



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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Gene sequences and annotations used as references for the study of orthologs structure, expression, and evolution

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Functional genomics studies

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Gene expression and molecular abundance profiles

HomoloGene

Homologous genes sets for selected organisms

PopSet

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

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Protein sequences grouped by identity

Protein

Protein sequences

Protein Clusters

Sequence similarity-based protein clusters

Protein Family Models

Models representing homologous proteins with a common function

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Experimentally-determined biomolecular structures

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Genome assembly information

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Museum, herbaria, and other biorepository collections

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Biological projects providing data to NCBI

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Descriptions of biological source materials

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Genome sequencing projects by organism

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SRA

High-throughput sequence reads

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Taxonomic classification and nomenclature

BLAST

A tool to find regions of similarity between biological sequences

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Search nucleotide sequence databases

blastp

Search protein sequence databases

blastx

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

ClinicalTrials.gov

Privately and publicly funded clinical studies conducted around the world

ClinVar

Human variations of clinical significance

dbGaP

Genotype/phenotype interaction studies

dbSNP

Short genetic variations

dbVar

Genome structural variation studies

GTR

Genetic testing registry

MedGen

Medical genetics literature and links

OMIM

Online mendelian inheritance in man

PubChem

Repository of chemical information, molecular pathways, and tools for bioactivity screening

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Bioactivity screening studies

Compounds

Chemical information with structures, information and links

Pathways

Molecular pathways with links to genes, proteins and chemicals

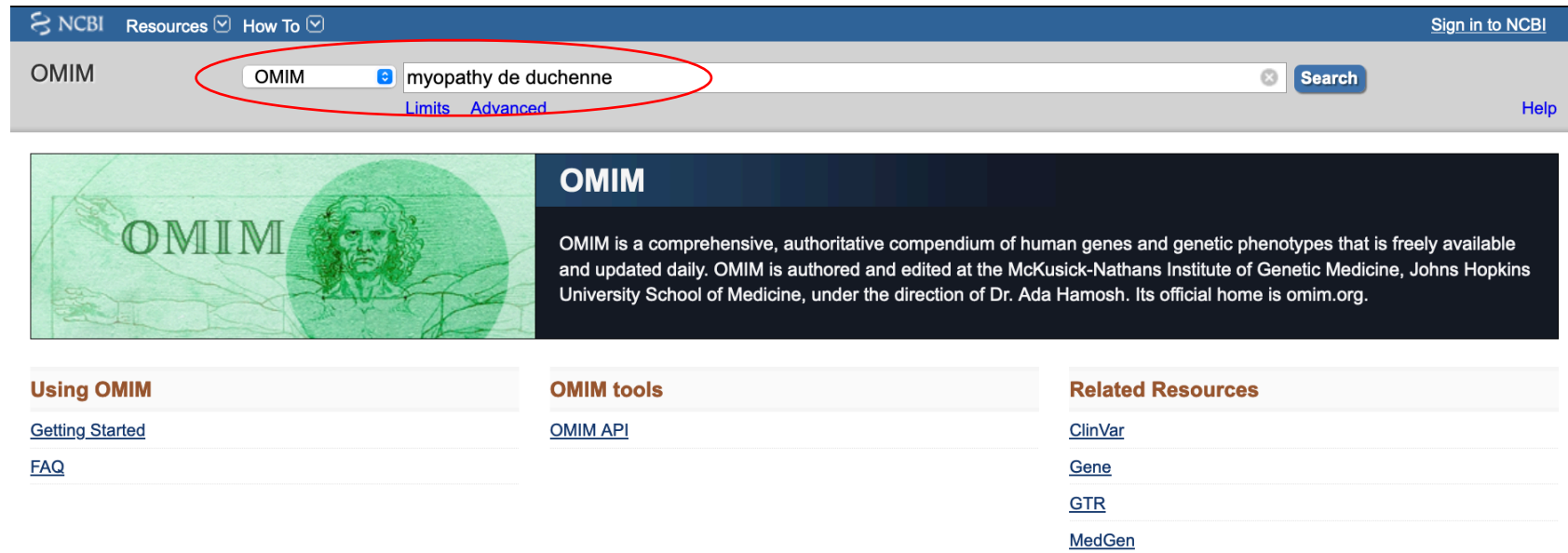
Substances

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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Limits Advanced Help

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

Find related data

Database: Select

Find items

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

Search

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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

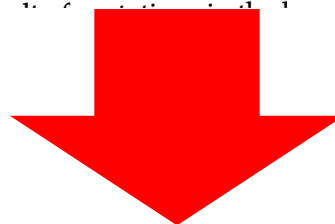
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▼ Description

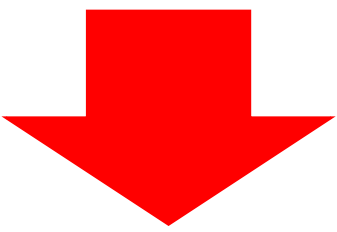
Dystrophin-associated muscular dystrophies range from the severe Duchenne muscular dystrophy (DMD) to the milder Becker muscular dystrophy (BMD; 300376). Mapping and molecular genetic studies indicate that both are the result of mutations in the huge gene that encodes dystrophin, also symbolized DMD. 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

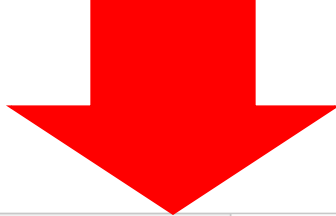
Skeletal Muscle

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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Cite Salehi L, Rahimzadeh M, Molaei E, Zaheri H, Esmaelzadeh-Saeieh S.
Share Brain Behav. 2020 Sep 23:e01835. doi: 10.1002/brb3.1835. Online ahead of print.
PMID: 32969190
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 ...

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

Experiences of breastfeeding during COVID-19: Lessons for future practical and emotional support.
3
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Mental health and sleep habits during preclinical years of medical school.
1 McKinley B, Daines B, Allen M, Pustispher K, Zapata I, Wilde B.
Cite Sleep Med. 2022 Sep 9;100:291-297. doi: 10.1016/j.sleep.2022.09.001. Online ahead of print.
Share PMID: 36148761
Additional assessments evaluated exercise habits, chronic disease, and impact of **COVID-19** Pandemic. The **COVID-19** Pandemic was evaluated directly in the model (pre- and post-**COVID-19** period variable), and through additional questions on th ...

Letter to the Editor: "Respiratory and peripheral muscular ultrasound characteristics in ICU COVID 19 ARDS patients".
2 Sajid DS.
Cite J Crit Care. 2022 Sep 20;72:154155. doi: 10.1016/j.jcrc.2022.154155. Online ahead of print.
Share PMID: 36148740 No abstract available.

Risk factors associated with COVID-19 infection and mortality in nursing homes.
3 Beobide Telleria I, Ferro Uriguen A, Laso Lucas E, Sannino Menicucci C, Enriquez Barroso M, López de Munain Arregui A.
Cite Aten Primaria. 2022 Sep 6;54(10):102463. doi: 10.1016/j.aprim.2022.102463. Online ahead of print.
Share PMID: 36148713
OBJECTIVE: The aim of this paper was to analyse the association of demographic, clinical and pharmacological risk factors with the presence of **SARS-COV-2** virus infection, as well as to know the variables related to mortality from **COVID-19** in nur ...

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Cite Salehi L, Rahimzadeh M, Molaei E, Zaheri H, Esmaelzadeh-Saeieh S.
Share Brain Behav. 2020 Sep 23:e01835. doi: 10.1002/brb3.1835. Online ahead of print.
PMID: 32969190
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 ...

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

[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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PMID: 32960881 DOI: [10.1371/journal.pmed.1003346](#)

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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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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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Diana Buitrago-Garcia^{1,2,c}, Dianne Egli-Gany^{1,c}, Michel J. Counotte^{1,c}, Stefanie Hossmann¹, Hira Imeri¹, Aziz Mert Ipekci¹, Georgina 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 Database 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 ^d |
|--|--------------------------|---------------------|----------------------------|----------------------------|---|-------------------------------|
| Contact investigation, single | | | | | | |
| Tong, ZD [44] | China, Zhejiang | 5 | 3 | 2 F, 3 M | 28 IQR 12–41 | 1, 3 |
| Huang, R [74] | China, Suqian | 2 | 1 | 1 F, 0 M | 54 | 3 |
| Jiang, XL [76] | 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 [49] | 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 [47] | China, Wuhan | 47 | 4 | NR | NR | 1 |
| Wu, J [105] | China, Zhuhai | 83 | 8 | NR | NR | 1, 2 |
| Luo, L [36] | China, Guangzhou | 129 | 8 | NR | NR | 1, 2, 3 |
| Bi, Q [60] | 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 |
| Roxby, AC [94] | USA | 6 | 3 | NR | NR | 1 |
| Yang, N [48] | China, Xiaoshan | 10 | 2 | 1 F, 1 M | NR | 1, 2 |
| Schwiezack, 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 [71] | United Kingdom | 126 | 46 | NR | NR | 2 |

(Continued)

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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.

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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.

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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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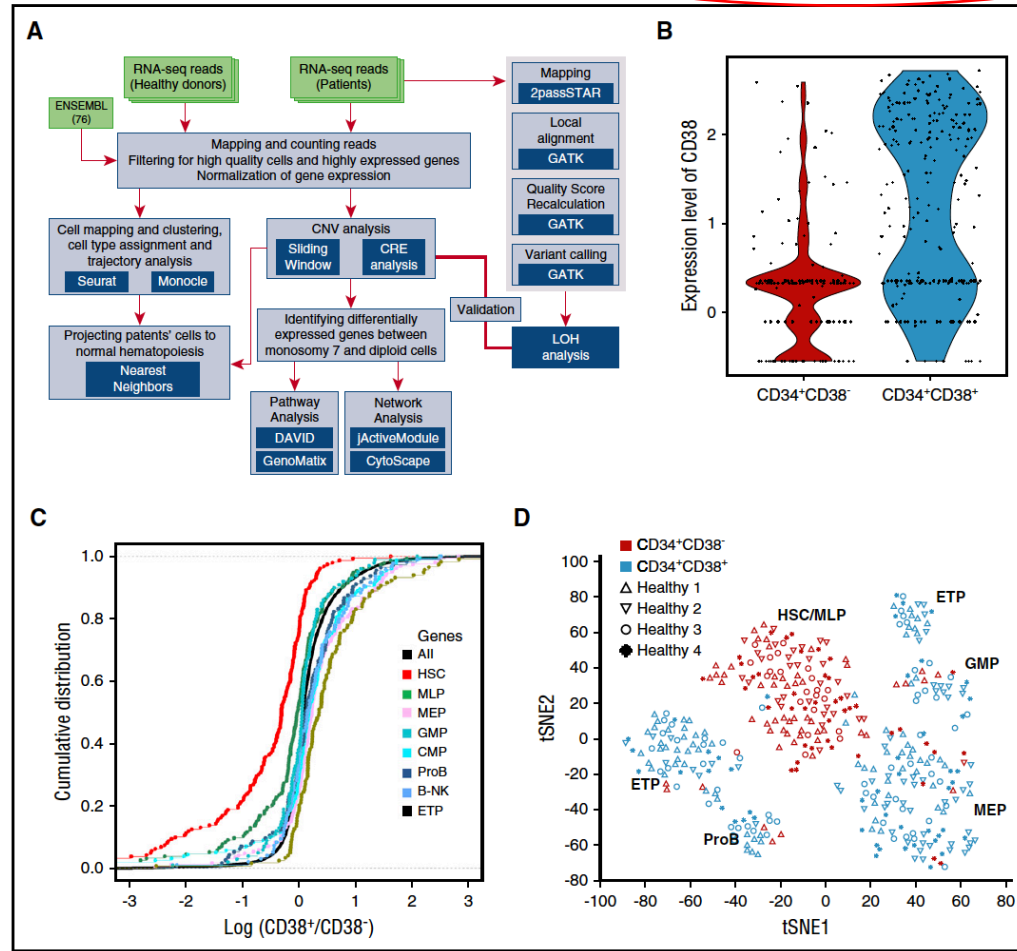


Figure 1. Hematopoietic heterogeneity in healthy donors quantified by scRNA-seq. CD34⁺CD38⁻ and CD34⁺CD38⁺ cells from 4 healthy donors (healthy 1-4) were sorted by surface-membrane markers and subjected to analyses. (A) The schematic pipeline consisting of 3 major analytic components: differentiation 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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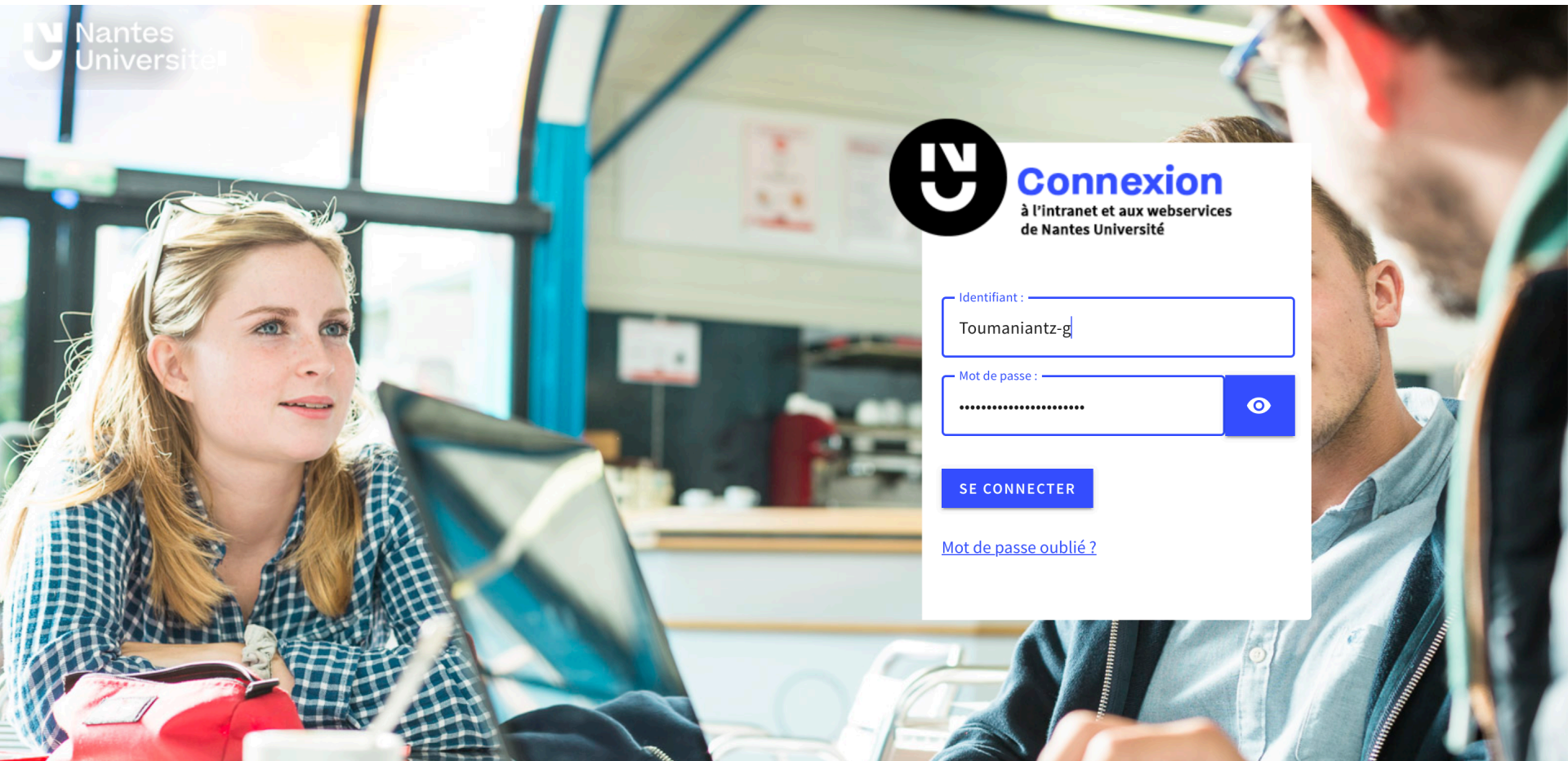


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Un exemple de recherche: Covid19 ?

nature

Titre de revue

Résultats de la recherche - nature

Affiner les résultats

En ligne ?

Non 27

Oui 14

Format

Revue 40

Base de données 1

Bibliothèque

BU Santé 12

BU Sciences 11

Bib. DCS (Droit et Changement Social) 3

Bib. Géothèque A. Vigarité 2

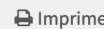
BU Droit 1

BU Lettres 1

Résultat(s) 1 - 20 résultats de 41 pour la requête 'nature', Temps de recherche: 0,05s

Trier Pertinence

Tout cocher | avec la sélection:



1



Nature

Macmillan Journals 1869-
La bibliothèque possède :

BU Sciences : Vol. 202 (1964) - Vol. 203 (1964) ; Vol. 206 (1965) - Vol. 257 (1975) ; Vol. 259 (1976) - Vol. 312 (1984) ; Vol. 322 (1986) - Vol. 565 (2019)

Egalement en ligne : [En ligne](#) [Via Nature](#)

[Sommaires en ligne](#)

Revue



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2



Nature

Nature
depuis 1869 jusqu'à 2012

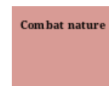
L'accès à cette ressource est contrôlé.

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3



Combat nature

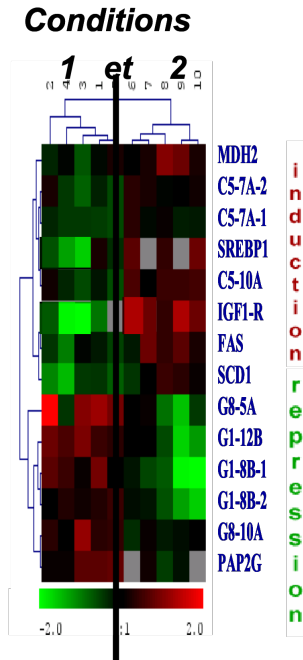
Société d'édition pour la nature et l'environnement 1974-2004
La bibliothèque possède :

Au labo : analyse à haut débit de cette bibliographie.

Les données expérimentales (en « omique ») => Biblio à au débit...

sont-elles cohérentes/incohérentes

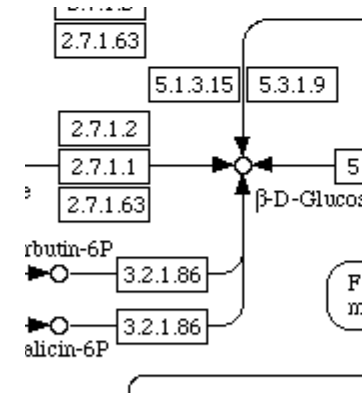
avec les connaissances du moment ?



littérature



Les modèles intégrés



→ Construire un modèle intégré de connaissance

→ Développer des méthodes pour comparer données expé et modèle permettant de trouver les cohérences/incohérences

2. Les analyses nucléotidiques

Question à étudier:

2. Les analyses nucléotidiques

NCBI
PubMed
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[www.pubmed.gov](#)

All Databases PubMed **Nucleotide** Protein Genome Structure OMIM PMC Journals Books

Search PubMed 101 Go Clear [Advanced Search \(beta\)](#)

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If you publish in one of [these journals](#), they will take care of the whole process.
If you publish *anywhere else*, deposit the manuscript in PubMed Central via one of the options described at [publicaccess.nih.gov](#).
Note: Other funding organizations, including [HHMI](#), [Wellcome Trust](#) and the [MRC](#) also require papers to be made freely available through PMC.

PubMed is a service of the [U.S. National Library of Medicine](#) that includes over 18 million citations from MEDLINE and other life science journals for biomedical articles back to the 1950s. PubMed includes links to full text articles and other related resources.

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Special Queries
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2. Les analyses nucléotidiques

NCBI

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Entrez Tools

Check sequence revision history

LinkOut

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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 38.2 statistics [Switch to previous build](#)

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

10 30 14 2 10

Hits: 14 15 16 17 18 19 20 21 22 X Y III not placed

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](#)).

2. Les analyses nucléotidiques

NIH U.S. National Library of Medicine NCBI National Center for Biotechnology Information Sign in to NCBI

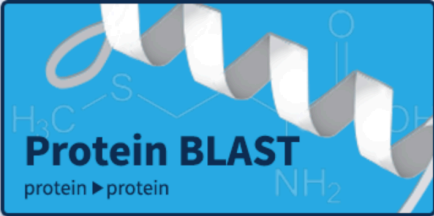



BLAST Home Recent Results Saved Strategies Help

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



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](#)

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

CCGCGTGGTGGCCCGAGCCAGCGAGGGGCTCAGCGCCGCTGCTGGAGCAGCGGACCCGGGGTATCGGGCCAC

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

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NCBI/ BLAST/ blastn suite/ Formatting Results - HRDEGBVV01R

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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 defline and scores, click to show alignments

Color key for alignment scores

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

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 |
| J05501.1 | 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 TGGGACTGCTGGTGGTGCCTTTTCGGGGCCACCATTTGGTG 240
Sbjct 301 GCCAGCGCCGATCTGGTCA TGGGACTGCTGGTGGTGCCTTTTCGGGGCCACCATTTGGTG 360
Query 241 TGGGGCCGCTGGGAGTACGGCTCCTTCTTCTGTGAGCTCTGGACTTCGGTAGACGTGCTA 300
Sbjct 361 TGGGGCCGCTGGGAGTACGGCTCCTTCTTCTGTGAGCTCTGGACTTCGGTAGACGTGCTA 420
Query 301 TGTGTGACGGCCAGCATCGAGACCCCTGTGTGCATCGCCCTGGAGCGCTTCCTCGGCATC 360
Sbjct 421 TGTGTGACGGCCAGCATCGAGACCCCTGTGTGCATCGCCCTGGAGCGCTTCCTCGGCATC 480
Query 361 ACGCTGCCCTTTTCGCTACCAGACCTGCTGACGCGCGCGGAGCGCGGGCCCTCGTGTGC 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

```

FEATURES             Location/Qualifiers
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                        /db_xref="RGD:2059"
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                        TLPFRYQSLLTRARARALVCTVWAI SALVSFLPILMHWRAESDEARRCYNDPKCCDF
                        VTNRAYAIASSVVSFYVPLCIMA FVYLRVRFREAQKQVKKIDSCERRFLTGP RPPSPA
                        PSPSPGPPRPADSLANGRSSKRRPSRLVALREKALKTLGIIMGVFTLCWL PFFFLANV
                        VKAFHRDLVDPDLV FVFNWLG YANSAFNP I IYCRSPDFRKA FQRLCCARRAACRRRA
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                        SLDEPGRQGFSSSESKV"
     STS                274..795
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                        /gene_synonym="BIAR"
                        /gene_synonym="RATBIAR"
                        /standard_name="Adrb1"
                        /db_xref="UniSTS:256461"
     STS                1252..1351
                        /gene="Adrb1"
                        /gene_synonym="BIAR"
                        /gene_synonym="RATBIAR"
                        /standard_name="Adrb1"
                        /db_xref="UniSTS:141043"
ORIGIN
1 atggggcggcgg gggcgcctgc cctgggcgcc tccgaacct gcaacctgtc gtcggcggcg
61 cgcctgcccc acggcgcggc caccgcggca cgactgctg tgcctcgcgc gcctcccggc
121 tcgctgctgc ctccagccag cgaggcctca gcgcgcctgt cgcagcagtg gaccgcgggt
181 atgggcctac tctggcgcct catcgtgctg ctcactgtag tgggcaactg gttggtgac
241 gtggccatcg ccaagacccc gcggctgcag acgctcacca acctcttcat catgtccctg
301 gccagcgcgg atctgtgcat gggactgctg gtggtgcctt tcggggccac cattgtggtg
361 tggggccgct gggagtacgg ctctctcttc tgtgagctct ggacttcggt agacgtgcta
421 tgtgtgacgg ccagcatcga gacctgtgtg gteatgcgcc tggaccgcta cctcggcact
481 acgctgcctt 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](#)

tcgctgctgcctccagccagcagggctcagcgcgcgtgctgcagcagtgaccgcgggtatggcctac

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

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NCBI/BLAST/tblast/ 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 |
|-----|-------|-------|--------|-------|

Query 0 100 200 300 400 500 600 700

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 |
| | | HCHEGPRSRARQQALVAKGQRDG | |
| Sbjct | 722 | EIAALGVVVAARFVALGPPPVHEDGQEGHQRGDGP | 543 |
| | | HCHEGPRSRARQQALVAKGQRDG | |
| Query | 354 | EEAVQGGDTQGLDAGRHT*HVVYRSP | 175 |
| | | ELTEEGAVLPAAPHHNGGPERHHQQSHDQIGAGQG | |
| Sbjct | 542 | EEAVQGGDTQGLDAGRHT*HVVYRSP | 363 |
| | | ELTEEGAVLPAAPHHNGGPERHHQQSHDQIGAGQG | |
| Query | 174 | HDEEVGERLQPRGLGDGHDHQHVAHYDEQHDERQE*AHTRG | 1 |
| | | PLLRR*ALAGWRQQR | |
| Sbjct | 362 | HDEEVGERLQPRGLGDGHDHQHVAHYDEQHDERQE*AHTRG | 189 |
| | | PLLRR*ALAGWRQQR | |

2. Les analyses nucléotidiques

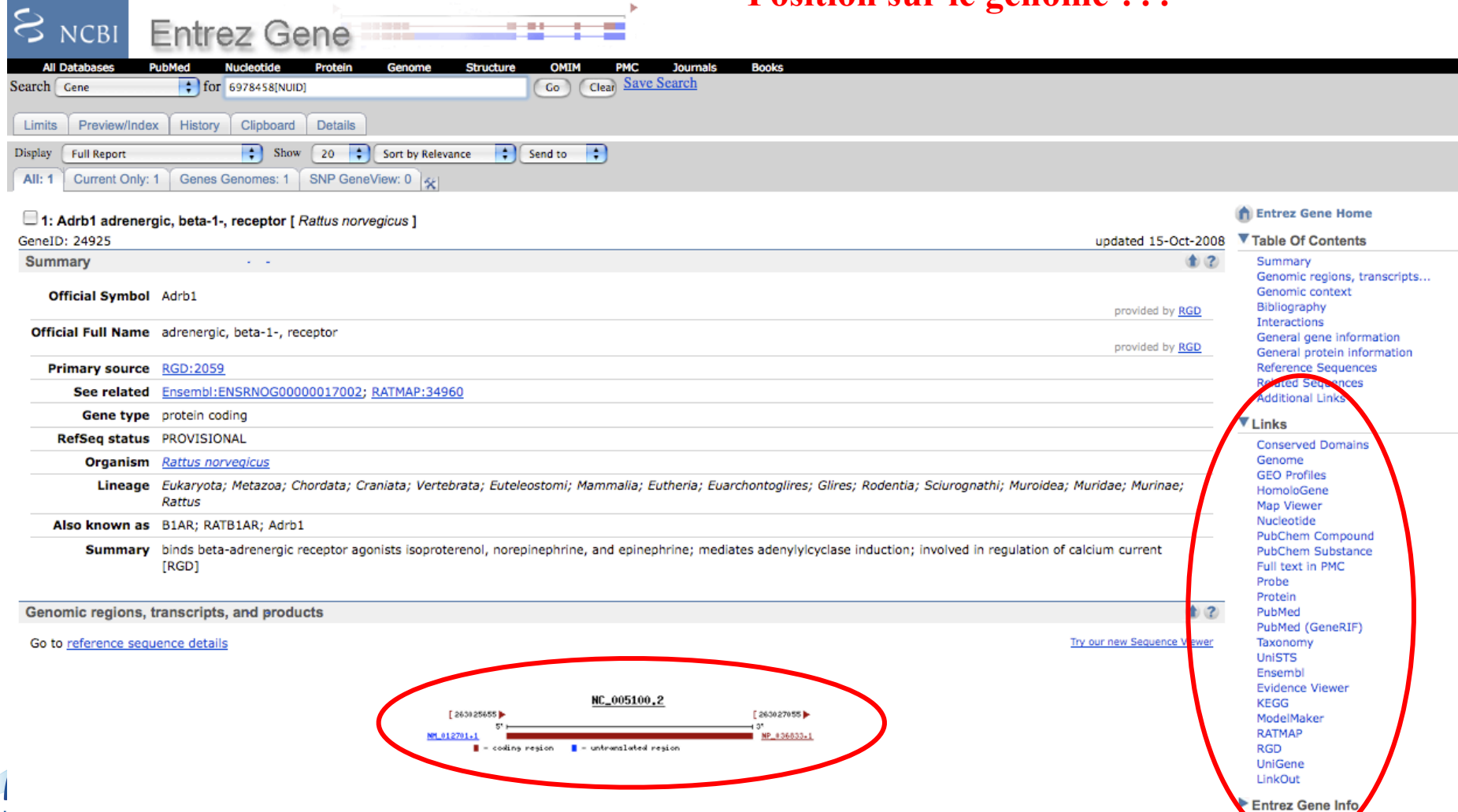
Legend for links to other resources: [U](#) UniGene [E](#) GEO [G](#) Gene [S](#) Structure [M](#) Map Viewer

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](#)

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 Home

Table Of Contents

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

NC_005100.2

[263925655] [263927959]

5' 3'

[NM_012701.1](#) [NP_036502.1](#)

■ = coding region ■ = untranslated region

2. Les analyses nucléotidiques

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

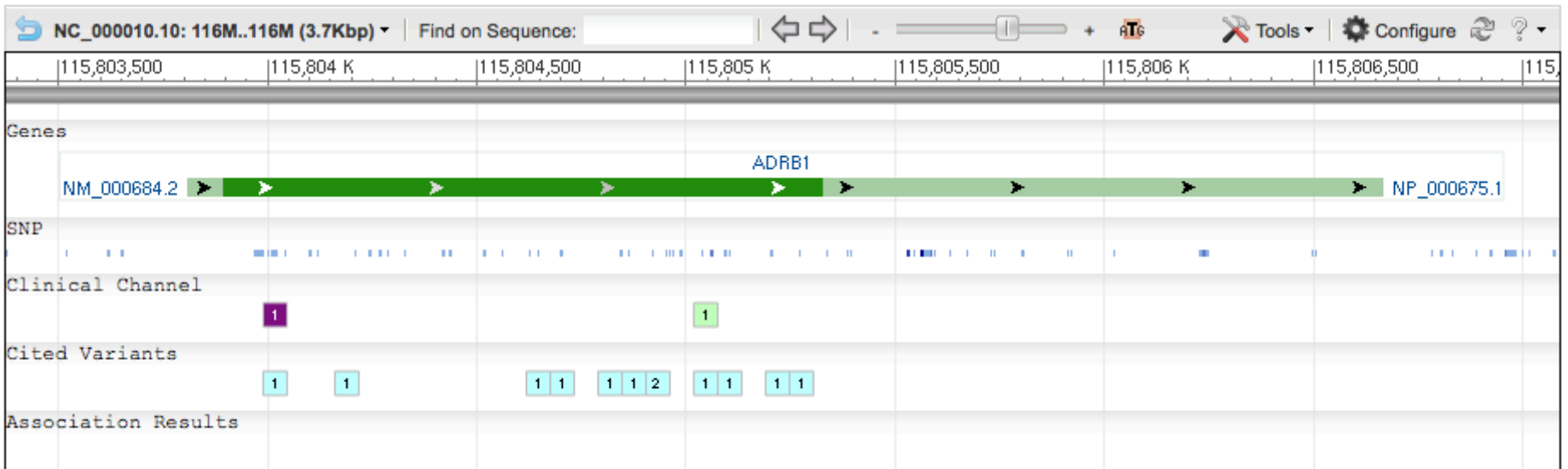
Position sur le génome ???

Genomic regions, transcripts, and products

Genomic Sequence

Go to [reference sequence details](#)

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



Exons, introns, SNP, etc...

2. Les analyses nucléotidiques

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PubMed Entrez BLAST OMIM

Search Find Find in This View

Map Viewer Home **Rattus norvegicus (rat) RGSC v3.4**

Map Viewer Help Rat Maps Help FTP

Data As Table View **Maps & Options**

Compress Map

Region Shown: 263,025,480 263,027,230 **Go**

out zoom in

You are here: **Ideogram**

default master

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

Query: 24925[[gene_id](#)] [\[clear\]](#)

Master Map: Genes On Sequence [Summary of Maps](#)

Region Displayed: 263,025,480-263,027,230 bp

| Hs | UniG | Model | Rn | UniG | ensGenes | RefSeq | RNR | Genes_seq | Symbol | Links | Cyto | E | Description |
|----|------|-------|----|------|----------|--------|-----|-----------|--------|---|------|-------------|-----------------------------|
| | | | | | | | | | Adrb1 | sv pr dl ev mm hm rgd sts | 1q55 | best RefSeq | adrenergic receptor, beta 1 |

Position sur le génome ???

La carte chromosomique...

3. Les pathologies héréditaires

3. Les pathologies héréditaires

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Search OMIM for beta drenergic receptor Go Clear

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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](#)

| Chromosome | Hit Count |
|------------|-----------|
| 1 | 1 |
| 2 | 10 |
| 3 | 30 |
| 4 | 1 |
| 5 | 1 |
| 6 | 1 |
| 7 | 1 |
| 8 | 1 |
| 9 | 14 |
| 10 | 2 |
| 11 | 1 |
| 12 | 10 |
| 13 | 1 |
| 14 | 1 |
| 15 | 1 |
| 16 | 1 |
| 17 | 109 |
| 18 | 1 |
| 19 | 1 |
| 20 | 1 |
| 21 | 1 |
| 22 | 1 |
| X | 1 |
| Y | 1 |
| III | 13 |

3. Les pathologies héréditaires

The screenshot shows the OMIM website interface. At the top, there is a search bar with the text 'OMIM' and 'for beta drenergic receptor'. Below the search bar, there are buttons for 'Limits', 'Preview/Index', 'History', 'Clipboard', and 'Details'. A message indicates that the term 'drenergic' was not found and suggests 'beta adrenergic receptor' (99 items). Below this, there are filters for 'All: 1464', 'OMIM UniSTS: 190', and 'OMIM dbSNP: 227'. The results are displayed as a list of items, with the first four items shown:

- 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* My NCBI [Sign In] [Register]

All Databases PubMed Nucleotide Protein Genome Structure PMC OMIM

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. 🗨

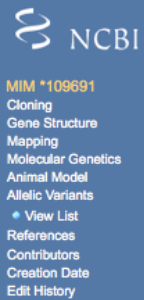
[Kim-Motoyama et al. \(1997\)](#) examined the frequency of the W64R variant in 278 Japanese men in relation to visceral obesity assessed by computerized tomography. They found that the mutation was more frequent in subjects with higher BMI. In subjects with a moderate degree of obesity, the mutation (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



4. Les analyses génomiques

4. Les analyses génomiques

Développement du séquençage

Des centaines de génomes séquencés

« Génomique et Protéomique » (USA & Europe)

4. Les analyses génomiques

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- [PASC \(Pairwise Sequence Comparison\)](#)

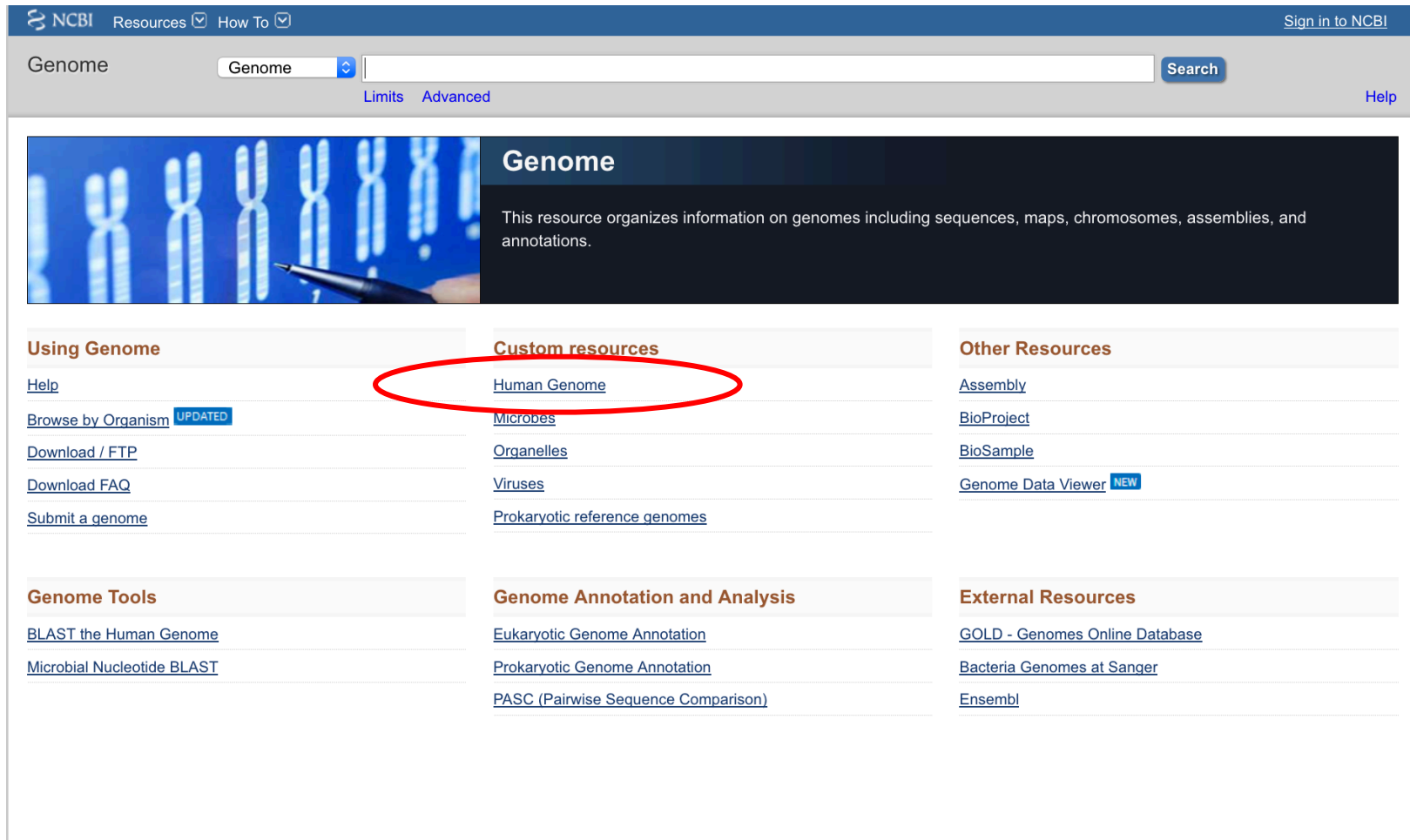
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- [BioProject](#)
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4. Les analyses génomiques



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4. Les analyses génomiques

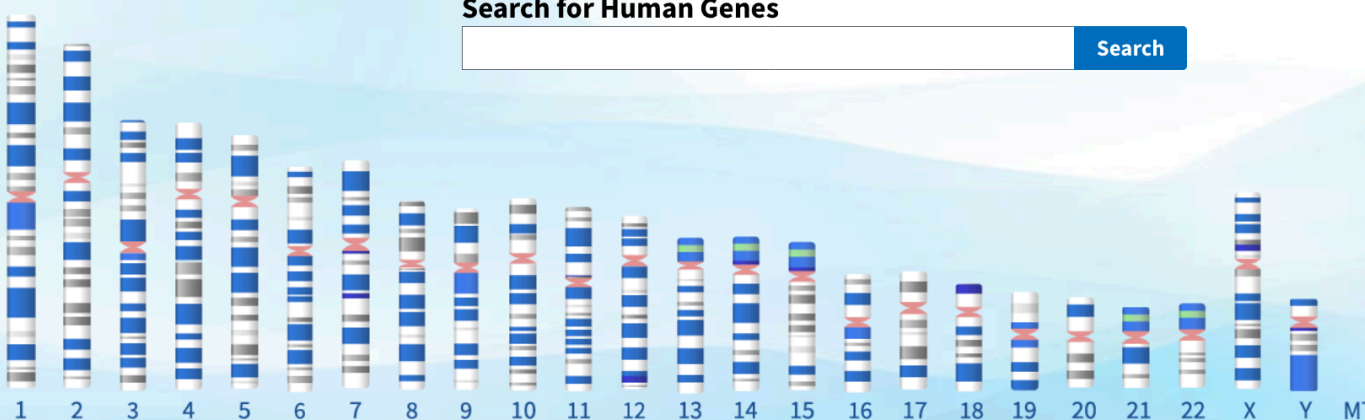
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| | GRCh38 | GRCh37 |
|------------------------------------|-----------------------|-----------------------|
| Reference Genome Sequence | Fasta | Fasta |
| RefSeq Reference Genome Annotation | gff3 | gff3 |

4. Les analyses génomiques

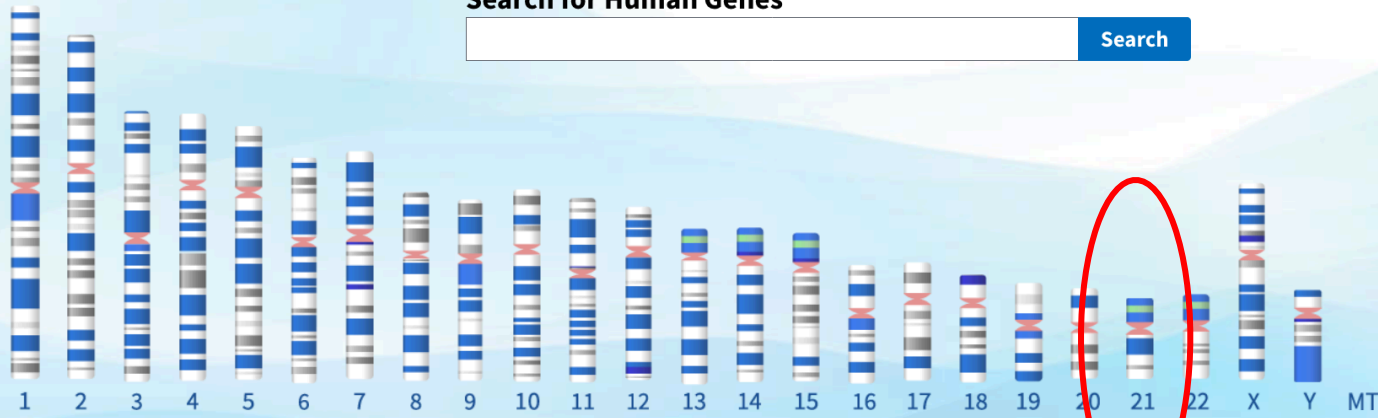
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|------------------------------------|-----------------------|-----------------------|
| Reference Genome Sequence | Fasta | Fasta |
| RefSeq Reference Genome Annotation | gff3 | gff3 |

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.

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Human genome overview page (Build 38.3) [BLAST The Hu](#)

Human genome overview page (Build 35.1)

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

Ideogram Contig Hs UniProt Genes_seq Symbol Links E Cyto Description

| 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 |
| TTTY7 | 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 |
| TTTY15 | 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 |
| TTTY17B | 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

NIH U.S. National Library of Medicine | NCBI National Center for Biotechnology Information | Sign in to NCBI

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](#)

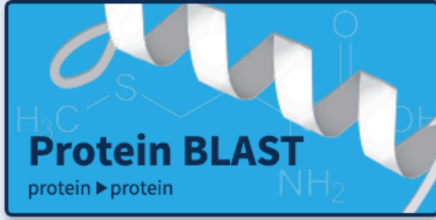
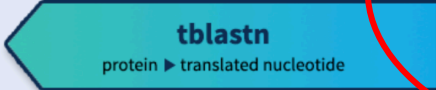


NEWS

[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



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

Idem sur les protéines...

5. Les analyses protéiques

BLAST Basic Local Alignment Search Tool

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► 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 FVAKRQRRFVRRELGRFPPEESPRSP

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

Home Recent Results Saved Strategies Help

My NCBI [Sign In] [Register]

NCBI/BLAST/blastp suite/ Formatting Results - HRGK4VXW013

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

Protein Sequence (138 letters)

Query ID |cl|7334
Description None
Molecule type amino acid
Query Length 138

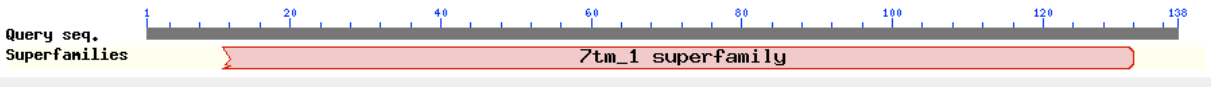
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.2.18+ [Citation](#)

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

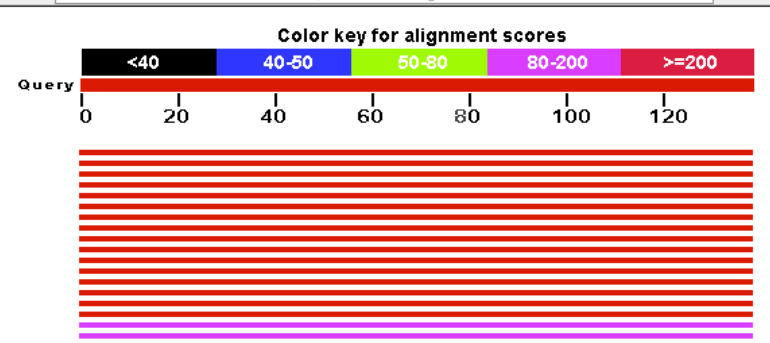
7tm_1 super-family

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   AQECHSNPRCCSFASNMPYALLSSSVSFYLP LLVMLFVYARVFV VAKRQRRFVRRELGRF 60
           AQECHSNPRCCSFASNMPYALLSSSVSFYLP LLVMLFVYARVFV VAKRQRRFVRRELGRF
  Sbjct 183 AQECHSNPRCCSFASNMPYALLSSSVSFYLP LLVMLFVYARVFV VAKRQRRFVRRELGRF 242

  Query 61  PPEESPRSPSRSPSPATVGTPTASDGV PSCGRRPARLLPLGEHRALRTLGLIMGIFSLCW 120
           PPEESPRSPSRSPSPATVGTPTASDGV PSCGRRPARLLPLGEHRALRTLGLIMGIFSLCW
  Sbjct 243 PPEESPRSPSRSPSPATVGTPTASDGV PSCGRRPARLLPLGEHRALRTLGLIMGIFSLCW 302

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

6. Exemple publication utilisant la bioinfo

Xu et al. *Orphanet Journal of Rare Diseases* (2023) 18:273
<https://doi.org/10.1186/s13023-023-02885-1>


Orphanet Journal of Rare
Diseases

RESEARCH


Open Access

The metabolomic plasma profile of patients with Duchenne muscular dystrophy: providing new evidence for its pathogenesis



Huayan Xu^{1†}, Xiaotang Cai^{2†}, Ke Xu¹, Qihong Wu¹ and Bei Xu^{3,4*} 

6. Exemple publication utilisant la bioinfo

Huayan Xu^{1†}, Xiaotang Cai^{2†}, Ke Xu¹, Qihong Wu¹ and Bei Xu^{3,4*} 

Abstract

Background Duchenne muscular dystrophy (DMD) is a fatal genetic muscle-wasting disease that affects 1 in 5000 male births with no current cure. Despite great progress has been made in the research of DMD, its underlying pathological mechanism based on the metabolomics is still worthy of further study. Therefore, it is necessary to gain a deeper understanding of the mechanisms or pathogenesis underlying DMD, which may reveal potential therapeutic targets and/or biomarkers.

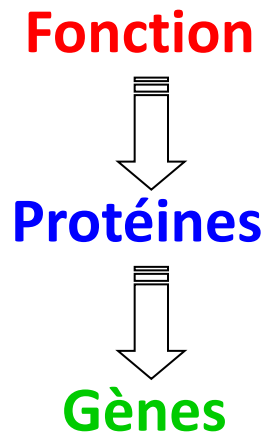
Results Plasma samples from 42 patients with DMD from a natural history study and 40 age-matched healthy volunteers were subjected to a liquid chromatography-mass spectrometry-based non-targeted metabolomics approach. Acquired metabolic data were evaluated by principal component analysis, partial least squares-discriminant analysis, and metabolic pathway analysis to explore distinctive metabolic patterns in patients with DMD. Differentially expressed metabolites were identified using publicly available and integrated databases. By comparing the DMD and healthy control groups, 25 differential metabolites were detected, including amino acids, unsaturated fatty acids, carnitine, lipids, and metabolites related to the gut microbiota. Correspondingly, linoleic acid metabolism, D-glutamine and D-glutamate metabolism, glycerophospholipid metabolism, and alanine, aspartate, and glutamate metabolism were significantly altered in patients with DMD, compared with those of healthy volunteers.

Conclusions Our study demonstrated the abnormal metabolism of amino acids, energy, and lipids in patients with DMD, consistent with pathological features, such as recurrent muscle necrosis and regeneration, interstitial fibrosis, and fat replacement. Additionally, we found that metabolites of intestinal flora were disordered in DMD patients, providing support for treatment of intestinal microbiota disturbance in DMD diseases. Our study provides a new research strategy for understanding the pathogenesis of DMD.

Keywords Duchenne muscular dystrophy, Metabonomics, Mass spectrometry, Plasma

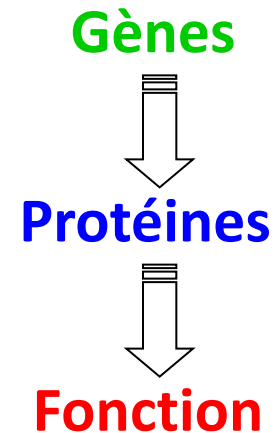
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Physiologie « classique »



Vision restreinte

Physiologie « inverse »

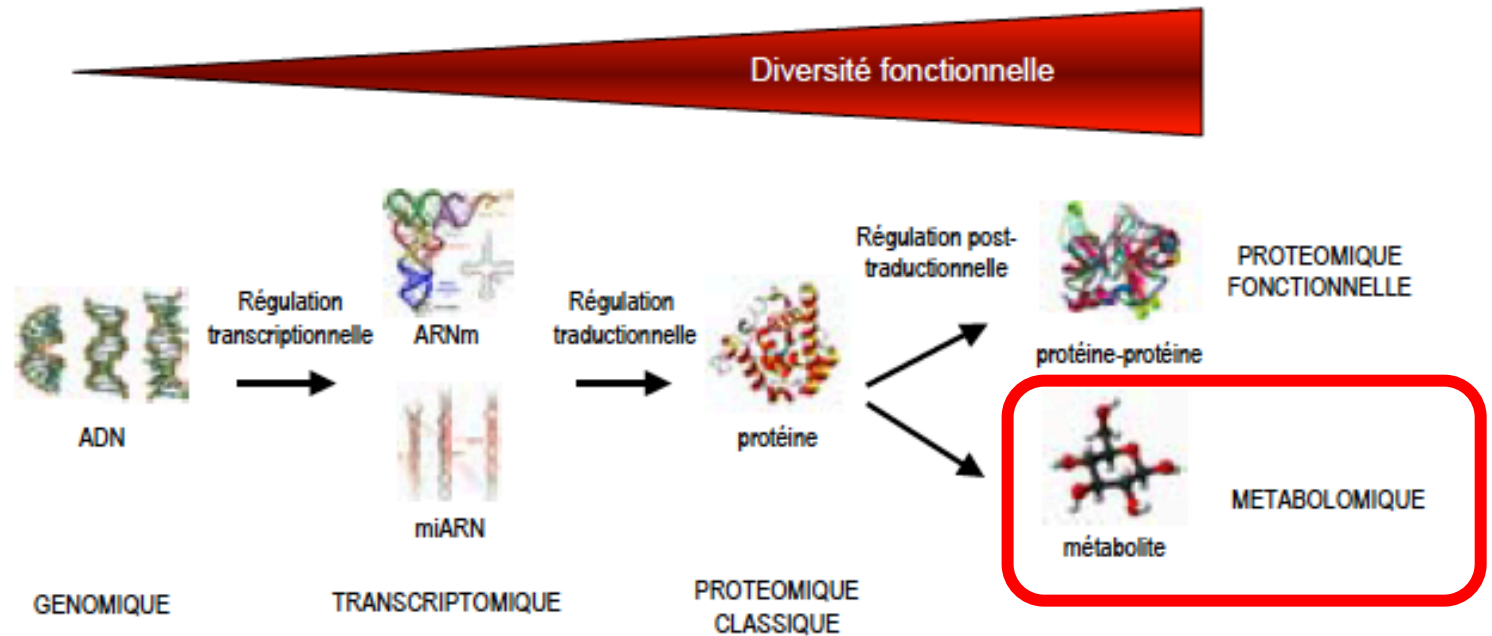


Vision globale

6. Exemple publication utilisant la bioinfo

Intérêt de la recherche « OMICS »

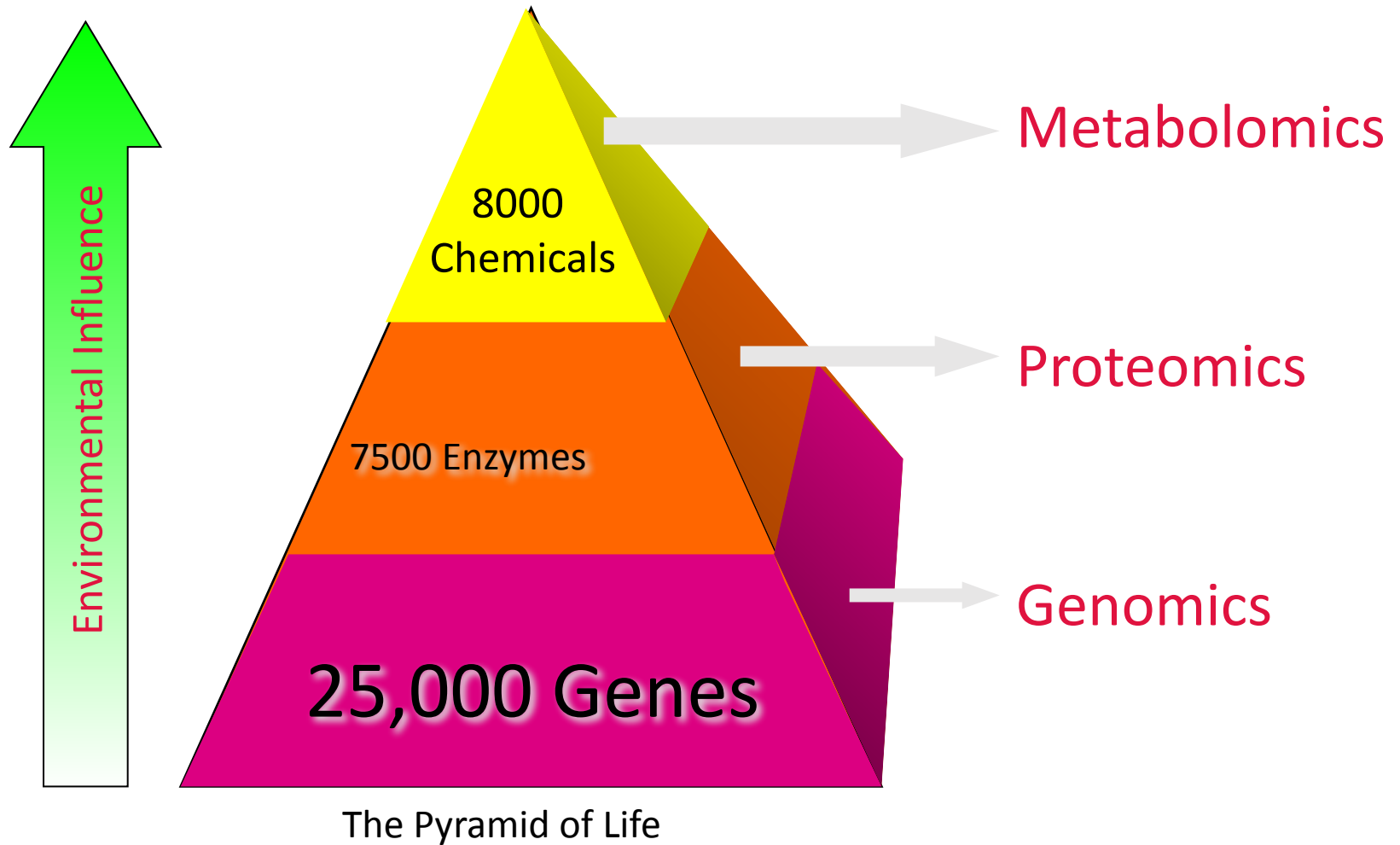
- Approche globale sans aucun *a priori*



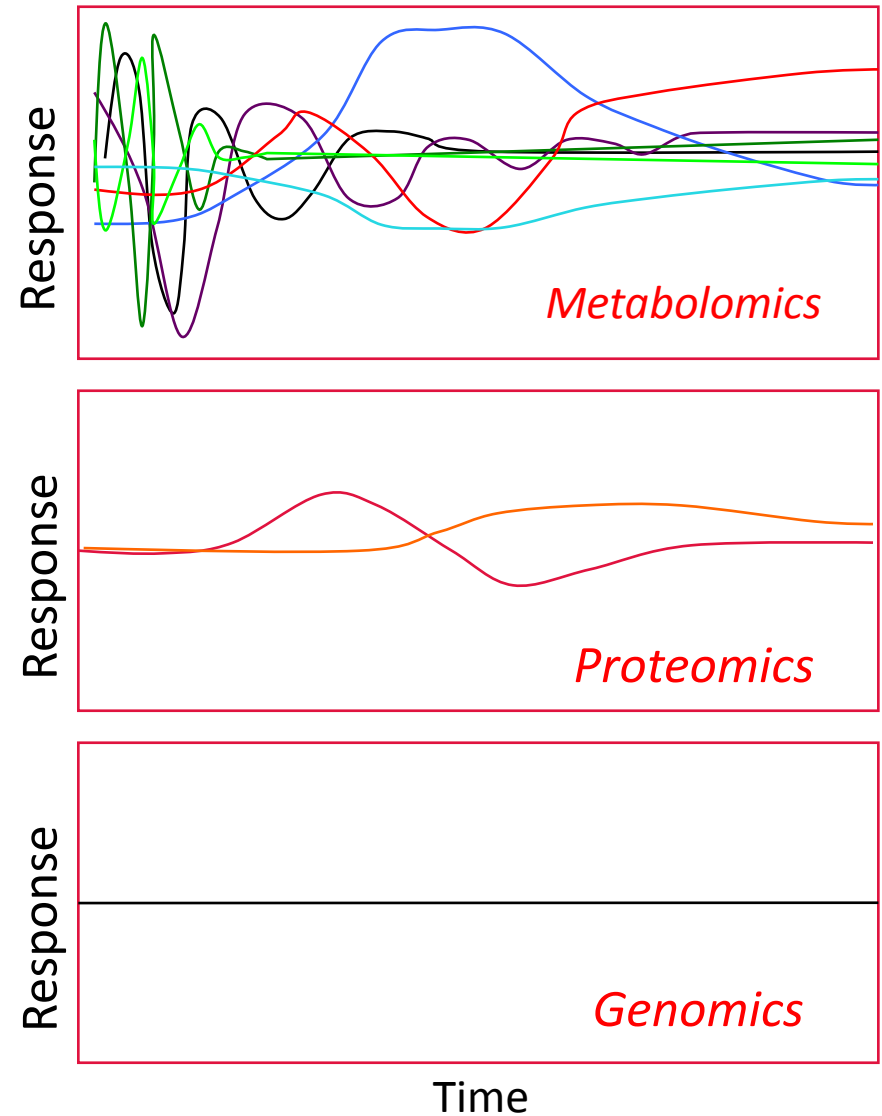
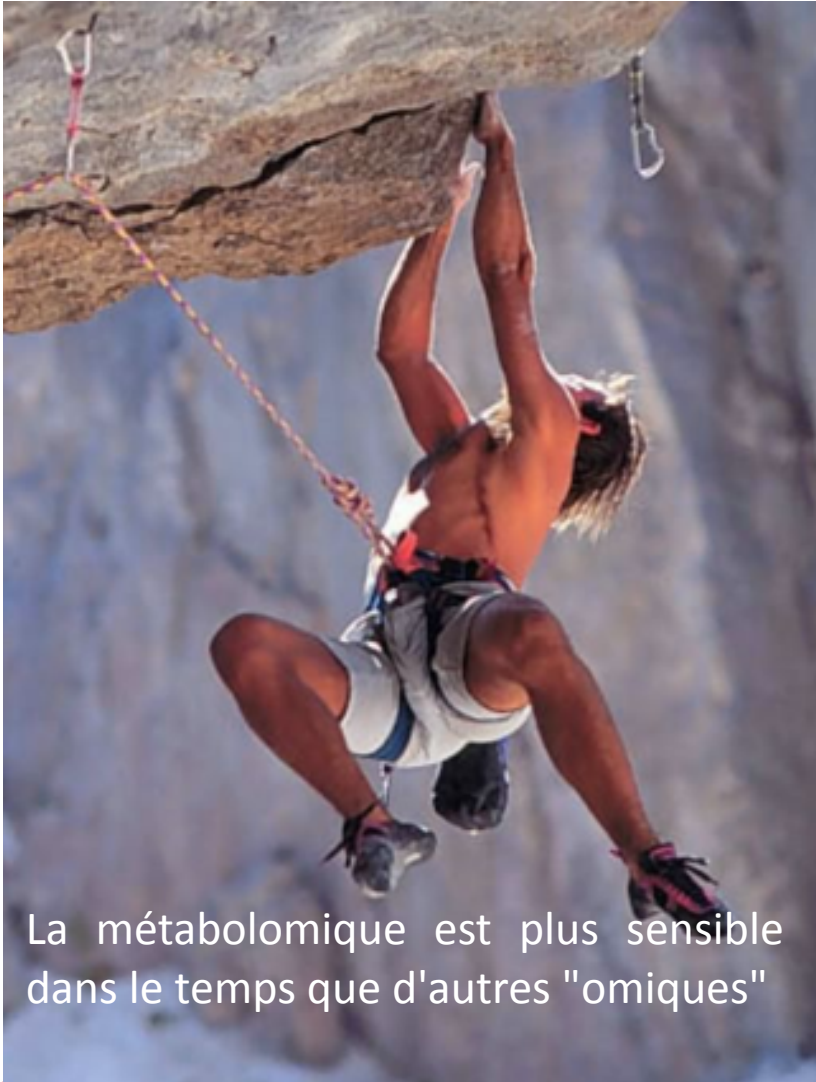
- Protéomique

Caractérisation qualitative et quantitative de l'ensemble des protéines présentes dans un échantillon biologique obtenu dans des conditions définies

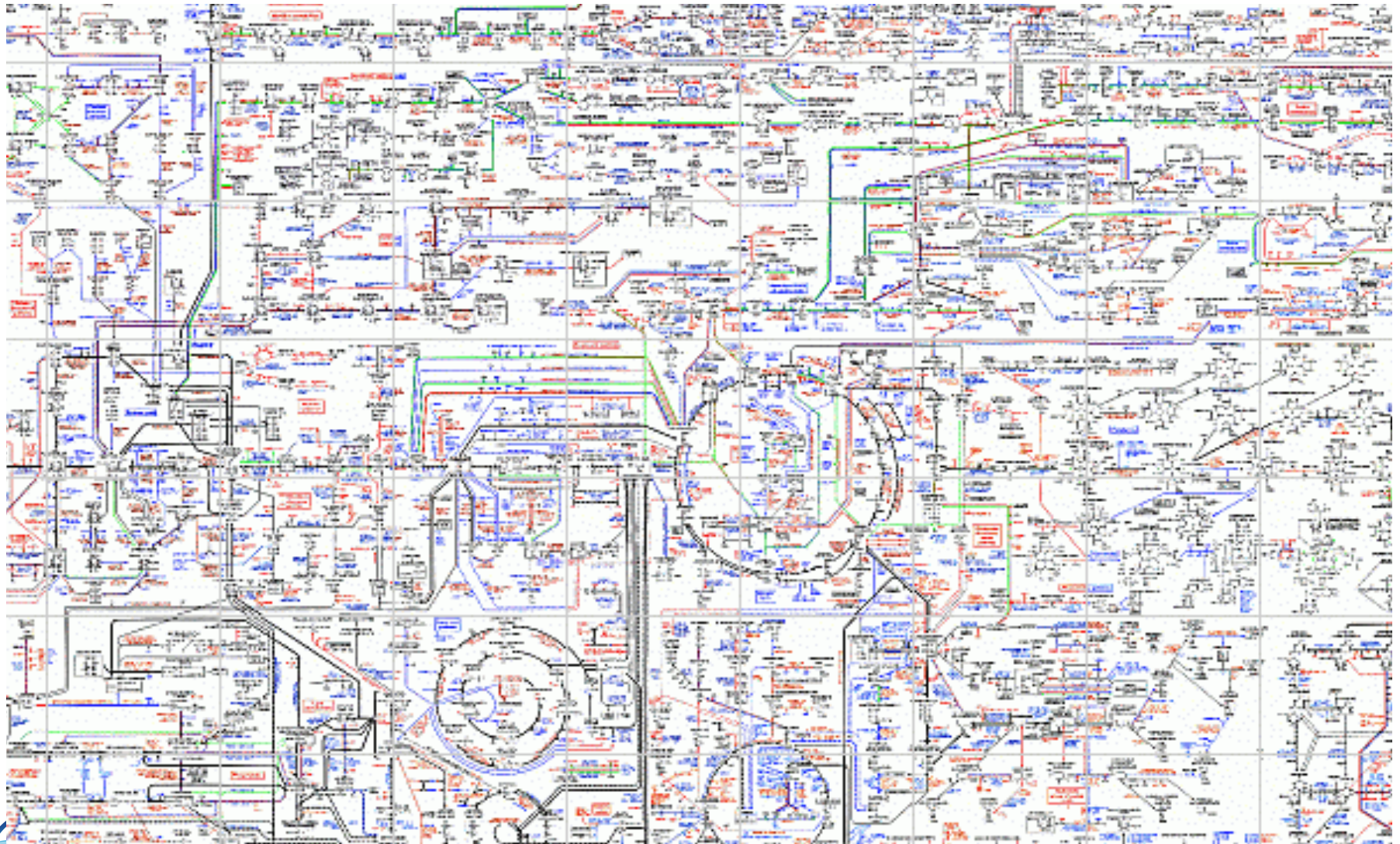
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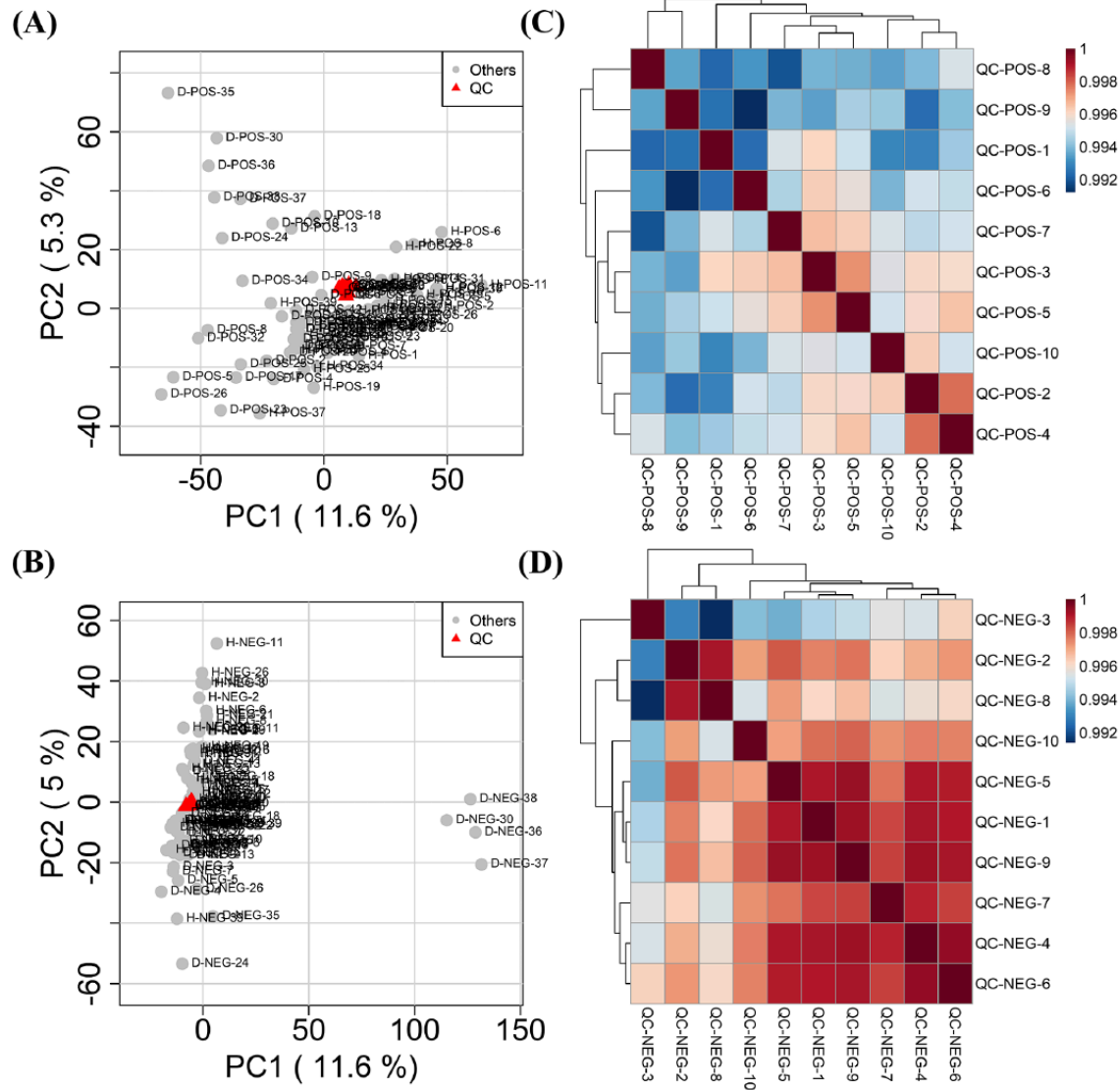


Fig. 1 PCA score plots and correlation analysis of QC samples in ESI+ (A, C) and ESI- (B, D) scan modes

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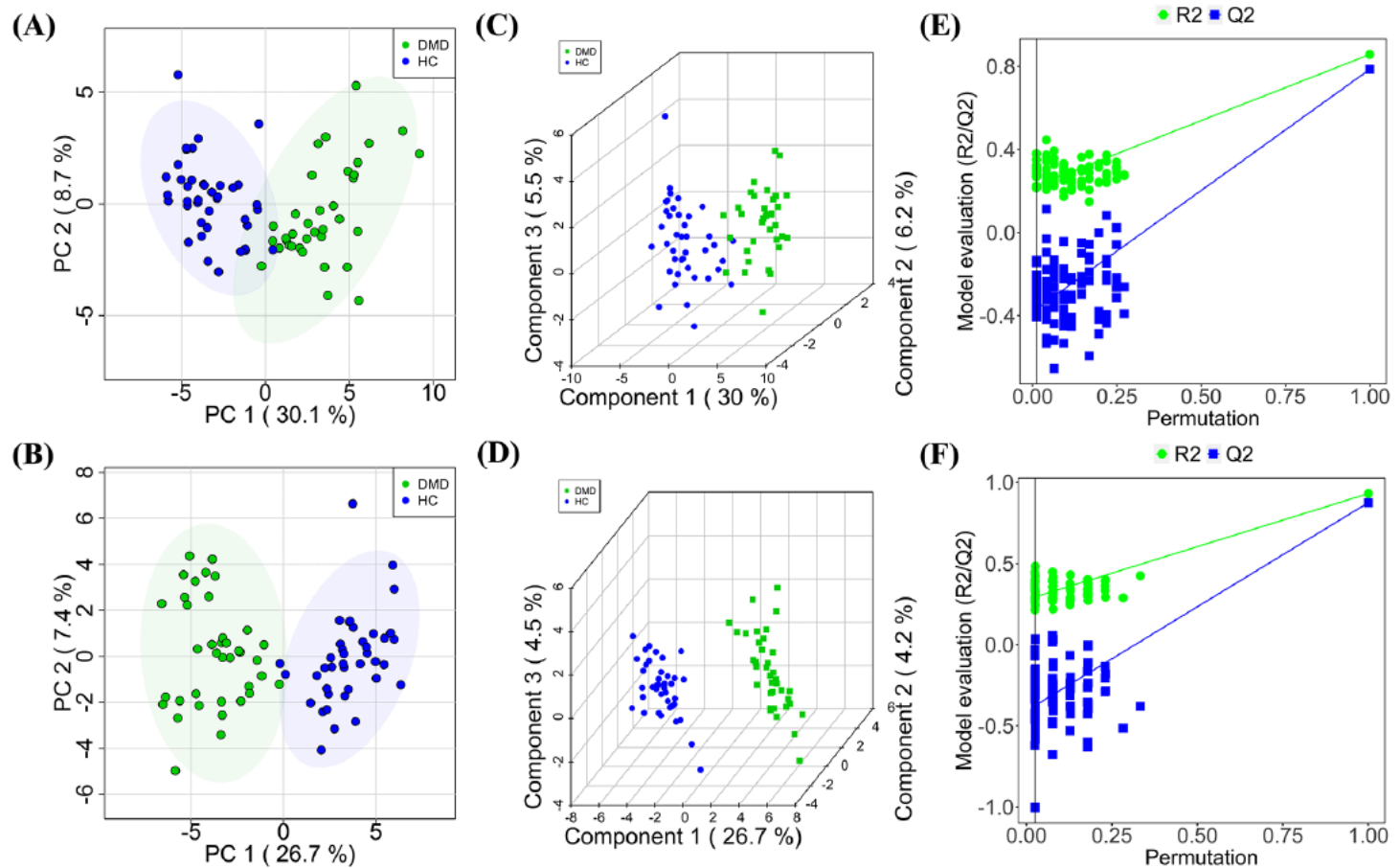


Fig. 2 Plots of PCA (A, B) and PLS-DA scores (C, D) with permutation testing (E, F) for healthy controls and DMD patients comparison in the ESI+ and ESI-scan modes

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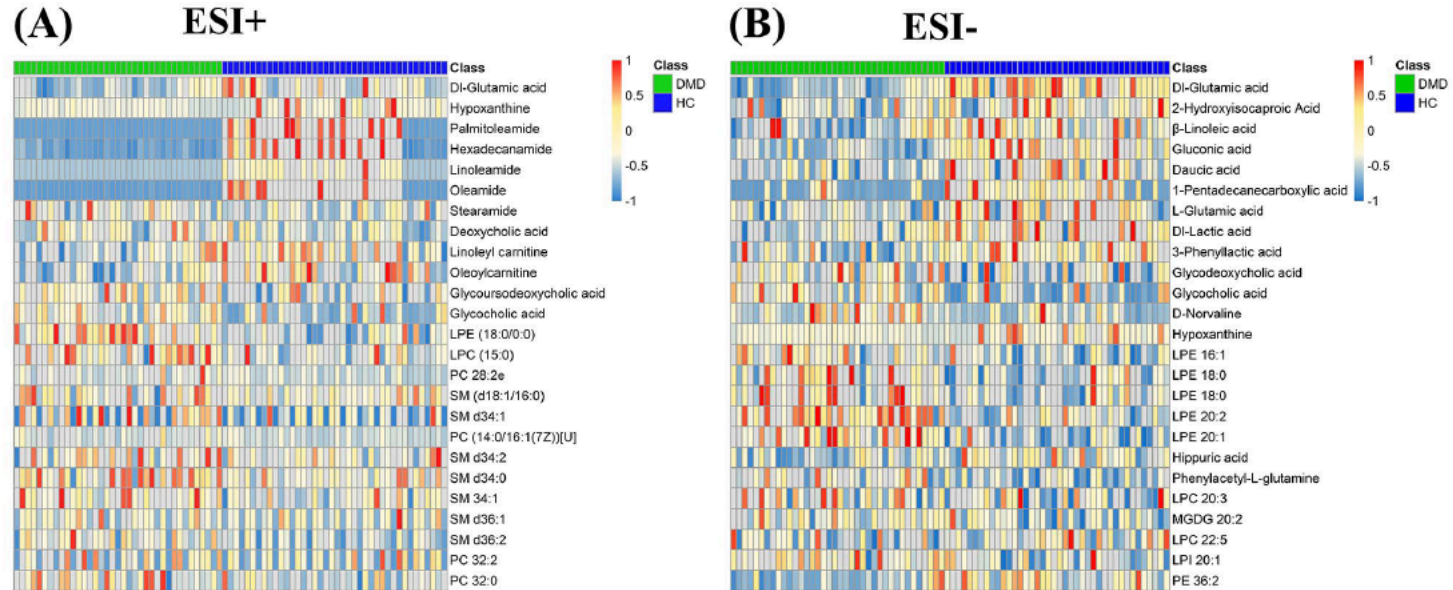


Fig. 3 Differential metabolite heat maps in ESI+ **(A)** and ESI- **(B)** scan modes. The columns represent samples, the rows represent metabolites, and the relative content of the metabolites is displayed by color

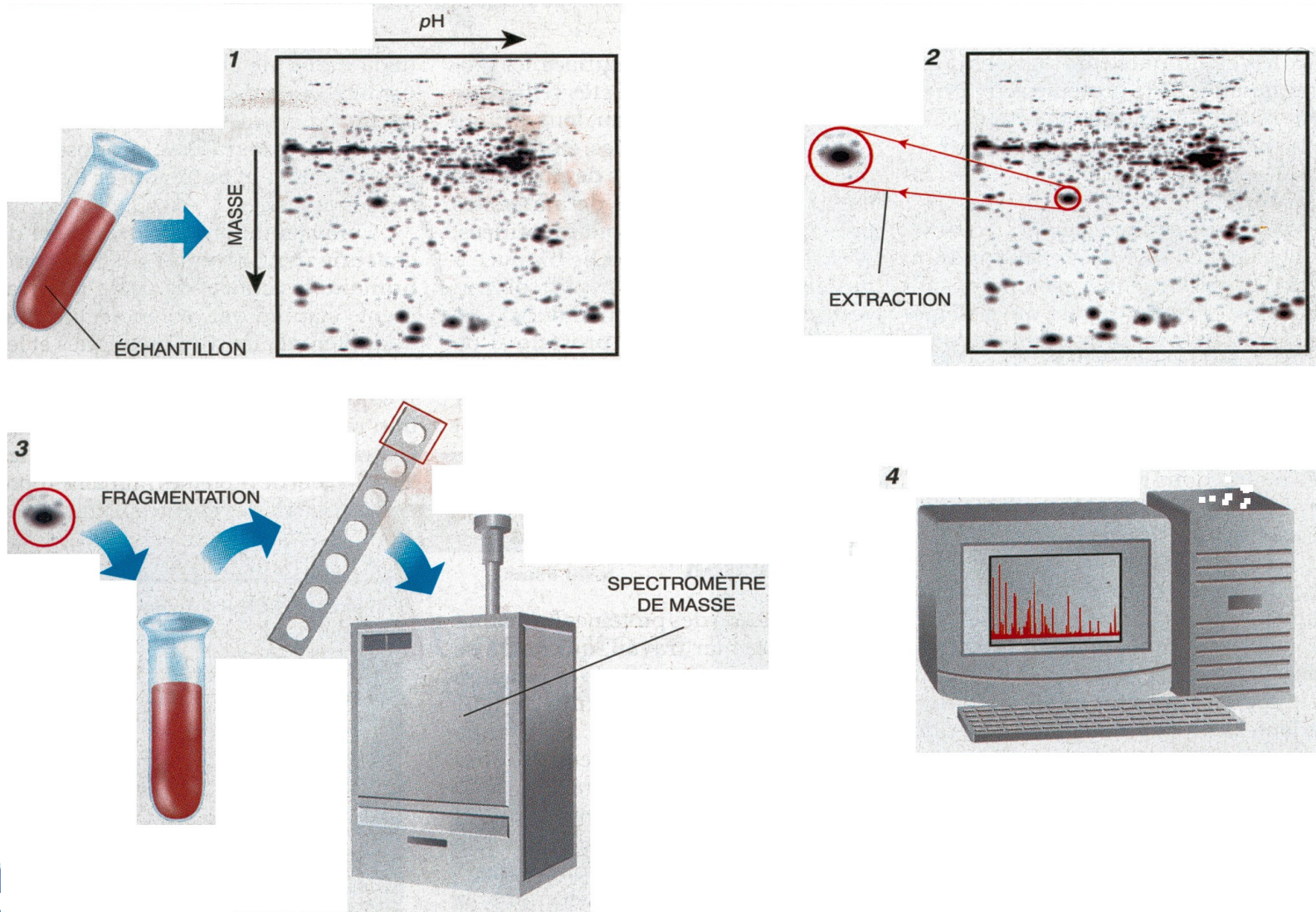
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Metabolite detection

An ultra-performance liquid chromatography (UPLC) system (Agilent1290 Infinity II; Agilent Technologies Inc., CA, USA) connected to a high-resolution tandem mass spectrometer (TripleTOF 5600 Plus; AB SCIEX, Framingham, MA, USA) was used to conduct the metabolomic analysis. Reversed-phase separation was performed on an ACQUITY HSS T3 column (100×2.1 mm, i.d. 1.8 µm; Waters, Milford, USA). The mobile phase composition was determined using a gradient elution of solvent A (0.1% formic acid in water) and solvent B (0.1% formic acid in acetonitrile), as previously described [19]. The flow rate was constant at 0.30 mL/min, and the column temperature was set at 30 °C.

- 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.

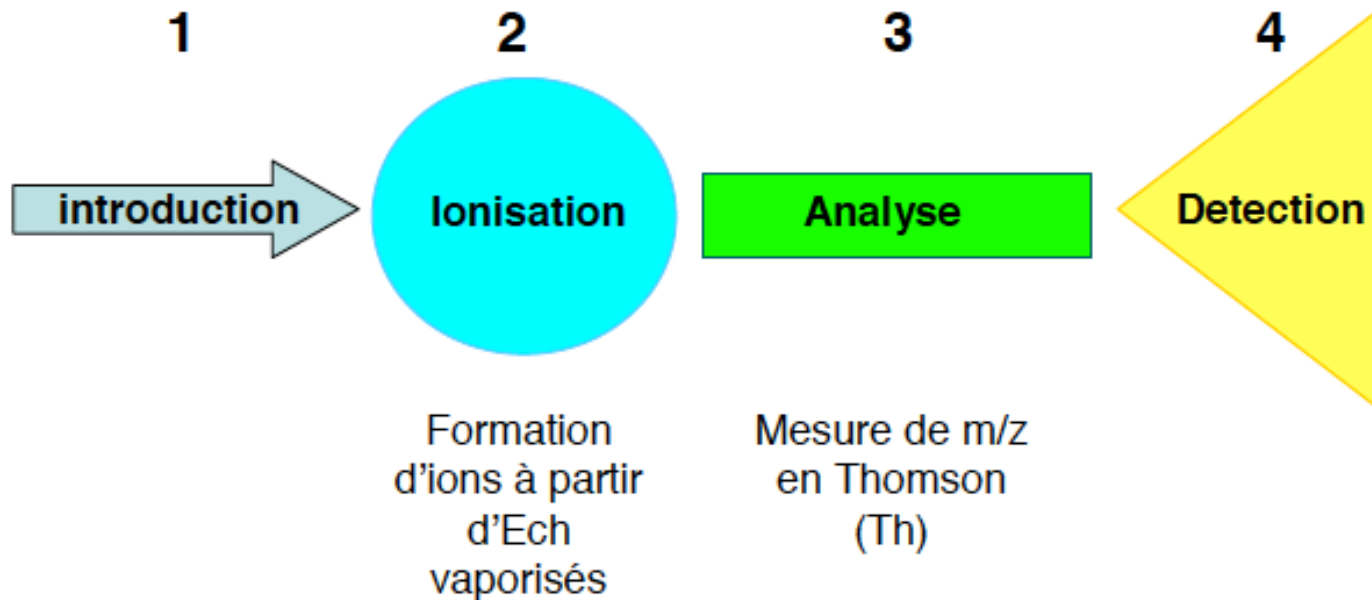
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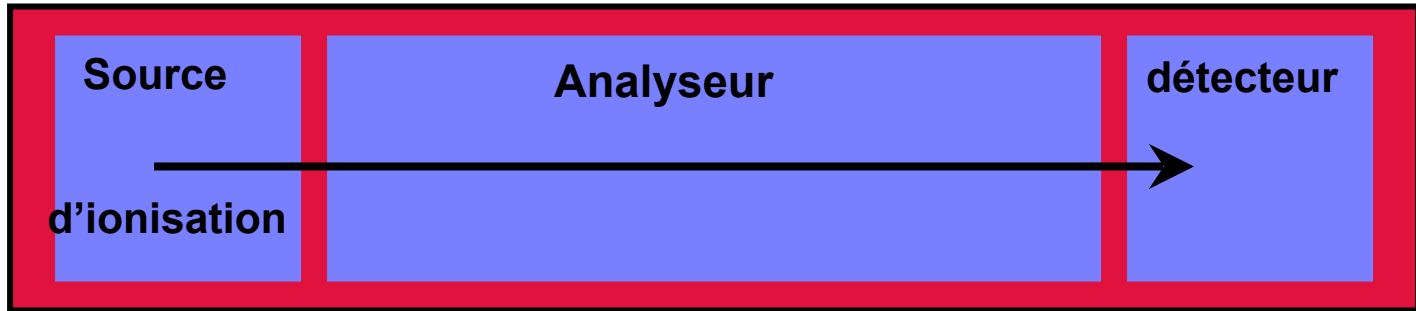
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Le spectromètre de masse se compose donc de quatre parties :

- 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

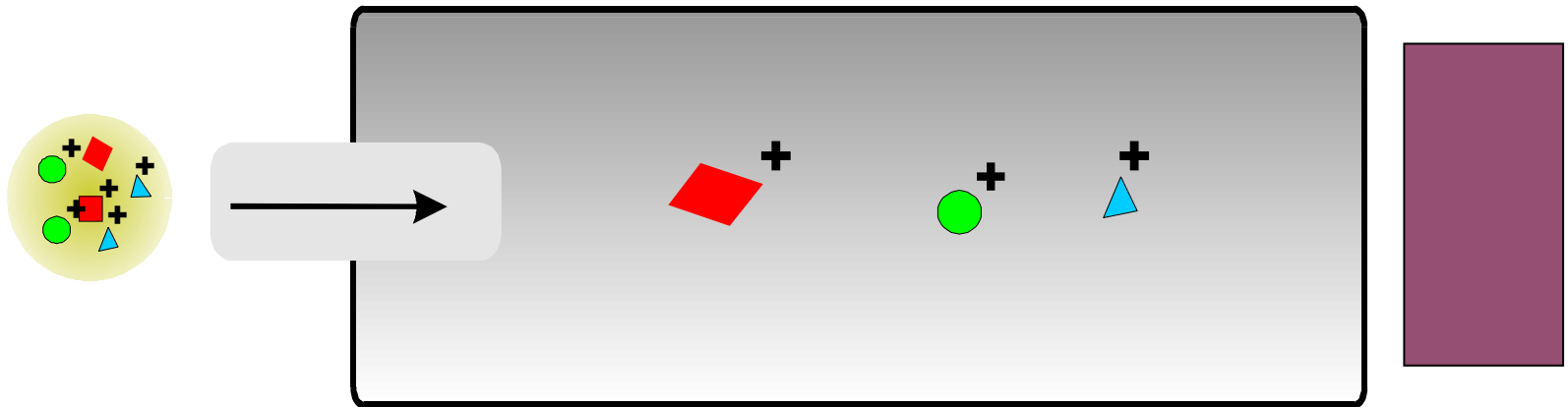


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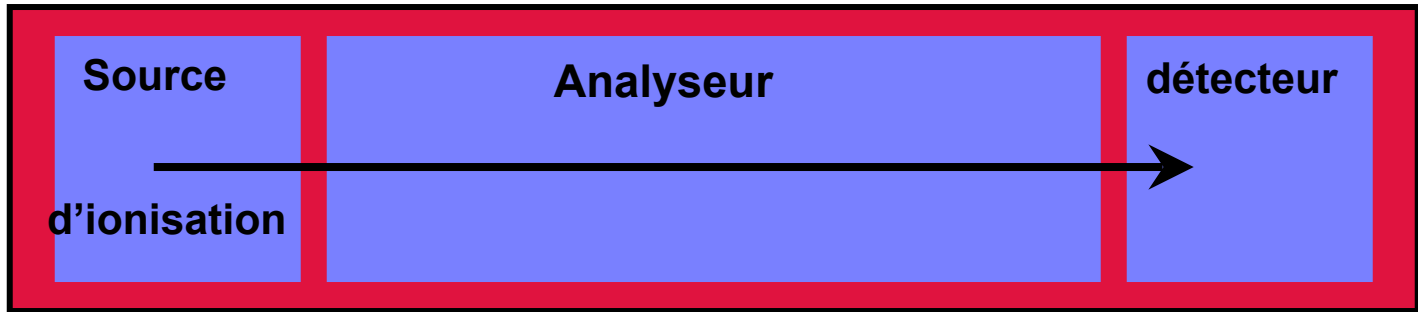


L'analyseur de masse

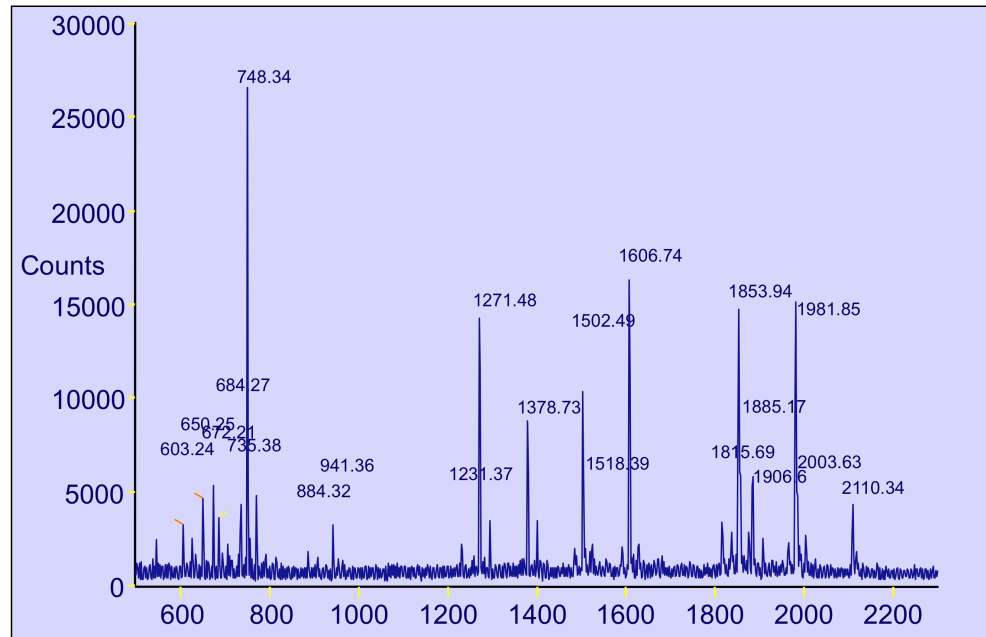
Détecteur



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Détecteur



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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
1288.7259
1134.6742
1008.5360
1008.5295
1065.5509
950.4499
1007.4714
880.4159
832.3658
792.3709

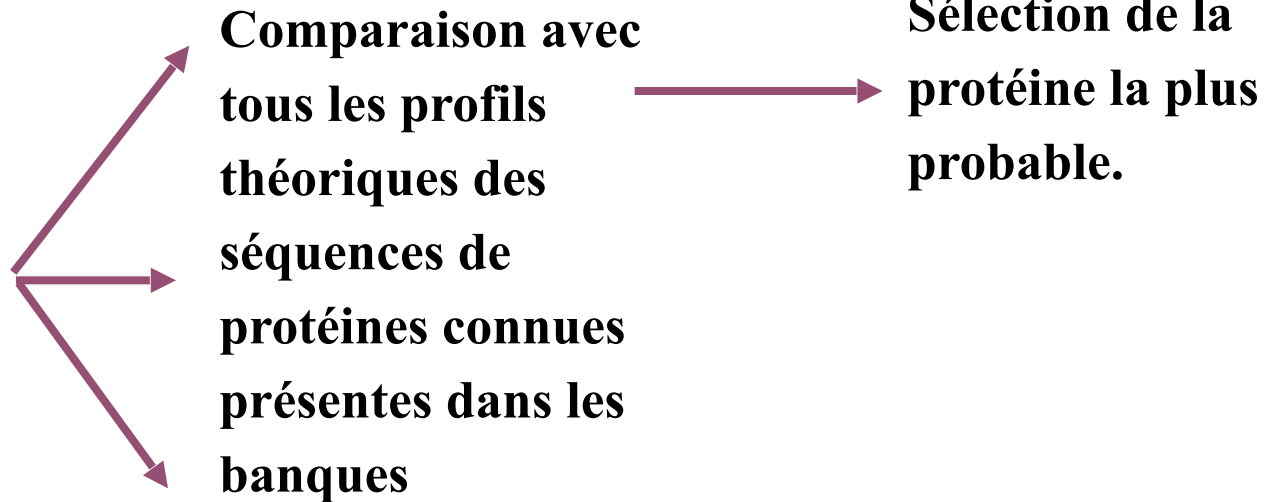
La carte massique obtenue est **l'empreinte massique** de la protéine. Elle est très spécifique.

6. Exemple publication utilisant la bioinfo

Liste de masses
expérimentale

| |
|-----------|
| 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 |
| 1288.7259 |
| 1134.6742 |
| 1008.5360 |
| 1008.5295 |
| 1065.5509 |
| 950.4499 |
| 1007.4714 |
| 880.4159 |
| 832.3658 |
| 792.3709 |

Interrogation des banques de données



6. Exemple publication utilisant la bioinfo

Table 2 List of statistically significant metabolites in DMD vs. HC comparisons

| Metabolites | Scan mode | Rt (s) | m/z | Adducts | DMD vs. HC | | | | |
|-------------------------|---------------------------|--------|----------|---------|-----------------------|------------|--------|--------|---|
| | | | | | Log2(FC) | P (T test) | VIP | Trends | |
| Amino acids | Glutamic acid | ESI- | 73.431 | 128.036 | M-H ₂ O-H | -1.181 | <0.001 | 1.955 | ↓ |
| | Glutamine | ESI+ | 47.218 | 146.080 | M+H | -1.072 | <0.001 | 1.857 | ↓ |
| | Hippuric acid | ESI- | 300.935 | 178.051 | M-H | -0.802 | 0.021 | 1.009 | ↓ |
| | Phenylacetyl-glutamine | ESI- | 348.896 | 527.213 | 2 M-H | 1.143 | <0.001 | 2.008 | ↑ |
| | Valine | ESI- | 420.136 | 293.176 | 2 M+Hac-H | 1.072 | 0.005 | 1.263 | ↑ |
| Unsaturated fatty acids | β-Linolenic acid | ESI- | 419.308 | 279.232 | M-H | -0.766 | 0.0001 | 1.582 | ↓ |
| Carnitine | Linoleyl carnitine | ESI+ | 435.747 | 424.342 | M+H | -0.784 | <0.001 | 1.536 | ↓ |
| | Oleoylcarnitine | ESI+ | 461.927 | 426.358 | M+H | -0.766 | <0.001 | 1.635 | ↓ |
| Bile acids | Glycocholic acid | ESI- | 372.288 | 464.302 | M-H | 1.121 | 0.005 | 1.122 | ↑ |
| | Glycodeoxycholic acid | ESI- | 406.477 | 448.307 | M-H | 0.950 | 0.0004 | 1.460 | ↑ |
| | Glycoursodeoxycholic acid | ESI+ | 406.026 | 450.322 | M+H | 1.031 | <0.001 | 1.543 | ↑ |
| | Deoxycholic acid | ESI+ | 462.698 | 357.279 | M+H-2H ₂ O | 1.174 | 0.002 | 1.323 | ↑ |
| Lipids | PC 32:0 | ESI+ | 1117.300 | 756.555 | M+Na | 0.712 | 0.006 | 1.058 | ↑ |
| | PC 32:2 | ESI+ | 730.026 | 730.539 | M+H | 0.872 | 0.029 | 1.018 | ↑ |
| | LPE 18:0 | ESI- | 552.975 | 480.310 | M-H | 0.655 | <0.001 | 2.289 | ↑ |
| | LPE 20:1 | ESI- | 590.366 | 506.326 | M-H | 0.748 | <0.001 | 1.656 | ↑ |
| | LPE 20:2 | ESI- | 526.317 | 504.311 | M-H | 0.856 | <0.001 | 2.269 | ↑ |
| | LPE (18:0/0:0) | ESI+ | 574.100 | 482.324 | M+H | 0.785 | <0.001 | 2.489 | ↑ |
| | LPI 20:1 | ESI- | 386.676 | 625.361 | M-H | 0.799 | <0.001 | 1.997 | ↑ |
| | LPE 16:1 | ESI- | 444.569 | 450.263 | M-H | 0.803 | <0.001 | 1.733 | ↑ |
| | LPC 20:3 | ESI- | 405.790 | 590.235 | M+FA-H | 0.976 | <0.001 | 1.525 | ↑ |
| | LPC 15:0 | ESI+ | 487.913 | 504.309 | M+Na | 0.634 | <0.001 | 1.675 | ↑ |
| | SM d34:0 | ESI+ | 1118.730 | 705.591 | M+H | 0.851 | <0.001 | 1.360 | ↑ |
| | SM d36:2 | ESI+ | 812.360 | 729.590 | M+H | 0.983 | 0.002 | 1.203 | ↑ |
| | SM 34:1 | ESI+ | 729.672 | 725.557 | M+Na | 1.034 | <0.001 | 1.383 | ↑ |

"↑": Compared with HC group, the differential metabolites were significantly increased in DMD group

"↓": Compared with HC group, the differential metabolites were significantly decreased in DMD group

6. Exemple publication utilisant la bioinfo

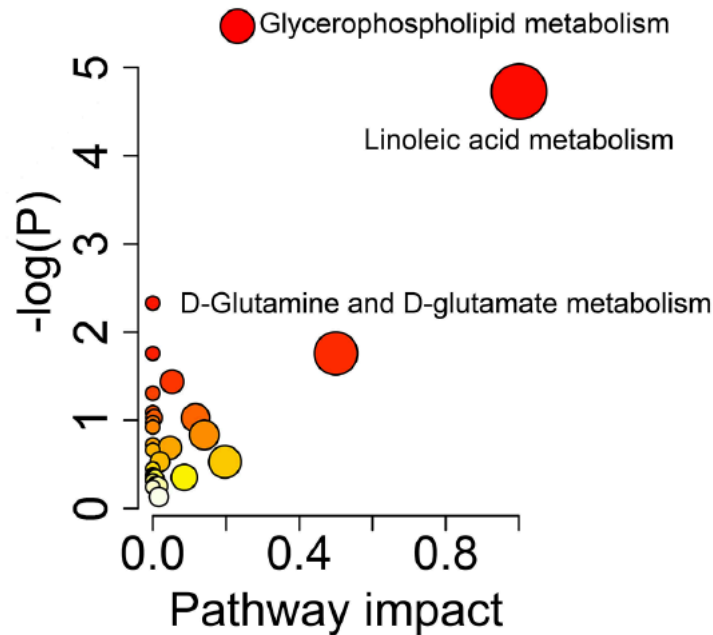


Fig. 5 Bubble diagram of metabolic pathways between DMD and HC groups

Table 3 Significantly altered metabolic pathways between DMD and HC groups

| Pathway name | KEGG.id | -log(P) | Impact | Hits |
|---|----------|---------|--------|------|
| Linoleic acid metabolism | Hsa00591 | 4.73 | 1 | 2 |
| D-Glutamine and D-glutamate metabolism | Has00471 | 1.76 | 0.5 | 1 |
| Glycerophospholipid metabolism | Hsa00564 | 5.47 | 0.23 | 5 |
| Alanine, aspartate and glutamate metabolism | Hsa00250 | 0.53 | 0.20 | 1 |

6. Exemple publication utilisant la bioinfo

Conclusions

Overall, our study demonstrated the abnormal metabolism of amino acids, energy, and lipids in patients with DMD, consistent with pathological features, such as recurrent muscle necrosis and regeneration, interstitial fibrosis, and fat replacement. In addition, we also identified a number of differential metabolites associated with gut microbiota, which may be related to nutritional disorders and intestinal muscle dysfunction in DMD patients. Although our study provides a new research strategy for the pathogenesis of DMD, there are some limitations. First, the sample size was small, so we hope to conduct a multi-center study with a large sample size in a later stage to reduce sampling error. Second, due to the different types, treatment courses, and doses of corticosteroids used by DMD group in this article, we were unable to completely distinguish the corticosteroid-treated group from the untreated group using PCA. Therefore, we could not obtain differences in disease metabolism at corticosteroid treated or nontreated conditions. Although we cannot separate DMD patients into treated and untreated group, this article can still be considered as the first exploratory study on metabolic changes in clinical patients with DMD (regardless of medication use) in natural research history. In the future, we will conduct a prospective study with larger samples to focus on drug treatments (such as glucocorticoids, calcium channel

blockers and vitamin D) and explore their impacts on the metabolic spectrum of DMD patients. Furthermore, target validation should be applied in an in-depth study to validate our selected metabolic indicators.

List of abbreviations

| | |
|------------|---|
| DMD | Duchenne muscular dystrophy |
| HC | healthy control |
| UPLC-MS/MS | ultra-high performance liquid chromatography-tandem mass spectrometry |
| IRB | Institutional Review Board |
| QC | quality control |
| UPLC | ultra-high performance liquid chromatography |
| IDA | independent data acquisition |
| KEGG | Kyoto Encyclopedia of Genes and Genomes |
| HMDB | Human Metabolome Database |
| PCA | principal component analysis |
| PLS-DA | partial least-squares discriminant analysis |
| VIP | variable importance in projection |
| ANOVA | analysis of variance |
| LDS | least significant difference |
| PC | phosphatidylcholines |
| LPE | lysophosphatidylethanolamines |
| SM | sphingomyelin |
| FDR | false discovery rate |
| GLS | glutaminases |
| LPC | lysophosphatidylcholine |
| PA | phosphatidic acid |
| PS | phosphatidylserine |
| PAGln | phenylacetylglutamine |
| FXR | farnesoid X receptor |
| GPBAR-1 | G-protein-coupled bile acid receptor-1 |
| GUDCA | glycoursodeoxycholic acid |
| FGF | fibroblast growth factor |

Acknowledgements

Not applicable.

MERCI à tous!

umr1087.univ-nantes.fr



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Inserm UMR 1087 / CNRS UMR 6291
Nantes, France



Daniel Buren et Patrick Bouchain, Les Anneaux, Quai des Antilles, Nantes, création pérenne Estuaire 2007 © Martin Argyrogis/LVAN