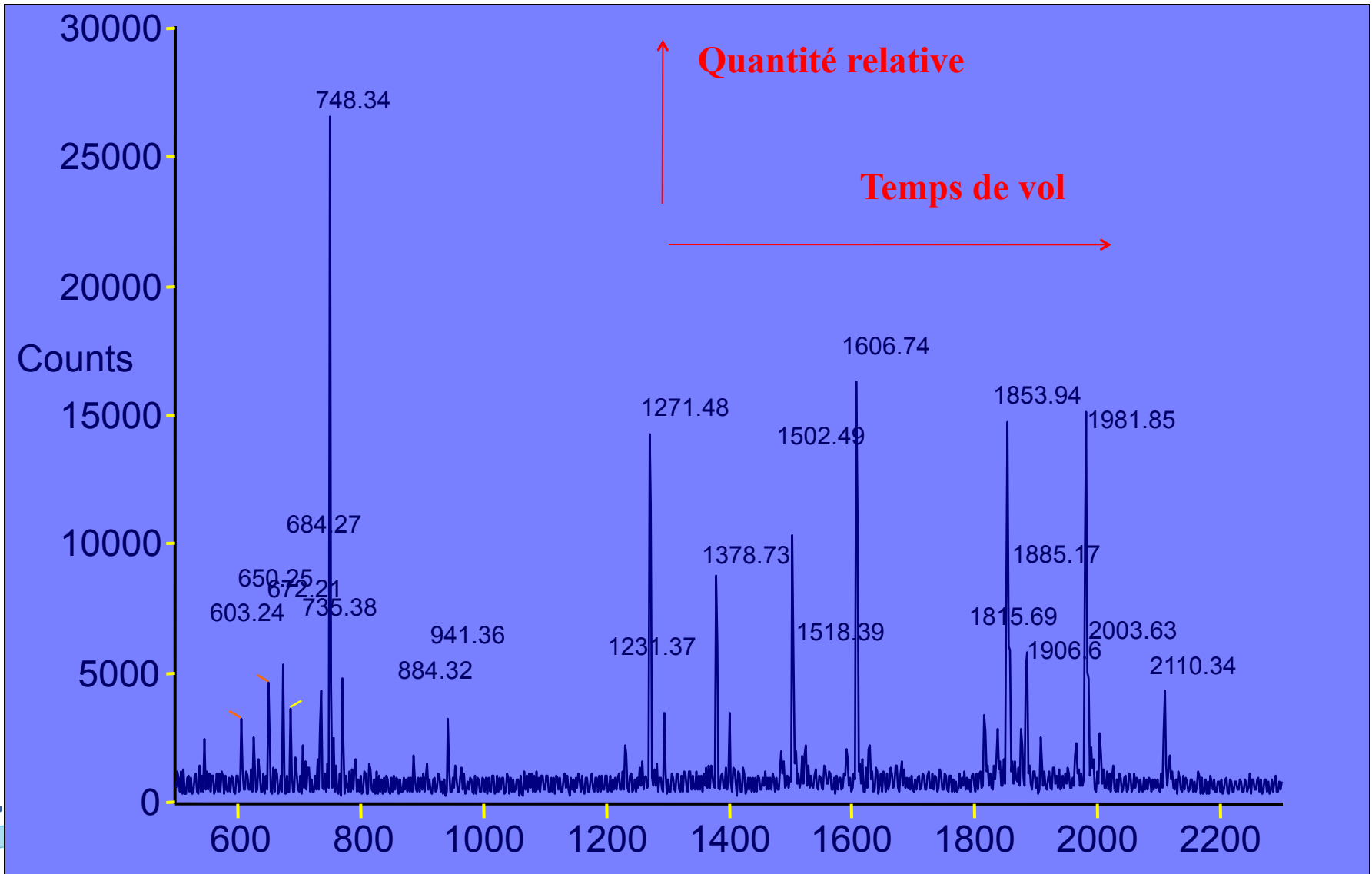
La spectrométrie de masse



Détecteur

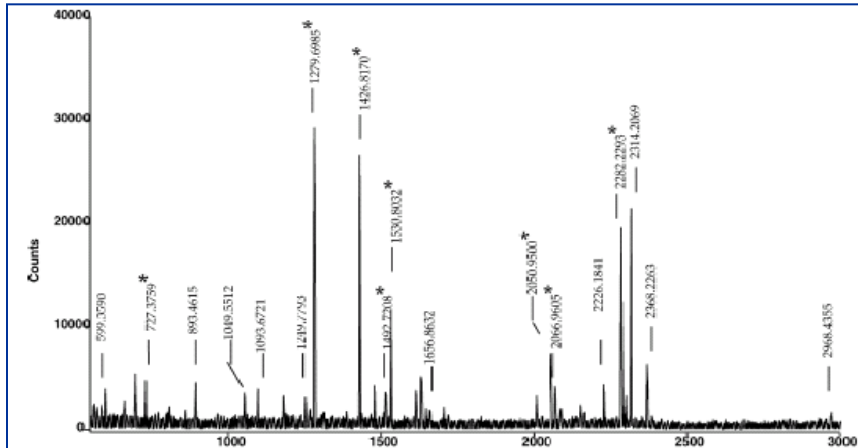


5. Les analyses protéiques



5. Les analyses protéiques

Cartographie massique par SM

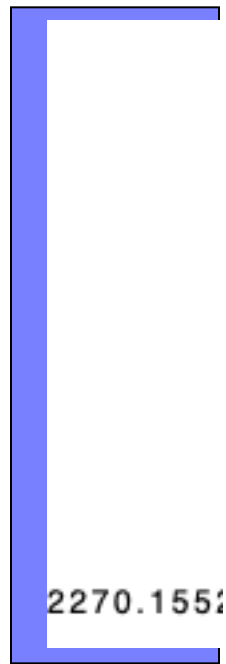


4148.1061
3221.5113
3392.5756
2993.3522
2468.2415
2325.0207
2144.9770
1948.9585
2005.9800
1906.8817
1883.0497
1721.7765
1618.7577
1732.8006
1508.7889
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950.4499
1007.4714
880.4159
832.3658
792.3709

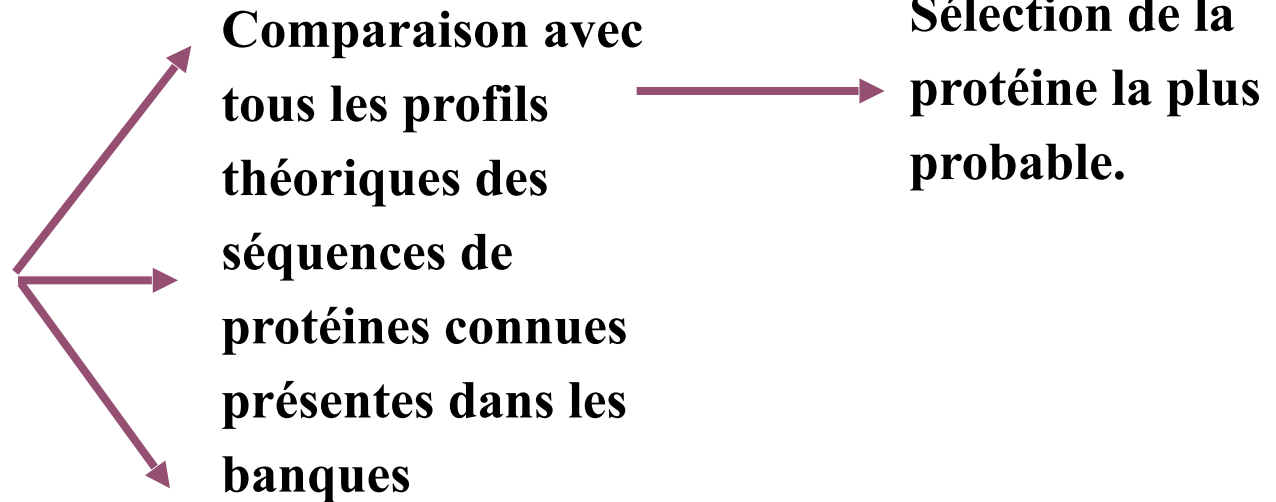
La carte massique obtenue est **l'empreinte massique** de la protéine. Elle est très spécifique.

5. Les analyses protéiques

Liste de masses
expérimentale



Interrogation des banques de données



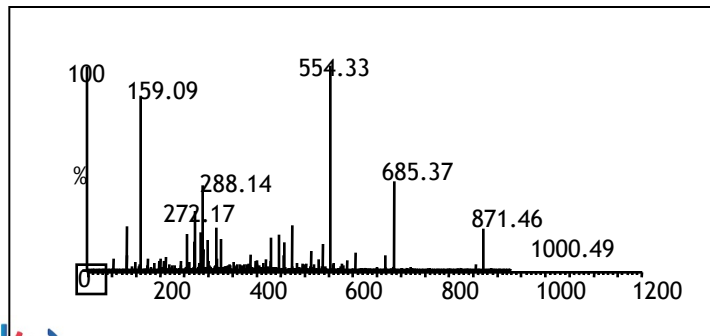
5. Les analyses protéiques

Données expérimentales

Masse du peptide tryptique (m)

+

Spectre MS/MS



Données théoriques

Digestion tryptique *in silico* des banques protéiques

Sélection des n protéines pour lesquelles on attend un peptide tryptique de masse m

n spectres MS/MS théoriques

MASCOT

6. Exemple publication utilisant la bioinfo

OPEN ACCESS Freely available online



A Rapid Screening Assay to Search for Phosphorylated Proteins in Tissue Extracts

Un papier de 2012 mais qui est représentatif du cours...

Ignazio Garaguso, Juergen Borlak*

Centre for Pharmacology and Toxicology, Hannover Medical School, Hannover, Germany

Abstract

Reversible protein phosphorylation is an essential mechanism in the regulation of diverse biological processes, nonetheless is frequently altered in disease. As most phosphoproteome studies are based on optimized *in-vitro* cell culture studies new methods are in need to improve *de novo* identification and characterization of phosphoproteins in extracts from tissues. Here, we describe a rapid and reliable method for the detection of phosphoproteins in tissue extract based on an experimental strategy that employs 1D and 2D SDS PAGE, Western immunoblotting of phosphoproteins, in-gel protease digestion and enrichment of phosphopeptides using metal oxide affinity chromatography (MOAC). Subsequently, phosphoproteins are identified by MALDI-TOF-MS/MS with the CHCA-TL or DHB ML sample matrix preparation method and further characterized by various bioinformatic software tools to search for candidate kinases and phosphorylation-dependent binding motifs. The method was applied to mouse lung tissue extracts and resulted in an identification of 160 unique phosphoproteins. Notably, TiO₂ enrichment of pulmonary protein extracts resulted in an identification of additional 17 phosphoproteins and 20 phosphorylation sites. By use of MOAC, new phosphorylation sites were identified as evidenced for the advanced glycosylation end product-specific receptor. So far this protein was unknown to be phosphorylated in lung tissue of mice. Overall the developed methodology allowed efficient and rapid screening of phosphorylated proteins and can be employed as a general experimental strategy for an identification of phosphoproteins in tissue extracts.

Citation: Garaguso I, Borlak J (2012) A Rapid Screening Assay to Search for Phosphorylated Proteins in Tissue Extracts. PLoS ONE 7(11): e50025. doi:10.1371/journal.pone.0050025

Editor: Christina Lynn Addison, Ottawa Hospital Research Institute, Canada

Received August 30, 2012; **Accepted** October 19, 2012; **Published** November 15, 2012

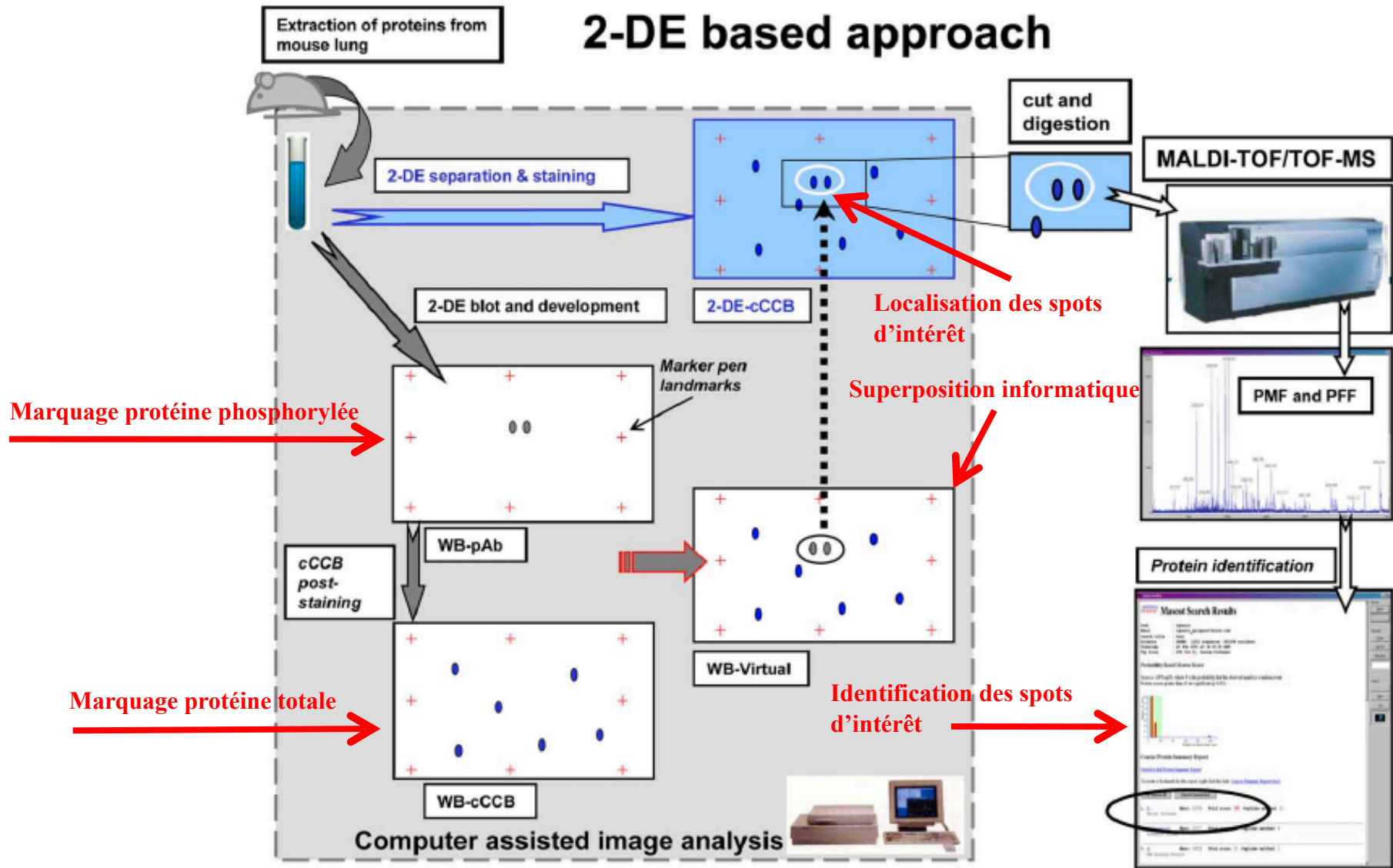
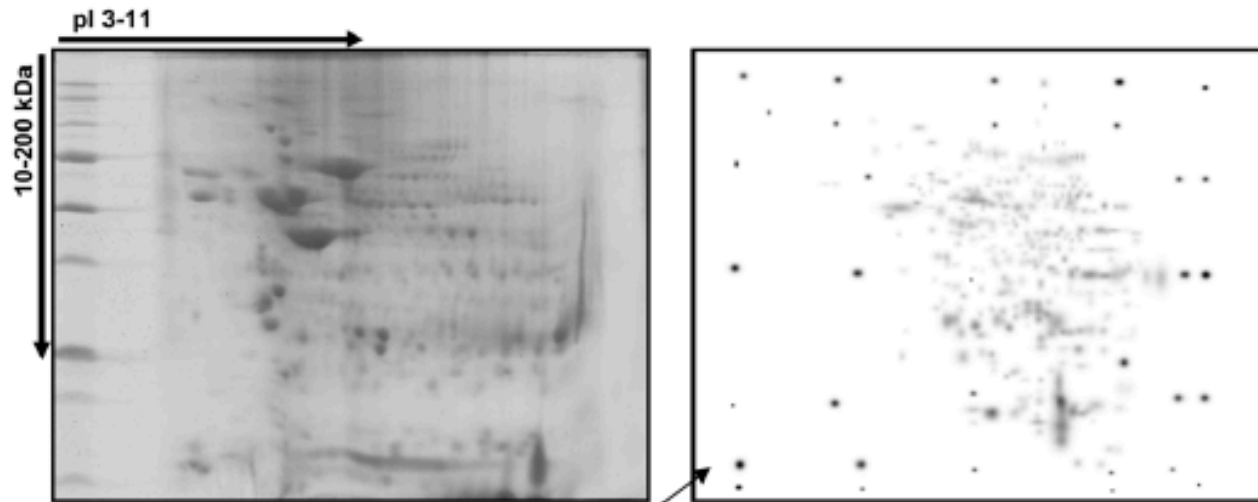


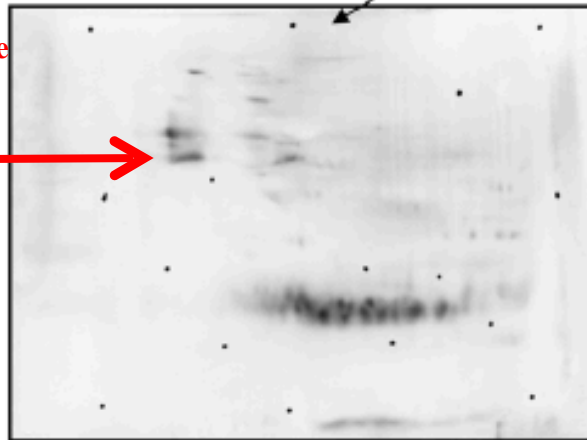
Figure 1. Description of the combined 2-DE-WB approach. 200 µg of tissue lysate protein extracts were separated on 2-DE, stained with Colloidal Coomassie G-250 and acquired as an image (2-DE-cCBB). In parallel 40 µg of total protein extract was separated by 2-DE and subsequently transferred onto PVDF membrane for incubation with antibodies directed against phosphorylated proteins. With a marker pen, landmarks points (crosses in Figure) were set around the membrane and the image of phosphorylated proteins was acquired (WB-pAb). Subsequently, the total proteins on the same membrane were revealed by cCBB-post staining and the image was recorded (WB-CBB). Using the marker added landmarks the two images were superimposed and combined by the image analysis software to create a virtual image showing the phosphoproteins and the total proteins together (WB-virtual). Several protein spots from this image, which are in common with the cCBB-2-DE image, were selected as additional landmarks and used to superimpose the WB-CBB image to the 2-DE-cCBB image. This allowed deciphering of phosphorylated proteins on the gel. Highlighted spots were then excised from the gel using a spot cutter, followed by in-gel digestion using trypsin. The proteins were identified using MALDI-TOF MS.

6. Exemple publication utilisant la bioinfo

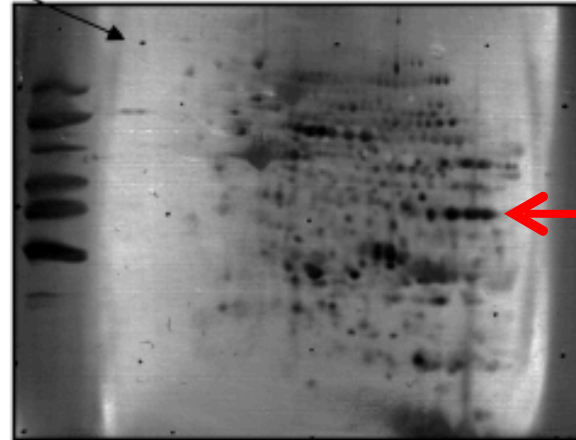


Marker pen Landmarks

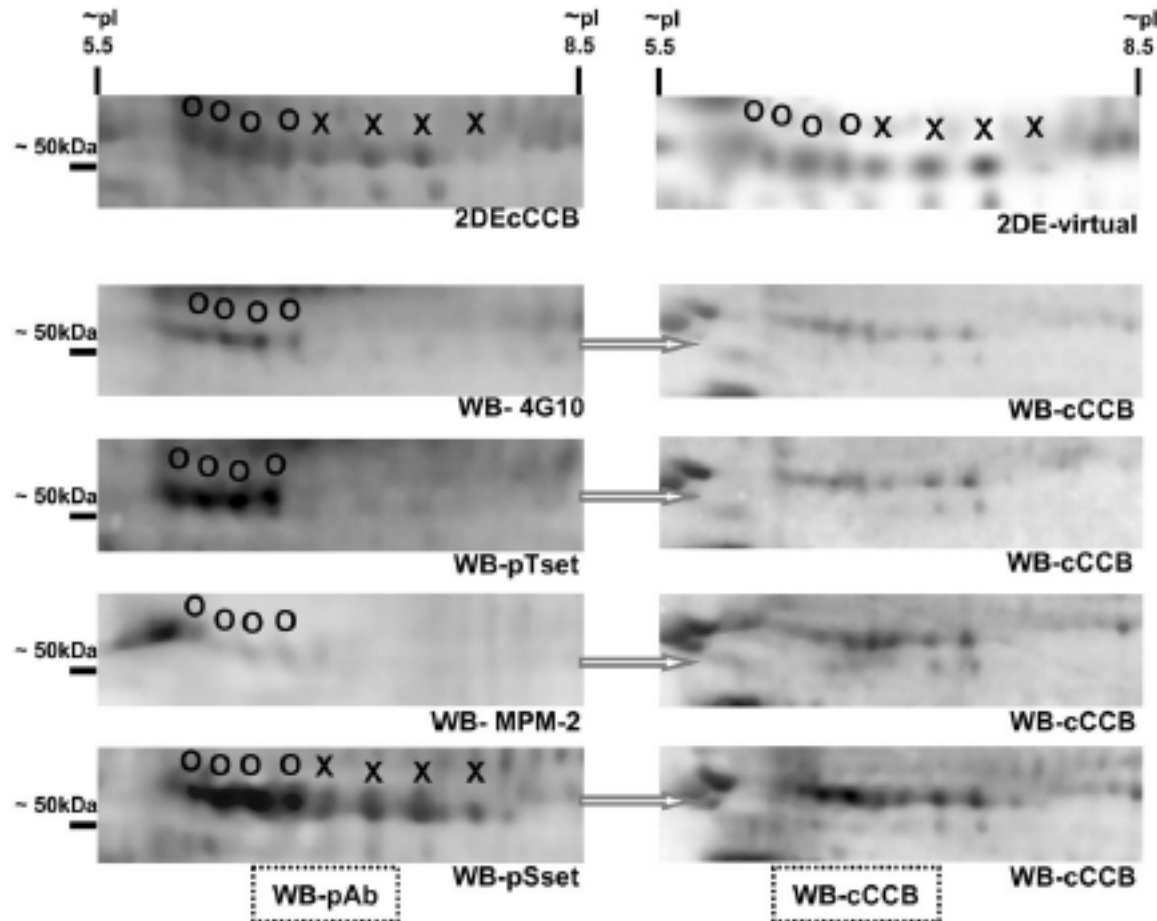
Marquage protéine phosphorylée sur tyrosine



Marquage protéine Phosphorylée sur sérine

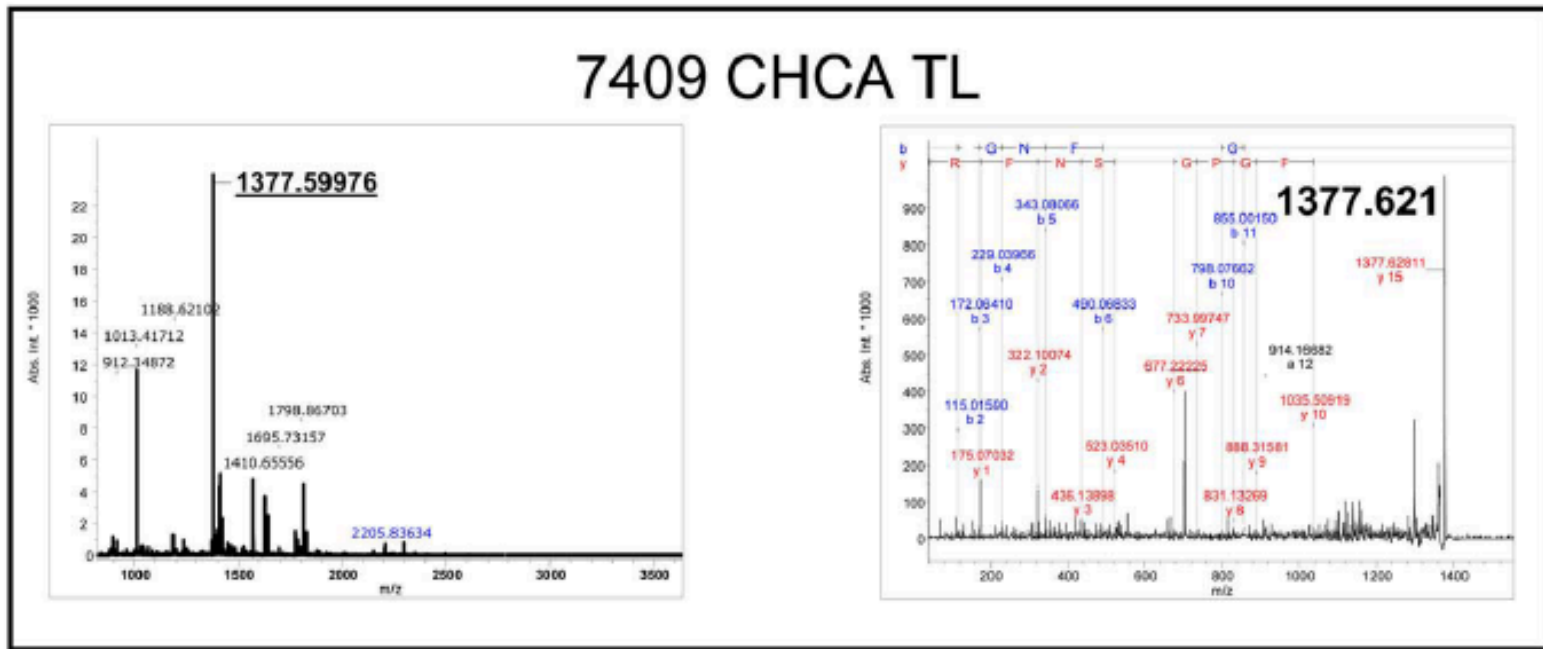
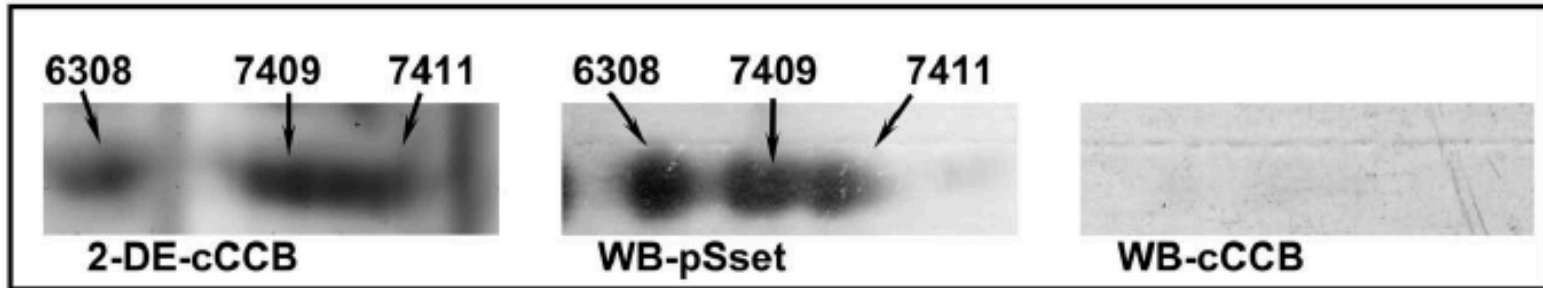


6. Exemple publication utilisant la bioinfo



Une phosphorylation modifie une immunoréactivité: notion de comètes:

6. Exemple publication utilisant la bioinfo



Analyse jusqu'à l'identification

6. Exemple publication utilisant la bioinfo

Table 1. Identified phosphopeptide by MALDI tandem MS using DHB ML sample preparation.

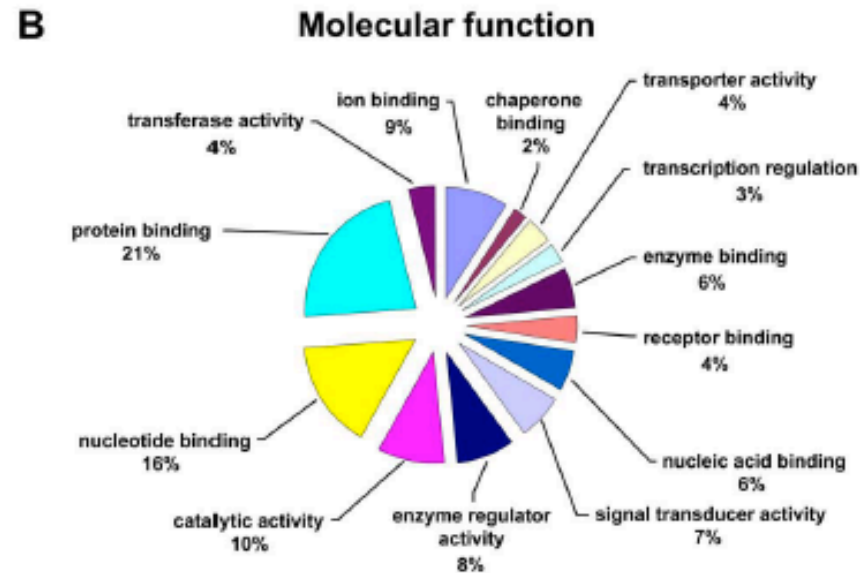
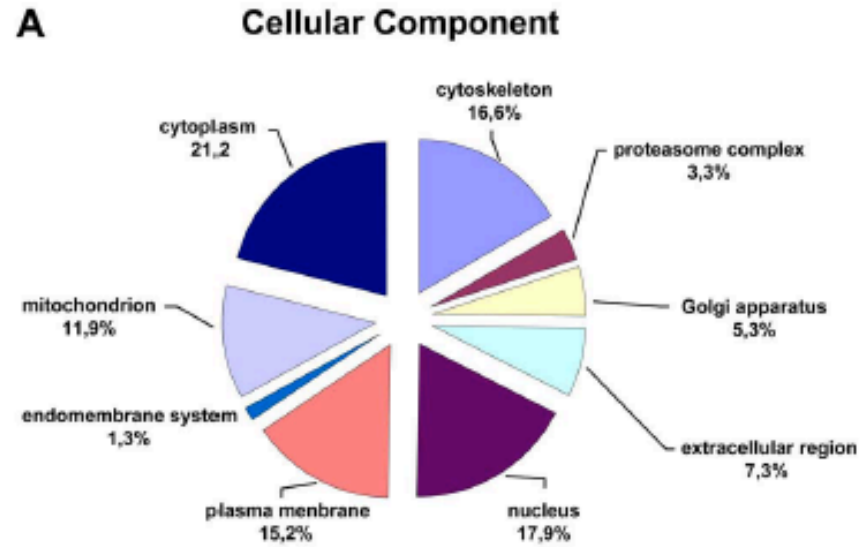
Protein Entry Name	Accession	Sequence	Start end	Meas. mass	Ion Score	Miss	MW
Angiotensin-converting enzyme	P09470	R.GPQFG <u>S</u> EVELR.H	1300–1310	1298.57765	63	0	151.888
Calnexin precursor	P35564	K.AEEDEILNRS <u>P</u> R.N	573–584	1508.67402	39	1	67.733
Advanced glycosylation end product-specific receptor	Q62151	R.KAPES <u>S</u> QEDEEERA	373–384	1526.60058	60	1	43.068
Nascent polypeptide-associated complex alpha subunit	P70670	R. <u>S</u> VTDPAMAPRTAK.N	588–600	1600.58786	20	1	221.603
Matrix-remodeling-associated protein 7	Q9CZH7	R.VAEPEE <u>S</u> EAEPPAAEGR.Q	73–89	1879.75921	82	0	19.516
Tensin	gi 226437589	R. <u>S</u> QSFPDVEPQLPQAPTR.G	790–806	1976.91134	56	0	203.317
Arginase-1	Q61176	- <u>M</u> SSKPK <u>S</u> LEIIGAPFSK.G	1–17	2075.89248	35	0	34.999
60S acidic ribosomal protein	P99027	K.KEE <u>S</u> EE <u>S</u> DD <u>M</u> GFGLFD.-	99–115	2125.68687	40	1	11.651
60S acidic ribosomal protein P1	P47955	K.KEE <u>S</u> EE <u>S</u> ED <u>M</u> GFGLFD.-	98–114	2139.70251	40	1	11.610
Myosin phosphatase Rho-interacting protein	P97434	R.AEEQLPPLLSP <u>P</u> SPTPHSR.R	280–299	2220.06959	27	0	117.357
Alpha-1 catenin	P26231	R.TPEELDD <u>S</u> DFETEDFDVR.S	634–651	2238.85983	127	0	100.896
Membrane-associated progesterone receptor component	O55022	K.EGEEPTV <u>S</u> DDDEPKDETAR.K	173–192	2375.93983	112	1	21.692
60S acidic ribosomal protein P0	P14869	K.AEAKE <u>S</u> EE <u>S</u> ED <u>M</u> GFGLFD.-	298–317	2410.81924	45	1	34.408
Septin-2	P42208	K.IYHLPDAE <u>S</u> DEDEDKFQEQL.R	210–229	2517.04527	115	0	41.783
EH domain-containing protein	Q8BH64	R.GPDEAIEDGEE <u>S</u> EDDAEWWVTK.D	426–448	2557.01375	112	1	50.135
Elongation factor 1-delta	P57776	K.GATPAEDDEDKIDILFG <u>S</u> DEEEEDKEAAR.L	145–173	3276.32225	144	2	31.916
Serum deprivation-response protein	Q63918	R.GNNSAVG <u>S</u> NADLTIEEDEEEEPVALQQAQ QVR.Y	356–387	3520.57109	135	0	46.806
		R.RGNNSAVG <u>S</u> NADLTIEEDEEEEPVALQQAQ QVR.Y	355–387	3676.67219	105	1	
		K.SSPFKV <u>S</u> PLSFRGK	287–299	1488.72465	53	1	

Phosphopeptides identified by MALDI-TOF-MS/MS from 50 µg of protein extracted from mouse lung and separated by SDS-PAGE.

S = phosphorylated serine determined by MALDI TOF-MS/MS. M = oxidized methionine.

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6. Exemple publication utilisant la bioinfo



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