

Bioinformática

Curso de Especialização na Área da Saúde – 2025/2026
Bases Técnicas em Vacinas e Biofármacos

PhD Flavio Lichtenstein

Bioinformatics, Systems Biology, and Biostatistics

Instituto Butantan – CENTD - Bioinformática



maio/2023

O que vimos até aqui?

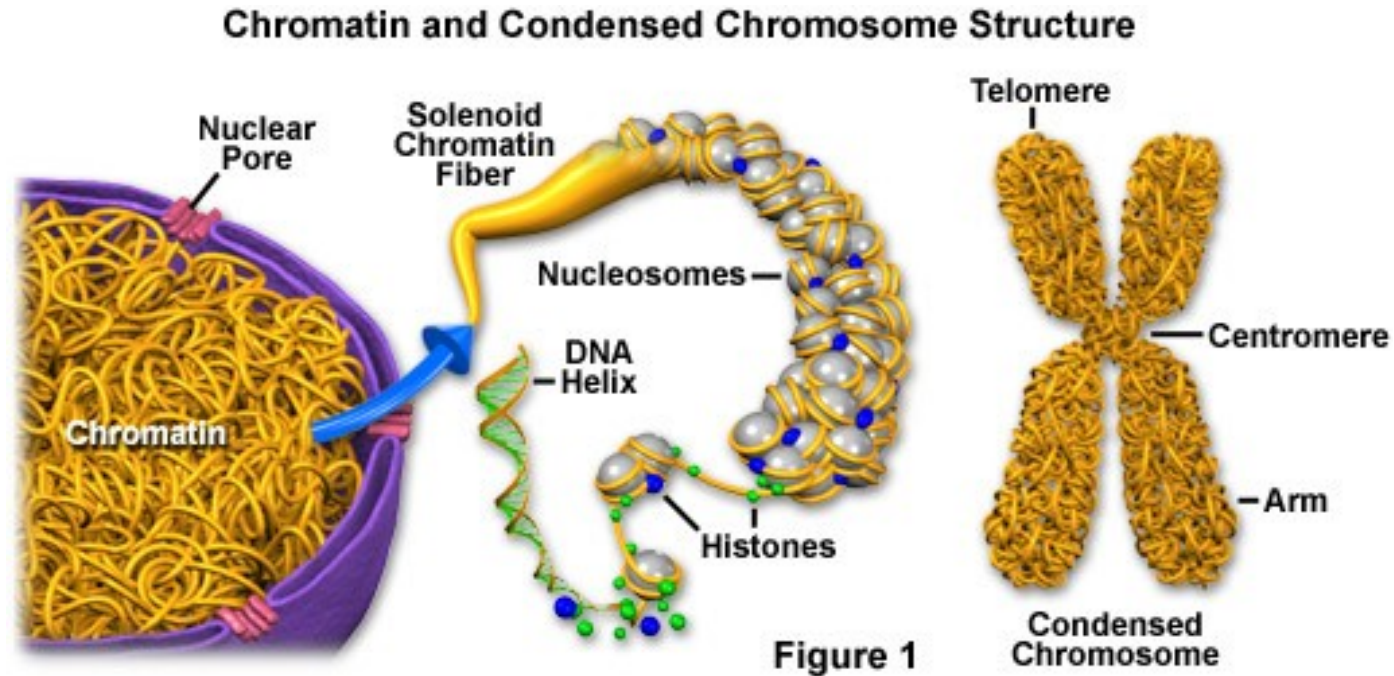
Constituição de um organismo eucarioto

- O corpo é constituído de órgãos
- Os órgãos não são homogêneos e divididos em diferentes tecidos
- Os tecidos são constituídos de células
- Há diferentes tipos de células
- As células têm vários organelas
 - Núcleo
 - Mitocôndria
 - Retículo endoplasmático
 - Lisossomo
 - Endossomo
 - Vacúolos
 - Golgi
 - etc

O que não vimos!

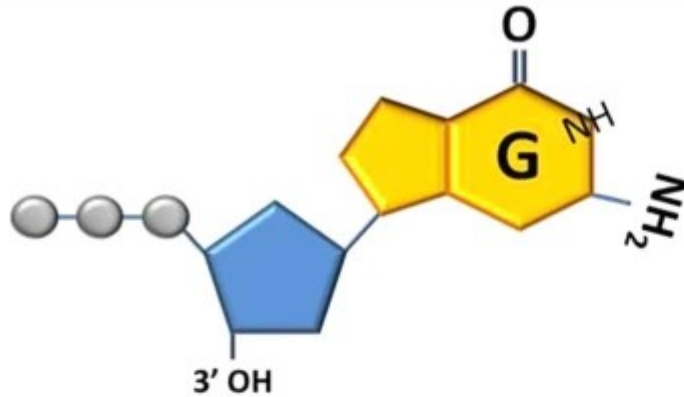
- O cromossomo é uma fita contendo material genético
- Os cromossomos estão enovelados dentro do núcleo
- Cada organismo (homem, coelho, abelha, etc) tem um número de cromossomos diferente
- O cromossomo tem milhões de nucleotídeos
- O cromossomo é formado de 2 fitas em forma de hélice
- Eles se pareiam via interações fracas ligando a fita dupla de DNA.

Os cromossomos estão enovelados dentro do núcleo

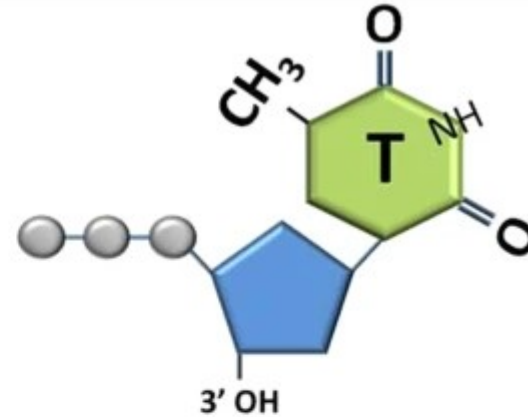


Os quatro nucleotídeos existentes no cromossomo

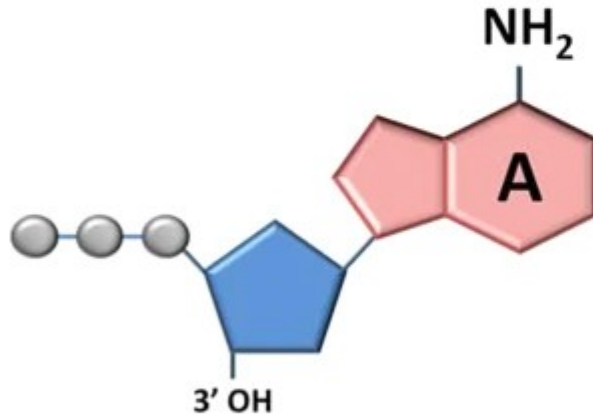
Guanina



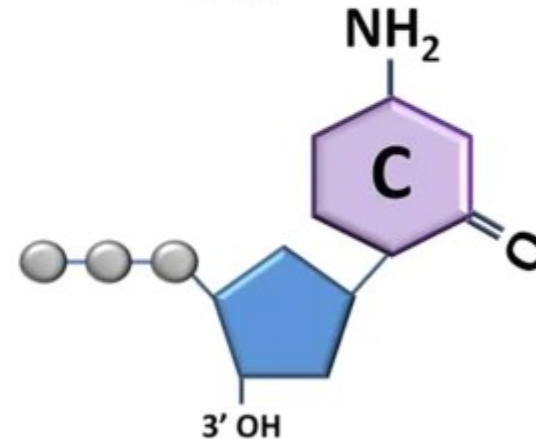
Timina



Adenina



Citosina

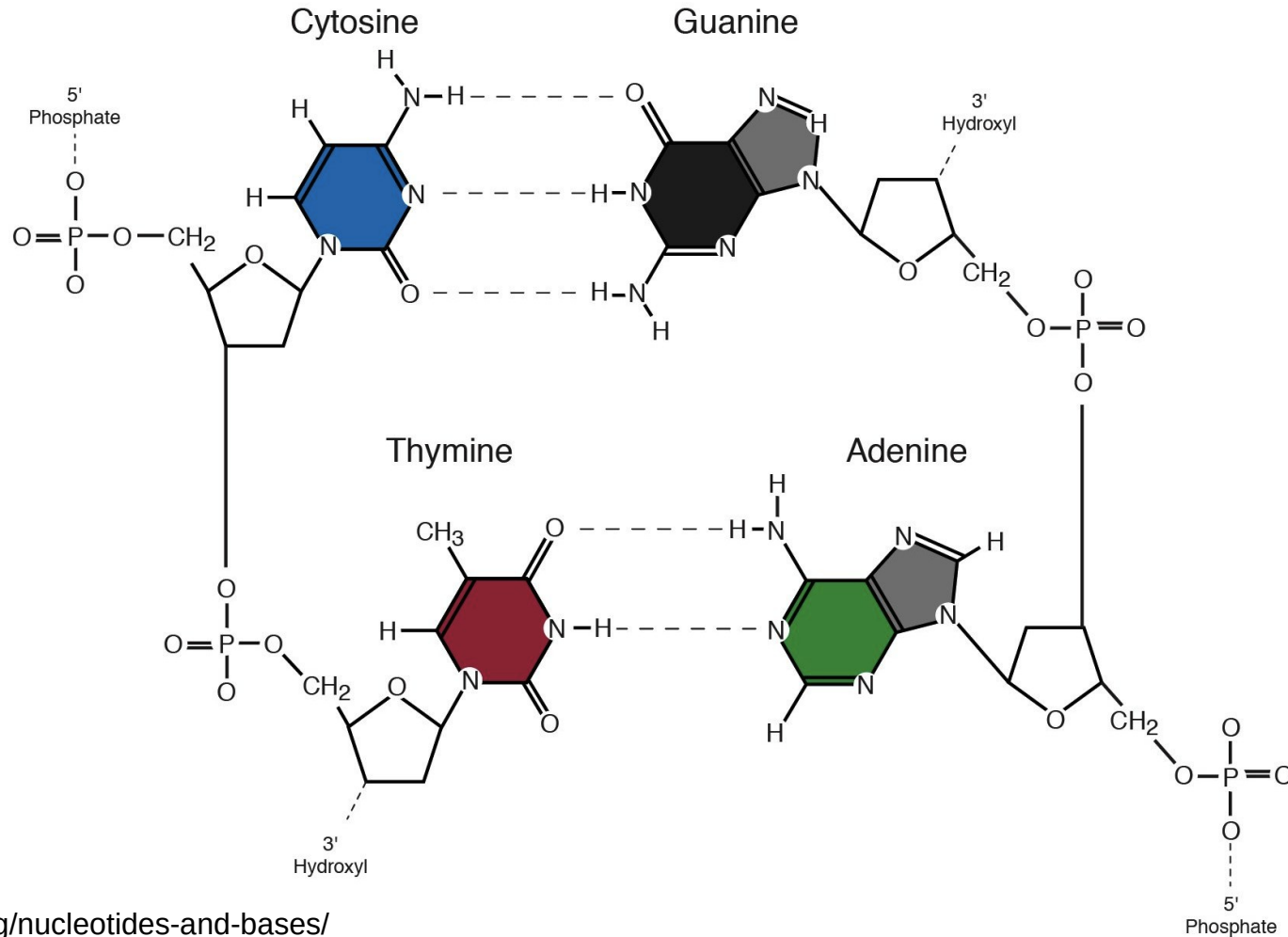


Purine
Deoxyribonucleotides

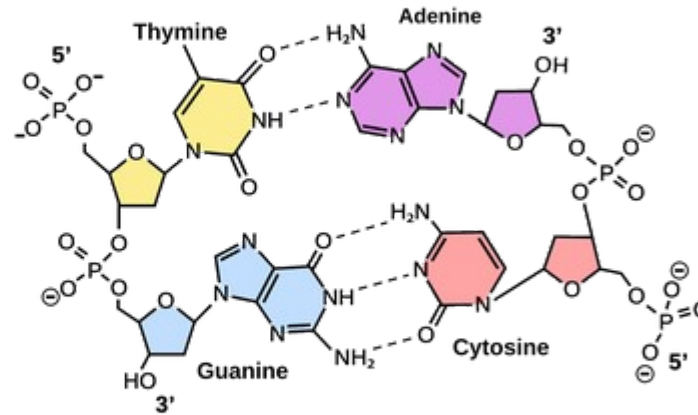
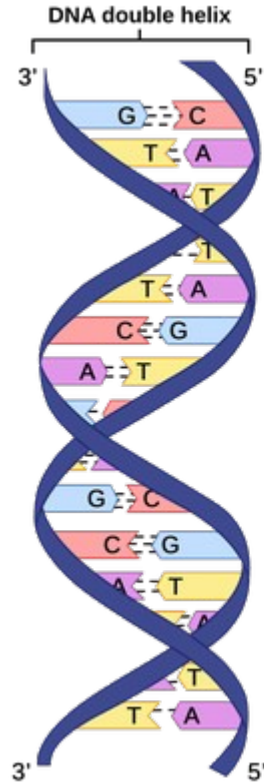
Pyrimidine
Deoxyribonucleotides

Ahmad, M., Panicker, N., Rizvi, T. et al. Electrical detection and quantification of single and mixed DNA nucleotides in suspension. Sci Rep 6, 34016 (2016).
<https://doi.org/10.1038/srep34016>

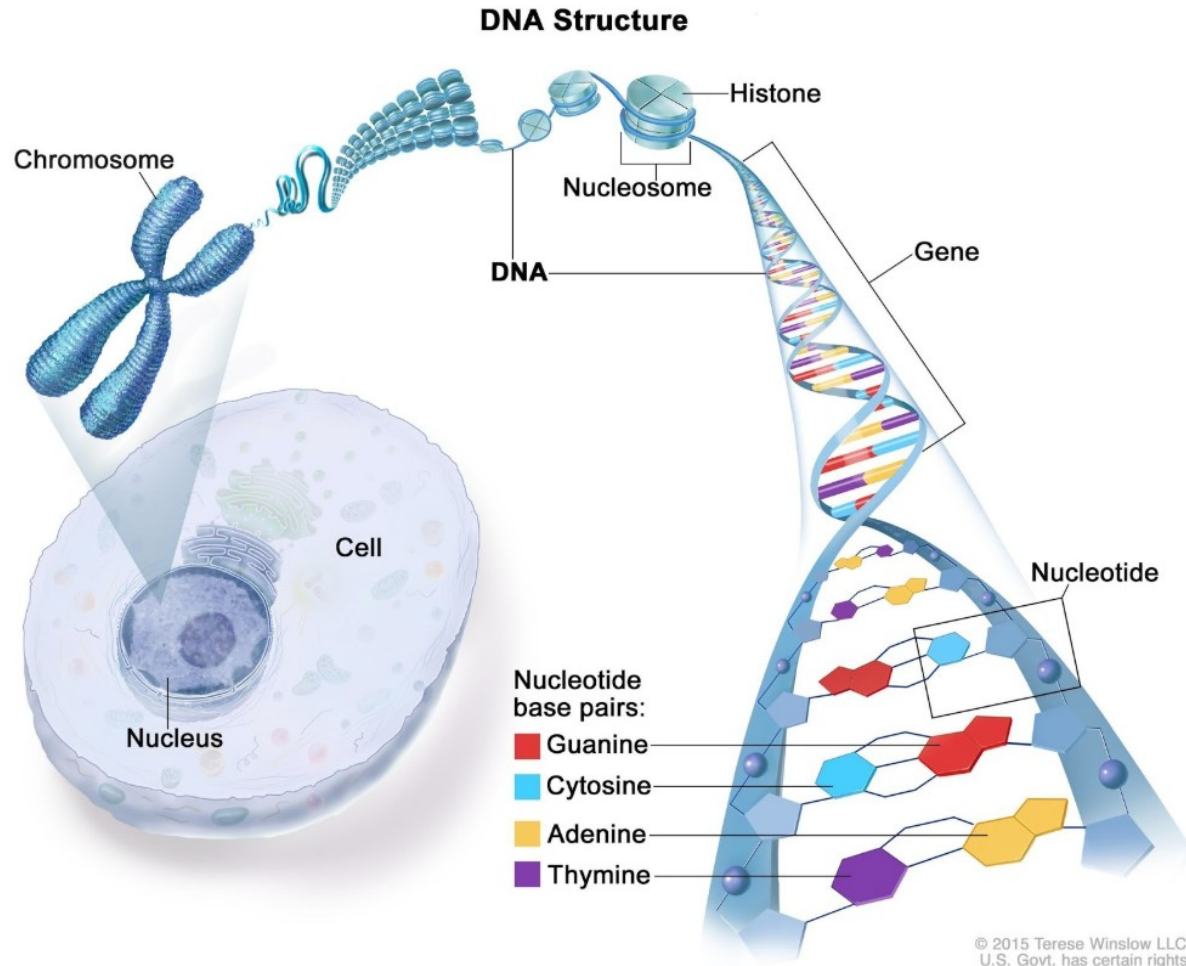
A interação fraca (ponte de hidrogênio) que segura as duas fitas de DNA



Fita dupla de DNA ~ dupla hélice



Hierarquia do cromossomo



Como estudar tudo isto?

Áreas de estudo

- Bioquímica & Química
- Biofísica
- Biologia Molecular
- Biologia Celular
- Genética
- ...
- e onde entra a matemática?

Biologia x Matemática

- Biomatemática (mathematical biology) ❌
- Matemática aplicada à Biologia de evolução ~ populações ✅
- Bioinformática (ômicas) ✅
- Immunoinformática ✅
- Biologia de Sistemas (redes – networks) ✅
- Bioestatística ✅
- Engenharia e Matemática aplicada a medicina ❌

exercício

Qual o comprimento do genoma mitocondrial?

Quantos genes existem no genoma mitocondrial?

O que é transferência horizontal e vertical de genes?

O que é bioinformática?

O que é imunoinformática?

O que é bioinformática

Bioinformática é o estudo de algoritmos matemáticos, aprendizado de máquina e bioestatística aplicados para melhor compreender sequências de nucleotídeos e proteínas e os resultados de experimentos das ômicas.

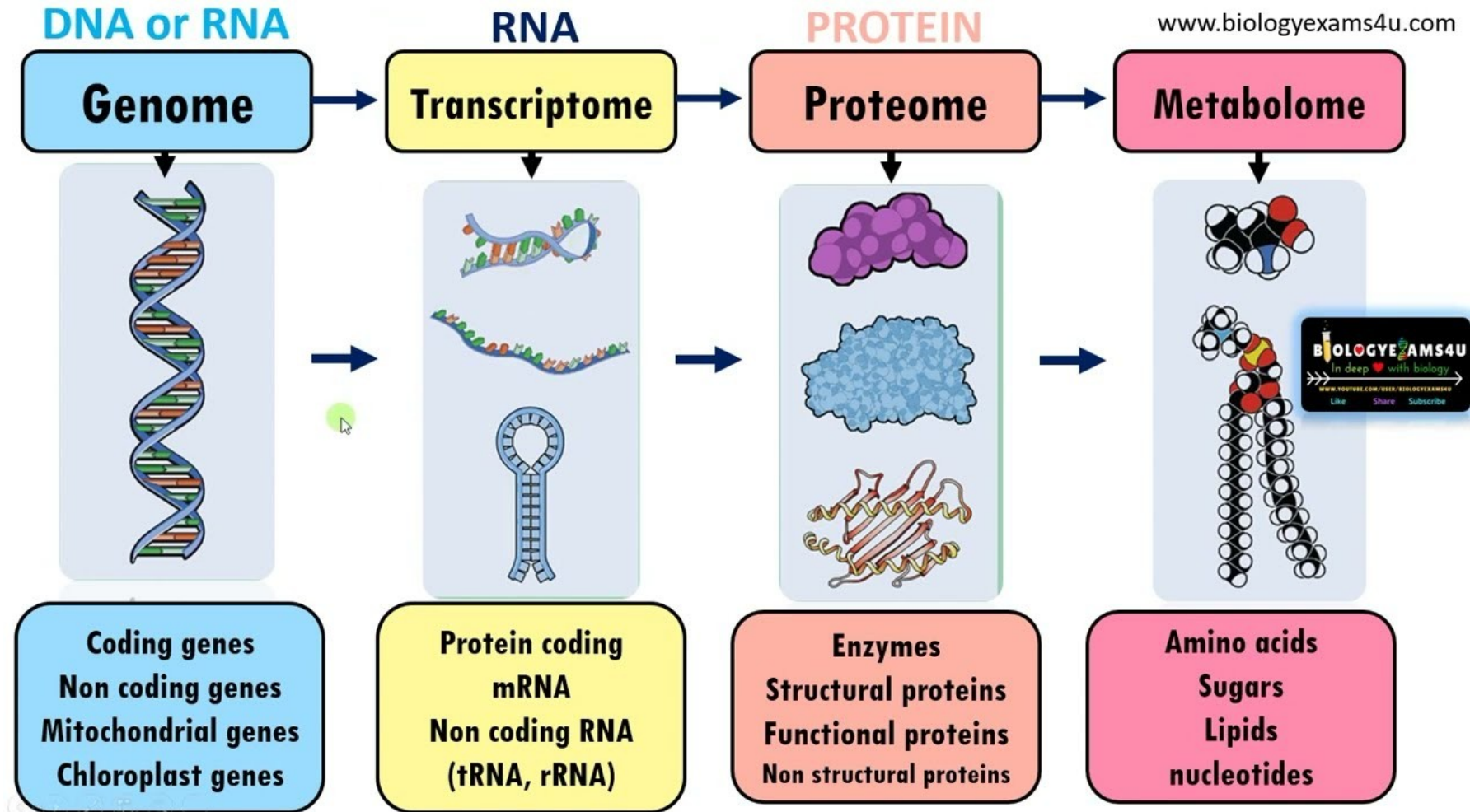
O que são ômicas? São estudos e experimentos relacionados a:

- Genômica
- Exômica
- Transcriptômica
- Epigenética

- Proteômica
- Metabolômica
- Single-cell



Qual a diferença entre Genoma, Transcriptoma, Proteoma and Metaboloma?



... me contaram que o COX2 é um gene interessante, será?

... me contaram que o COX2 é um gene interessante, será?

O que posso fazer?

Busca de genes / proteínas

Posso perguntar:

- Onde tem uma boa descrição deste gene?
- Em que vias ele participa?
- Como posso localizá-lo?

Busca de genes / proteínas

Posso perguntar:

- Onde tem uma boa descrição deste gene?

Genecards <https://www.genecards.org/>

- Em que vias ele participa?

KEGG” [KEGG: procure no google “COX2 pathway
https://www.genome.jp/dbget-bin/www_bget?dha:cox2](https://www.genome.jp/dbget-bin/www_bget?dha:cox2)

- Como posso localizá-lo?

<https://genome.ucsc.edu/>

UCSC genome browser

COX2 na verdade é MT-CO2

Genecard

genecards.org/cgi-bin/carddisp.pl?gene=MT-CO2&keywords=COX2

Free for academic non-profit institutions. Other users need a [Commercial license](#)

WEIZMANN INSTITUTE OF SCIENCE LifeMap SCIENCES

Search GeneCards (supports boolean, parenthesis and quotes) [Advanced](#)

Home | User Guide | Analysis Tools | Release Notes | About | Data Access | GeneCards Team | My Genes | Log In / Sign Up

MT-CO2 Gene - Mitochondrially Encoded Cytochrome C Oxidase II

Protein Coding (Updated: Mar 21, 2023 ; GCMP007587 ; GIFTS: 40)

Search in Gene [Follow Gene](#)

Jump to section	Aliases Paralogs	Disorders Pathways	Domains Products	Drugs Proteins	Expression Publications	Function Sources	Genomics Summaries	Localization Transcripts	Orthologs Variants
-----------------	---------------------	-----------------------	---------------------	-------------------	----------------------------	---------------------	-----------------------	-----------------------------	-----------------------

R&D Proteins Primary Antibodies
ELISAs Antibody Arrays
Activity Assays

VectorBuilder Online Vector Design Platform
Virus Packaging (AAV/Lenti)
CRISPR Library Construction

ORIGENE Proteins Antibodies Assays
Genes shRNA Primers
CRISPR Lentiviral Particles

SYNTHEGO CRISPR Knockout Kit sgRNA
KO Pools iPSC SNV Clone
Free Bioinformatics Tools

Aliases for MT-CO2 Gene

Aliases for MT-CO2 Gene

GeneCards Symbol: **MT-CO2** ² [?]

Mitochondrially Encoded Cytochrome C Oxidase II ² ⁵

COX2 ² ³ ⁴ ⁵

MTCO2 ³ ⁴ ⁵

COII ³ ⁴

CO2 ² ⁵

Cytochrome C Oxidase Polypeptide II ⁴

Cytochrome C Oxidase Subunit II ³

Cytochrome C Oxidase Subunit 2 ⁴

Cytochrome C Oxidase II ²

EC 7.1.1.9 ⁴

EC 1.9.3.1 ⁴⁸

COXII ⁴

External Ids for MT-CO2 Gene

HGNC: 7421 NCBI Entrez Gene: 4513 Ensembl: ENSG00000198712 UniProtKB/Swiss-Prot: P00403

GeneALaCart
GENECARDS BATCH QUERIES

> 190 Integrated Biomedical Sources

API, JSON, CSV, EXCEL



<https://www.genecards.org/>

Entry	cox2 CDS T01026
Name	(RefSeq) cytochrome c oxidase subunit 2
KO	K02261 cytochrome c oxidase subunit 2
Organism	dha Debaryomyces hansenii
Pathway	dha00190 Oxidative phosphorylation dha01100 Metabolic pathways
Module	dha_M00154 Cytochrome c oxidase
Brite	KEGG Orthology (KO) [BR:dha00001] 09100 Metabolism 09102 Energy metabolism 00190 Oxidative phosphorylation cox2 09180 Brite Hierarchies 09182 Protein families: genetic information processing 03029 Mitochondrial biogenesis [BR:dha03029] cox2 Mitochondrial biogenesis [BR:dha03029] Mitochondrial DNA transcription, translation, and replication fac Mitochondrial DNA-encoded proteins Cytochrome c oxidase cox2
SSDB	Ortholog Paralog Gene cluster GFIT
Motif	Pfam: COX2 COX2_TM DUF6169 Motif
Other DBs	NCBI-GeneID: 5845854 NCBI-ProteinID: YP_001621413 UniProt: A9RAG1
Position	MT:2603..3343 Genome browser
AA seq	246 aa AA seq DB search MIWTDVPTPWGMRFQDAATPNAEGMHLYDHMMYYLALMLGLVSYMLYVMMKDYKNNTFA YKYIKHGQTLEIMWMTMPAVMLLLMAFP SFMLLYLCDEVLTPAMTVKVVGLQWYWKYEYS DFVSETGETVEYESYVMPEDMLEEGQLRLD TDTS MVVPVDTHVRFMTANDVLHCFTMP SLGIKVDACPGRLNQVSALMQRTGVYYGQCSELCGVNHGLMPIKTECVPIGDFVEWLGEQ ENVYVA
NT seq	741 nt NT seq +upstream 0 nt +downstream 0 nt atgatttgactagatgtaccaacaccttgaggaatagctttccaagatgccgaacacct

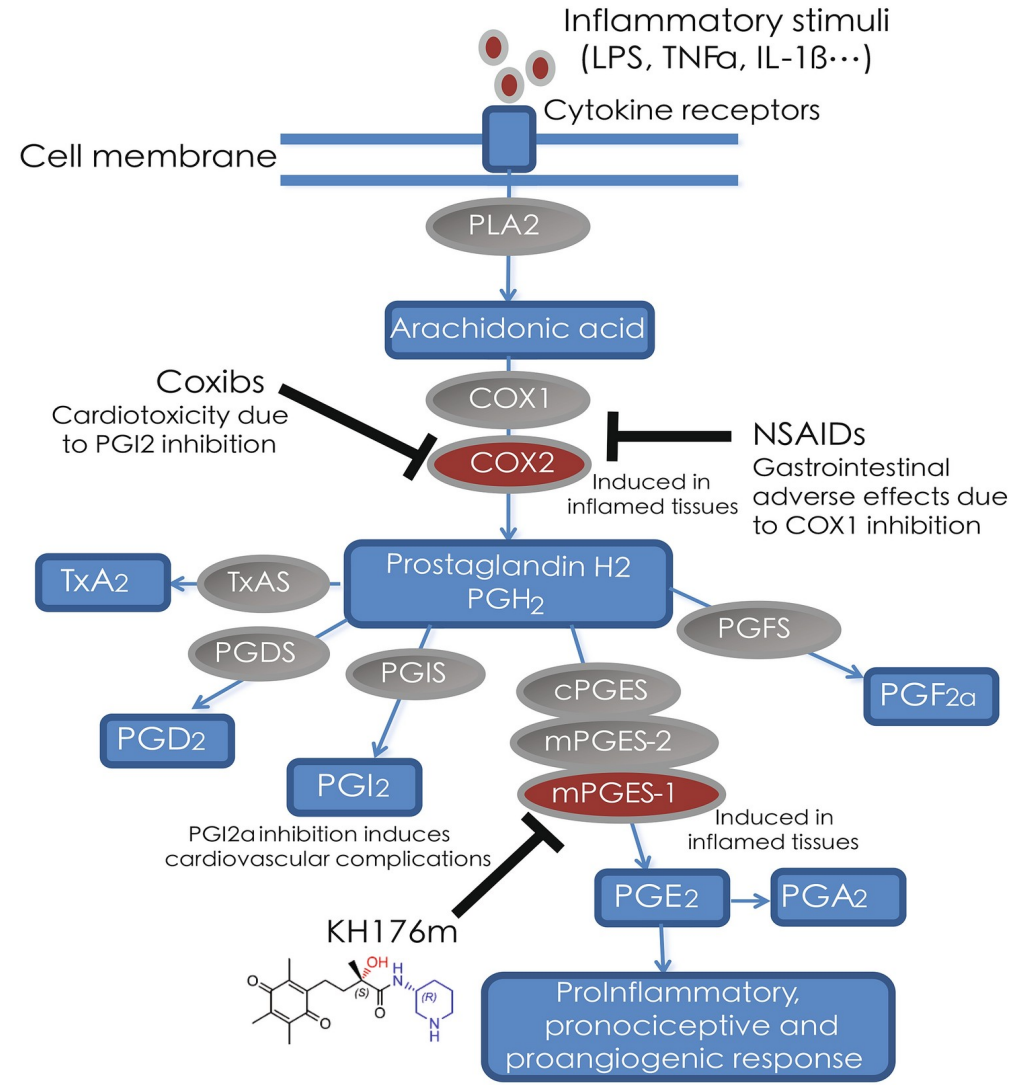
All links

Ontology (2)
 KEGG BRITE (2)
 Pathway (3)
 KEGG PATHWAY (2)
 KEGG MODULE (1)
 Genome (1)
 KEGG GENOME (1)
 Gene (17)
 KEGG ORTHOLOGY (1)
 RefGene (13)
 NCBI-PROTEINID (1)
 NCBI-Gene (1)
 OC (1)
 Protein sequence (3)
 UniProt (1)
 SWISS-PROT (1)
 RefSeq(pep) (1)
 Protein domain (3)
 Pfam (3)
 All databases (29)

[Download RDF](#)

Entry	K11987	K0
Symbol	PTGS2, COX2	
Name	prostaglandin-endoperoxide synthase 2 [EC:1.14.99.1]	
Pathway	<p>map00590 Arachidonic acid metabolism ←</p> <p>map01100 Metabolic pathways ←</p> <p>map04064 NF-kappa B signaling pathway ←</p> <p>map04370 VEGF signaling pathway ←</p> <p>map04625 C-type lectin receptor signaling pathway ←</p> <p>map04657 IL-17 signaling pathway ←</p> <p>map04668 TNF signaling pathway ←</p> <p>map04723 Retrograde endocannabinoid signaling</p> <p>map04726 Serotonergic synapse</p> <p>map04913 Ovarian steroidogenesis</p> <p>map04921 Oxytocin signaling pathway</p> <p>map04923 Regulation of lipolysis in adipocytes</p> <p>map05010 Alzheimer disease</p> <p>map05022 Pathways of neurodegeneration - multiple diseases</p> <p>map05140 Leishmaniasis</p> <p>map05163 Human cytomegalovirus infection</p> <p>map05165 Human papillomavirus infection</p> <p>map05167 Kaposi sarcoma-associated herpesvirus infection</p> <p>map05200 Pathways in cancer</p> <p>map05204 Chemical carcinogenesis - DNA adducts</p> <p>map05206 MicroRNAs in cancer</p> <p>map05222 Small cell lung cancer</p>	
Disease	<p>H00017 Esophageal cancer</p> <p>H00025 Penile cancer</p> <p>H00046 Cholangiocarcinoma</p>	
Brite	<p>KEGG Orthology (K0) [BR:ko00001]</p> <p>09100 Metabolism</p> <p>09103 Lipid metabolism</p> <p>00590 Arachidonic acid metabolism</p> <p>K11987 PTGS2, COX2; prostaglandin-endoperoxide synthase 2</p> <p>09130 Environmental Information Processing</p> <p>09132 Signal transduction</p> <p>04370 VEGF signaling pathway</p> <p>K11987 PTGS2, COX2; prostaglandin-endoperoxide synthase 2</p> <p>04064 NF-kappa B signaling pathway</p> <p>K11987 PTGS2, COX2; prostaglandin-endoperoxide synthase 2</p> <p>04668 TNF signaling pathway</p> <p>K11987 PTGS2, COX2; prostaglandin-endoperoxide synthase 2</p> <p>09150 Organismal Systems</p> <p>09151 Immune system</p> <p>04625 C-type lectin receptor signaling pathway</p>	

Exemplo de um pathway contendo COX2



Jiang, X., Renkema, H., Pennings, B. et al. Mechanism of action and potential applications of selective inhibition of microsomal prostaglandin E synthase-1-mediated PGE₂ biosynthesis by sonlicromanolTM's metabolite KH176m. Sci Rep 11, 880 (2021). <https://doi.org/10.1038/s41598-020-79466-w>

Vamos achar genes? e regiões intergênicas...



UCSC genome browser

← → ↻ 🔒 genome.ucsc.edu

UNIVERSITY OF CALIFORNIA SANTA CRUZ Genomics Institute UCSC Genome Browser

Genomes Genome Browser Tools Mirrors Downloads My Data Projects Help About Us

Tools

-  **Genome Browser** - Interactively visualize genomic data
- BLAT** - Rapidly align sequences to the genome
- In-Silico PCR** - Rapidly align PCR primer pairs to the genome
-  **Table Browser** - Download and filter data from the Genome Browser
- LiftOver** - Convert genome coordinates between assemblies
- REST API** - Returns data requested in JSON format
- Variant Annotation Integrator** - Annotate genomic variants
- More tools...**

News

- May 04, 2023 - **EVA SNP release 4 for 36 assemblies**
- Apr. 24, 2023 - **New DGV Gold Standard track for hg38**
- Apr. 14, 2023 - **Problematic Regions for hg38 and a new public hub**
- Apr. 10, 2023 - **New Cross Tissue Nuclei track for hg38**
- Mar. 29, 2023 - **Updated DGV tracks for hg19/hg38**
- Mar. 08, 2023 - **TOGA Gene Prediction tracks for 41 assemblies**

[More news...](#) [Subscribe](#)



<https://genome.ucsc.edu/>

Vamos achar genes? e regiões intergênicas...

UCSC genome browser

The screenshot shows the UCSC Genome Browser homepage. At the top is a navigation bar with links: Genomes, Genome Browser, Tools, Mirrors, Downloads, My Data, Projects, Help, and About Us. Below this is a 'Browse/Select Species' section with a search box and a list of popular species: Human, Mouse, Rat, Zebrafish, Fruitfly, Worm, and Yeast. An orange arrow points to the 'Human' icon. To the right is a 'Find Position' section with a 'Human Assembly' dropdown set to 'Dec. 2013 (GRCh38/hg38)' and a 'Position/Search Term' input box. An orange arrow points to the search box, and a yellow callout bubble with the text 'Digite MT-CO2' points to it. Below the search box is a 'Human Genome Browser - hg38 assembly' section with a 'view sequences' link. To the left of the main content is a 'UCSC SPECIES TREE AND CONNECTED ASSEMBLY HUBS' section showing a phylogenetic tree of various primates. At the bottom right is a small graphic of a human figure with the text 'Homo sapiens (Graphic courtesy of CBSE)'. At the bottom of the page, an orange arrow points to the URL: <https://genome.ucsc.edu/cgi-bin/hgGateway>.

Browse/Select Species

POPULAR SPECIES

Human Mouse Rat Zebrafish Fruitfly Worm Yeast

Search through thousands of genome browsers
Enter species, common name or assembly ID

[Unable to find a genome? Send us a request.](#)

UCSC SPECIES TREE AND CONNECTED ASSEMBLY HUBS

Find Position

Human Assembly
Dec. 2013 (GRCh38/hg38)

Position/Search Term
Enter position, gene symbol or search terms
Current position: chr2:25,160,000-25,168,903

Human Genome Browser - hg38 assembly

view sequences

UCSC Genome Browser assembly ID: hg38
Sequencing/Assembly provider ID: Genome Reference Consortium
Assembly date: Dec. 2013 initial release; June 2022 update
Assembly accession: [GCA_000001405.29](#)
NCBI Genome ID: [51](#) (Homo sapiens (human))
NCBI Assembly ID: [GCF_000001405.40](#) (GRCh38.p14, GCA_000001405.29)
BioProject ID: [PRJNA31257](#)

Search the assembly:

- **By position or search term:** Use the "position or search term" box to find areas of the genome associated with many different attributes, such as a specific chromosomal coordinate range; mRNA, EST, or STS marker names; or keywords from the GenBank description of an mRNA. [More information](#), including sample queries.
- **By gene name:** Type a gene name into the "search term" box, choose your gene from the drop-down list, then press "submit" to go directly to the assembly location associated with that gene. [More information](#).
- **By track type:** Click the "track search" button to find Genome Browser tracks that match specific selection criteria. [More information](#).

UCSC SPECIES TREE AND CONNECTED ASSEMBLY HUBS

Human
Chimp
Bonobo
Gorilla
Orangutan
Gibbon
Green monkey
Crab-eating macaque
Rhesus
Baboon (anubis)
Baboon (hamadryas)
Proboscis monkey
Golden snub-nosed monkey
Marmoset
Squirrel monkey

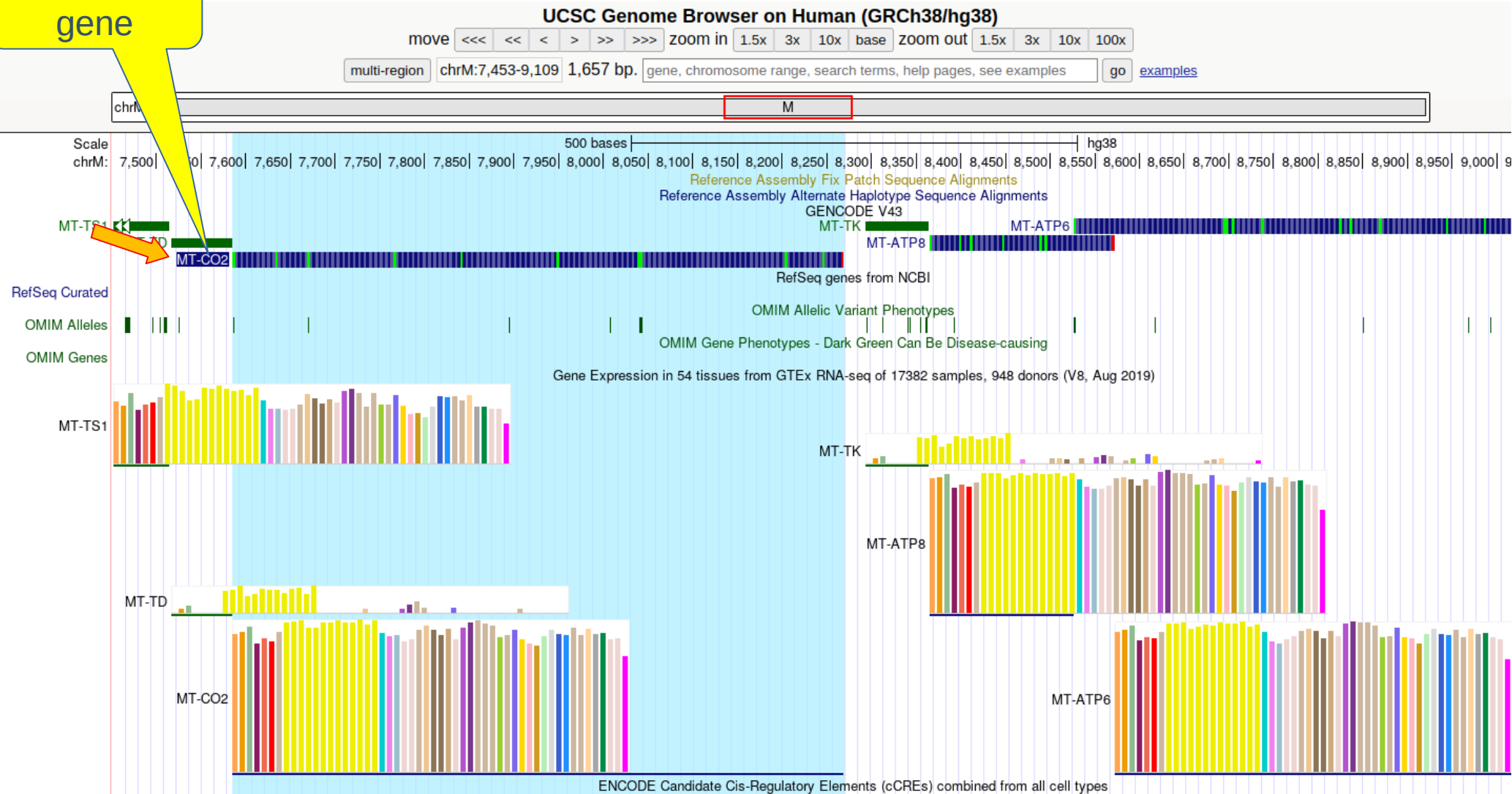
UCSC

Homo sapiens
(Graphic courtesy of CBSE)

<https://genome.ucsc.edu/cgi-bin/hgGateway>

achei o
gene

COX2 - MT-CO2

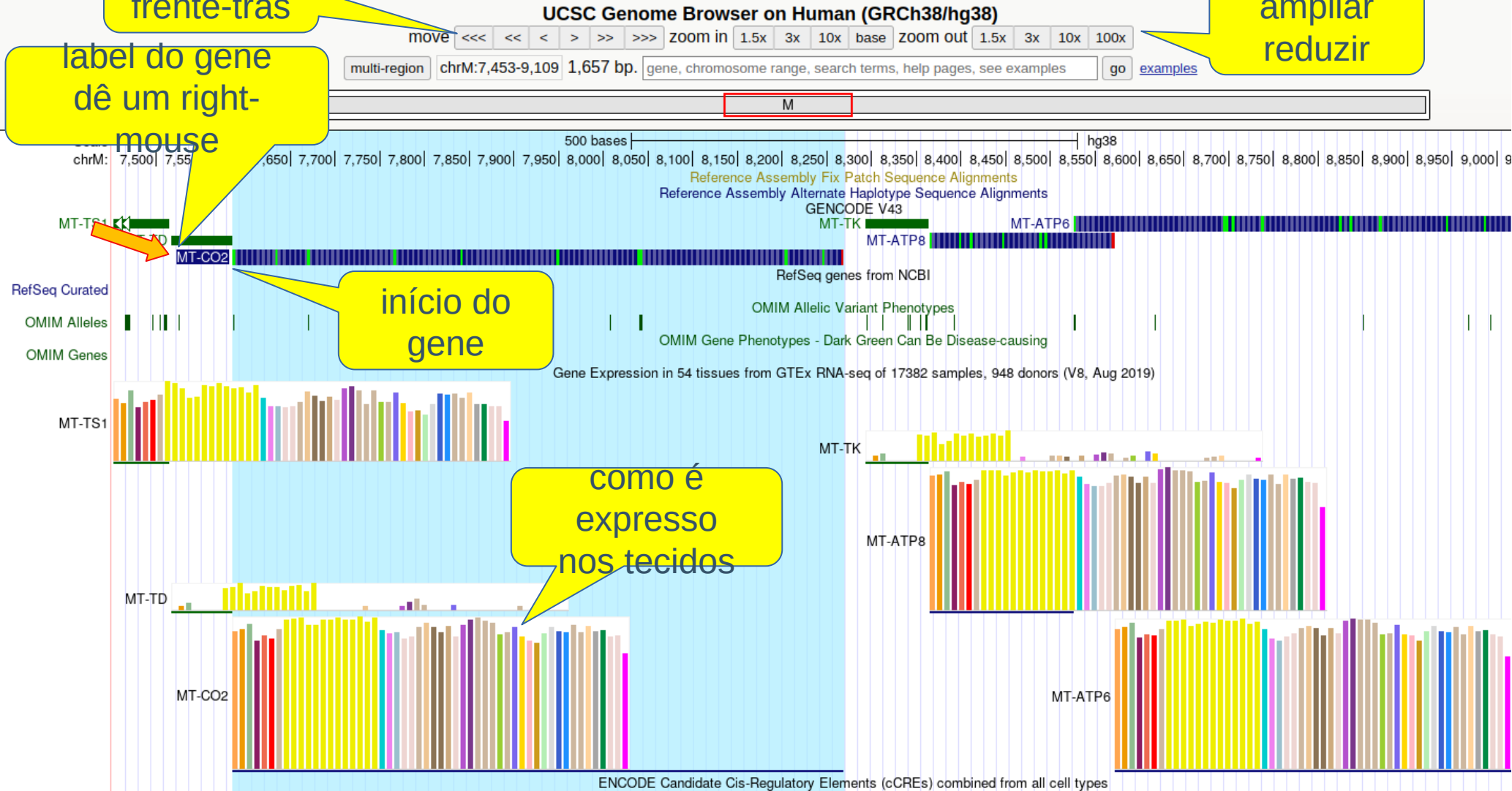


COX2 - MT-CO2

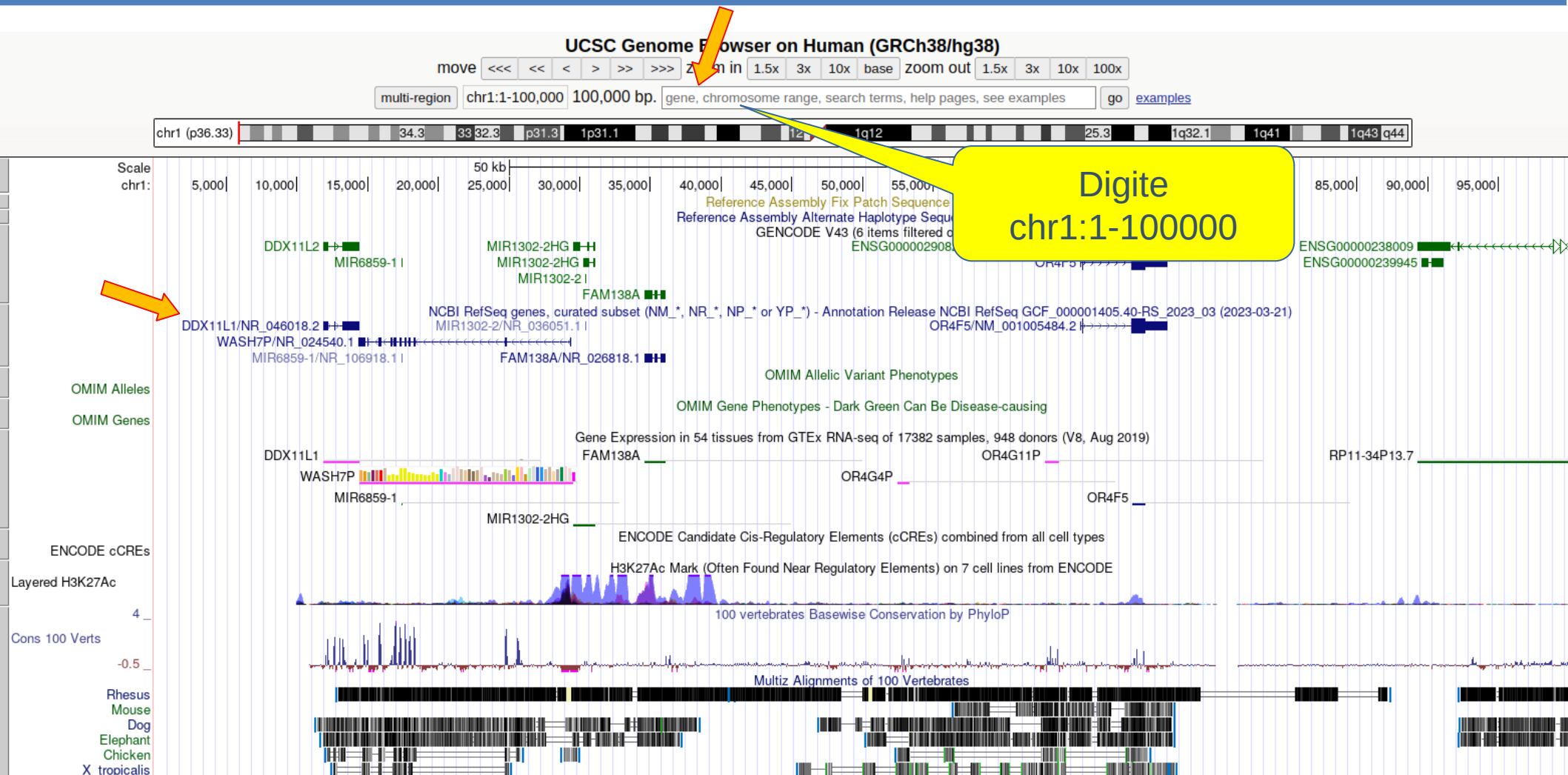
navegar
frente-trás

label do gene
dê um right-
mouse

ampliar
reduzir



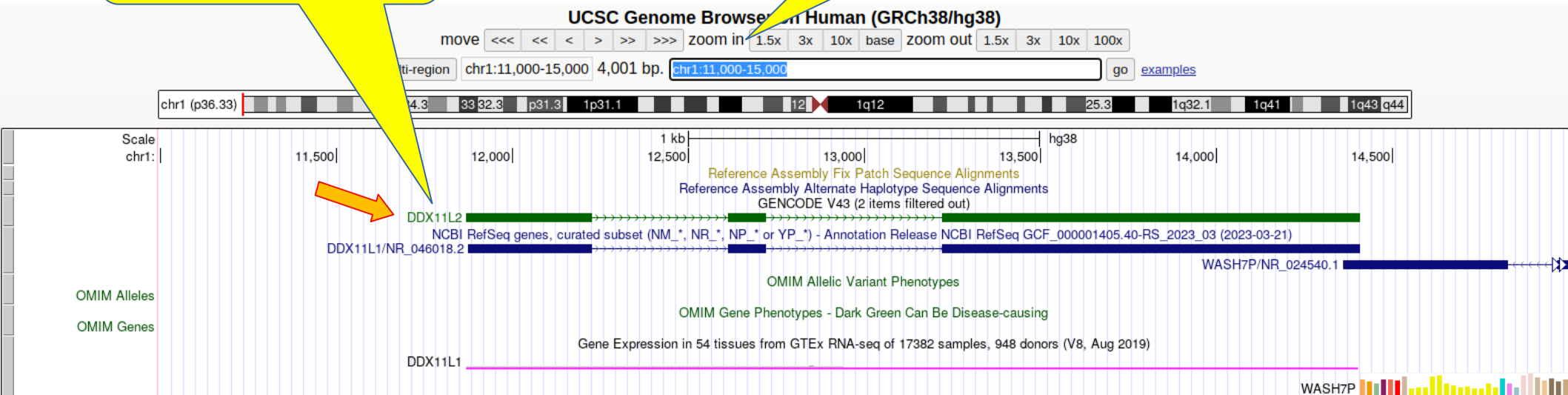
Cromossomo 1 de 1:100000



Zoom: chr1:11,000-15,000

Right-mouse
get DNA

Procure por
DDX11



Vamos fazer um BLAST de nucleotídeos

Basic Local Alignment Search Tool



<https://blast.ncbi.nlm.nih.gov/Blast.cgi>

BLAST - nucleotides

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

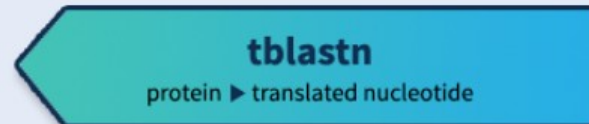
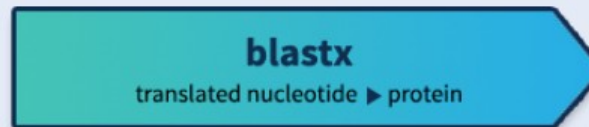
BLAST+ 2.14.0 is here!

BLASTP, BLASTX, and TBLASTN are faster than before.

Fri, 28 Apr 2023

[More BLAST news...](#)

Web BLAST



<https://blast.ncbi.nlm.nih.gov/Blast.cgi>

BLAST – copie a sequência e dê um blast

Standard Nucleotide BLAST

BLASTN programs search nucleotide databases using a nucleotide query. more...

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s) [?](#) [Clear](#) Query subrange [?](#)

From to

Or, upload file No file chosen [?](#)

Job Title

Enter a descriptive title for your BLAST search [?](#)

☐ Align two or more sequences [?](#)

Choose Search Set

Database ☒ Standard databases (nr etc.): ☐ rRNA/ITS databases ☐ Genomic + transcript databases ☐ Betacoronavirus

[New](#) ☐ Experimental databases [Try experimental taxonomic nt databases](#) [Download](#)

For more info see [What are taxonomic nt databases?](#)

Nucleotide collection (nr/nt) [?](#)

Organism Optional ☐ exclude [Add organism](#)

Enter organism common name, binomial, or tax id. Only 20 top taxa will be shown [?](#)

Exclude Optional ☐ Models (XM/XP) ☐ Uncultured/environmental sample sequences

Limit to Optional ☐ Sequences from type material

Entrez Query Optional [YouTube](#) Create custom database

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 [?](#)

BLAST Search database Nucleotide collection (nr/nt) using Megablast (Optimize for highly similar sequences)

☐ Show results in a new window

copie aproximadamente os primeiros 60 nucleotídeos

BLAST achou DDX11 mais similares com a sequência enviada

Job Title	Nucleotide Sequence		
RID	6ANVHZR6013	Search expires on 05-19 06:38 am	Download All ▼
Program	BLASTN 	Citation ▼	
Database	nt	See details ▼	
Query ID	lcl Query_59665		
Description	None		
Molecule type	dna		
Query Length	1450		
Other reports	Distance tree of results	MSA viewer	

Filter Results

Organism

only top 20 will appear

☐ exclude

+

Add organism

Percent Identity

E value

Query Coverage

to

to

to

Filter

Reset

- Descriptions
- Graphic Summary
- Alignments
- Taxonomy

Sequences producing significant alignments

Download ▼

Select columns ▼

Show

100 ▼

[?](#)

☒ select all 100 sequences selected

[GenBank](#)

[Graphics](#)

[Distance tree of results](#)

[MSA Viewer](#)

	Description ▼	Scientific Name ▼	Max Score ▼	Total Score ▼	Query Cover ▼	E value ▼	Per. Ident ▼	Acc. Len ▼	Accession
<input checked="" type="checkbox"/>	Homo sapiens DEAD/H-box helicase 11 (DDX11), RefSeqGene on chromosome 12	Homo sapiens	2678	2678	100%	0.0	100.00%	37947	NG_023352.1
<input checked="" type="checkbox"/>	Homo sapiens 12 BAC RP11-551L14 (Roswell Park Cancer Institute Human BAC Library) complete seque...	Homo sapiens	2678	2678	100%	0.0	100.00%	168986	AC008013.8
<input checked="" type="checkbox"/>	Homo sapiens chromosome 12 clone CH17-321K24, complete sequence	Homo sapiens	2632	2632	100%	0.0	99.45%	210014	AC277891.1
<input checked="" type="checkbox"/>	Homo sapiens FOSMID clone ABC13-48569500C5 from chromosome 12, complete sequence	Homo sapiens	2503	2503	100%	0.0	97.80%	37211	AC215997.4
<input checked="" type="checkbox"/>	Homo sapiens BAC clone CH17-138H12 from chromosome 12, complete sequence	Homo sapiens	2497	2497	100%	0.0	97.73%	211866	AC254631.1
<input checked="" type="checkbox"/>	Homo sapiens 12p13 PAC RPC11-726G1 (Roswell Park Cancer Institute Human PAC Library) complete s...	Homo sapiens	2486	2486	100%	0.0	97.59%	180685	AC006432.15

BLAST achou DDX11 mais similar

Estatística:

- Score: nucleotídeos alinhados
- E-value: ~ p-valor (se pequeno é significativo)
- Porcentagem de identidades
- Comprimento
- Accession Number – link para o registro

Job Title

Nucleotide Sequence

RID

[6ANVHZR6013](#) Search expires on 05-19 06:38 am [Download All](#) ▼

Program

BLASTN [?](#) [Citation](#) ▼

Database

nt [See details](#) ▼

Query ID

lcl|Query_59665

Description

None

Molecule type

Query Length

Other reports

[Viewer](#) [?](#)

Sequências encontradas

Organismo

accession ID

Descriptions

Graphic Summary

Alignments

Taxonomy

Sequences producing significant alignments

Download ▼

Select columns ▼

Show 100 [?](#)

☒ select all 100 sequences selected

[GenBank](#) [Graphics](#) [Distance tree of results](#) [MSA Viewer](#)

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
<input checked="" type="checkbox"/>	Homo sapiens DEAD/H-box helicase 11 (DDX11), RefSeqGene on chromosome 12	Homo sapiens	2678	2678	100%	0.0	100.00%	37947	NG_023352.1
<input checked="" type="checkbox"/>	Homo sapiens 12 BAC RP11-551L14 (Roswell Park Cancer Institute Human BAC Library) complete sequence	Homo sapiens	2678	2678	100%	0.0	100.00%	168986	U08013.8
<input checked="" type="checkbox"/>	Homo sapiens chromosome 12 clone CH17-321K24, complete sequence	Homo sapiens	2632	2632	100%				
<input checked="" type="checkbox"/>	Homo sapiens FOSMID clone ABC13-48569500C5 from chromosome 12, complete sequence	Homo sapiens	2503	2503	100%				
<input checked="" type="checkbox"/>	Homo sapiens BAC clone CH17-138H12 from chromosome 12, complete sequence	Homo sapiens	2497	2497	100%	0.0	97.73%	211866	AC254631.1
<input checked="" type="checkbox"/>	Homo sapiens 12p13 PAC RPC11-726G1 (Roswell Park Cancer Institute Human PAC Library) complete sequence	Homo sapiens	2486	2486	100%	0.0	97.59%	180685	AC006432.15

clique aqui

DDX11 registro do NG_023352 no Genbank do NCBI

GenBank ▾

Send to: ▾

Homo sapiens DEAD/H-box helicase 11 (DDX11), RefSeqGene on chromosome 12

NCBI Reference Sequence: NG_023352.1

[FASTA](#) [Graphics](#)

[Go to:](#) ☐

LOCUS	NG_023352	37947 bp	DNA	linear	PRI 25-MAR-2023
DEFINITION	Homo sapiens DEAD/H-box helicase 11 (DDX11), RefSeqGene on chromosome 12.				
ACCESSION	NG_023352				
VERSION	NG_023352.1				
KEYWORDS	RefSeq; RefSeqGene.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo.				
REFERENCE	1 (bases 1 to 37947)				
AUTHORS	Alkhunaizi,E., Brosh,R.M. Jr., Alkuraya,F.S. and Chitayat,D.				
TITLE	Warsaw Syndrome				
JOURNAL	(in) Adam MP, Mirzaa GM, Pagon RA, Wallace SE, Bean LJH, Gripp KW and Amemiya A (Eds.); GENEREVIEWS(R); (1993)				
PUBMED	31169992				
COMMENT	REVIEWED REFSEQ : This record has been curated by NCBI staff. The reference sequence was derived from AC008013.8 . This sequence is a reference standard in the RefSeqGene project.				

Summary: DEAD box proteins, characterized by the conserved motif

Aonde estão os Éxons?

Onde começa este gene? start-codon ATG

```
>hg38 dna range=chr12:31073860-31104799 5'pad=0 3'pad=0 strand=+ repeatMasking=none
GTTGTTCCGGCTGCCTTTCACTGAGGGGACCCGCCAGTTTCTAACTCAGT
GGCGTTTGCCCTGATTCCCGGGGCTGGCTTTCAGCGTAGCAATTCTGCC
GGCGAAGAAGGTGAGCGCAGTGCTGTGTGGCAGCAGAGCTCCTTAGGACG
AGGAGCAGCGGGACGAGGAAGGGCAGACTGGTGAATCGCAAACCTGGGCG
TCTGTTCCGGCGCCGGACCCCTATTTGCAAAGGTGGGTGGCCCGTCCGGA
GCGGGAACAAACATTCCGGAAGTGGAGGGCCGGGCCAGCGTGATTGACAAGC
GGGAACCCCTGTGTGGGACGGGTAGGCCTAGGAAGGTTGTGCCTGCGGT
GGAACCTGGGCGGTGCGCAGAAGTGGGCATTAAACGACAGCCGCGTGTCTGG
GTCTTAGATTTGGCCAGCTGTGTTGAGCTTTTCATG GATTATCTTACGT
AGATAAGACACTGCAACAGTGAGTGAGCGCTTGTAAACCACTGTCTCTT
ACGGAAACTGAGCCCCAGCGATGCTAACTTTAGCAAGGATACAGCTGGGA
TCCTAAACTTGGCAATCAGAGCCAGAGCCGATAAAAGTTAGCTGCATGAG
TCTAGCTTCCCCAGGGCGGGAATCGAGGCGGAGCAGGGTACAGTACGGA
GGCCAGGAATGAGTGCACTTGACCAGATTGTTGACGGAAGTGTCATAAAA
ATG GACTTAAATGCTGATAAGCAGCTGTTTGGGTTCCACACAGGGTGCGA
GCTCAGGATGCACGTTGGAGGGGACACAGGGCCAGAGCAAGGTGGGAATG
CGGGTATTATGGGCCAGGCCATCCTCCAGCTGGTGGAGCACCGCAGTACT
GCAGTGTGTGGCCCTGGCTTAACAGCAGTGCGGAAAGCTTTTTCTTGG
GGCTGTGGTGCTTCCAGGTGTGTGAAGTAAAAACATTTTAGGGCCATAC
GGTAGATAGTACCTGCCACATAGTTGTCTTGGTCAGCCCCGGCTGCCATG
ACAAAATACCATAAACTGGGTGGCTTAGACACAGAAATG GTTTTCTCAC
AGTCCCAGAGGCTTGGGATGCCAAGATCAATG TGGGAGGACACAACCTG
AGCCCAACAACAATAGTCTGTACTCAGTAATGAGTGATAATTGGGGACTGA
AGAAAATGAACACGTAAAGAACTAATATGTTCTGAAGTGCTTTCACAAC
TCTAACCTCGTTTTATGAGCGTGAGCTTTGCTGTCTGGTGTGTGCTTG
GCACTGGGAGGTGATGTTGTCTCCACACAGCCAACCTGAAGAGGGCTG
AACAGTCACTGCAAATGTTTTAATAGGGCTTAGTGAATCCGTTATACT
CAGATTTATCTAAACCTCTATGATTTAGCCTGTGCTGCTTCTGGAATAAT
GAGATCCATAATTACCACTGATGGGAAGTGAAATAATACTTACGTTTCT
TCTGTATTGTTAGTGTTGTCTTCTAGAGTTTGGTAACCAAGTCTGTCT
TTTTATCCCACTTATCCTGGTGGGAGGAAAAGTGAGGAGATAGAAAGTT
TCAGGTGGCTTGGGGGTCTGGCAGATGTTGGTTCAAATCCTGAGTTCAGC
ACTTGCTGAGTGACCTTGGGCAAGTCATATAAGTTTACTGAGTCTCAGTT
TCTTCTCTATAAAATAGAGCTTATAAAATACCACACAGGGTTTTGTG
GGGTTATCTGAAAACGGTTTGAAACCATTAAGAACTGGCCATTTAACTA
```

Aonde estão os Éxons?

Onde começa este gene? start-codon ATG

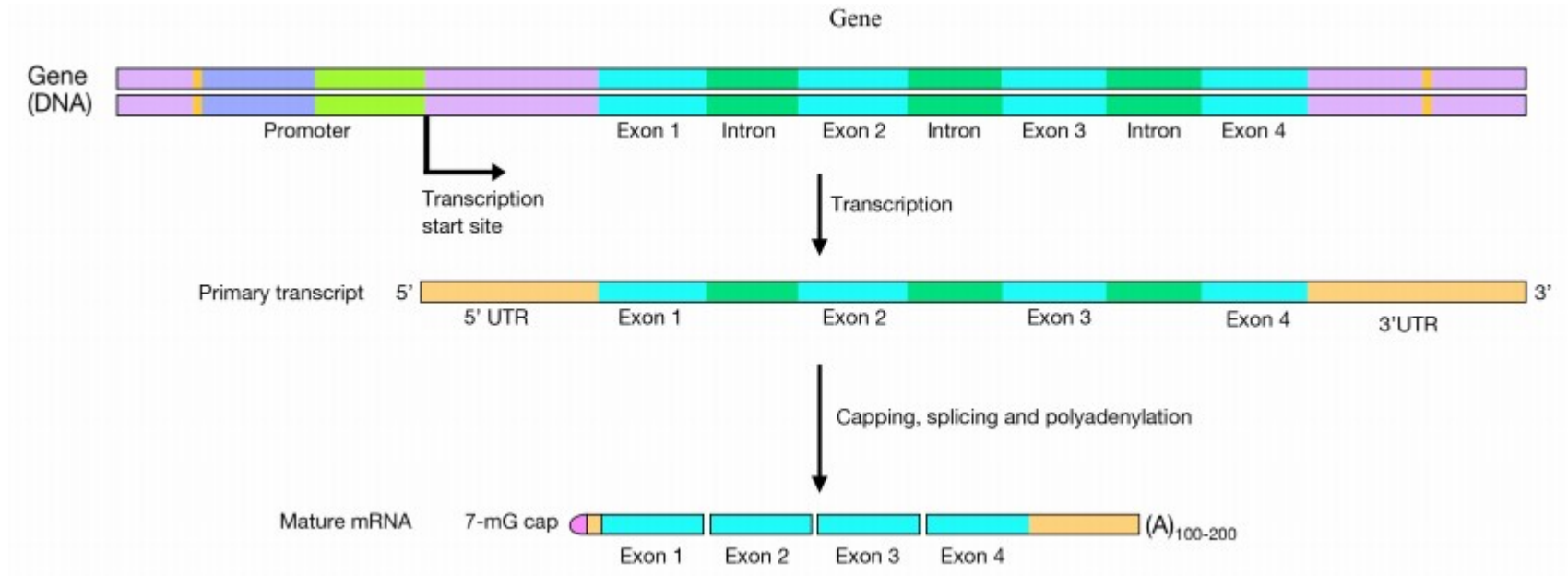
>hg38 dna range=chr12:31073860-31104799 5'pad=0 3'pad=0 strand=+ repeatMasking=none

GTGTTCCGGCTGCCTTTCACTGAGGGGACCGCCAGTTTCTAAGTCACT
GGCGTTTGCCCTGATTCCCGGGGCTGGCTTTAGCGTAGCAATTCAGCC
GGCGAAGAAGGTGAGCGCAGTGTGTGTGGCAGCAGAGCTCCTTAGGACG
AGGAGCAGCGGGACGAGGAAGGGCAGACTGGTGAATCGCAAACCTGGGCG
TCTGTTCCGGCGCCGACCCCTATTTGCAAAGGTGGGTGGCCCGTCCGGA
GCGGGAAAAACATTCGGAAAGTGGAGGGCCGGCCAGCGTGATTGACAAGC
GGGAACCCCTGTGTGGGACGGGTAGGCCTAGGAAGGTTGTGCTGCGGT
GGAAGTGGGCGGTGCGCAGAAAGTGGGCATTAAACAGCAGCCGCGTGTCTGG
GTCTTAGATTTGGCCAGCTGTGTTGAGCTTTTCATGGAATTATCTTACGT
AGATAAGACACTGCAACAGTGAGTGAGCGCTTGAACCCACTGTCTCTT
ACGGAACTAGACCCAGCGATGCTAACTTTAGCAAGGATACAGCTGGGA
TCCTAAACTTGGCAATCAGAGCCAGAGCCGATAAAGTTAGCTGCATGAG
TCTAGCTTCCCCAGGGCGGGAATCAGAGCGGAGCAGGGTACAGTACGGA
GGCGAGGAATGAGTGCACCTTGACCAGATTGTTGACGGAAGTGTCAAAAA
ATGGAATTAATGCTGATAAGCAGCTGTTTGGGTTCCACACAGGGTGCAG
GCTCAGGATGACGTTGGAGGGGACACAGGGCCAGAGCAAGGTGGGAATG
CGGGTATTATGGGCGAGCCATCCTCCAGCTGGTGGAGCACCAGTACT
GCAGTGTGTGGCCCTGGCTTAAACAGCAGTGCGGAAAAAGCTTTTCTTGG
GGCTGTGGTCTTCCAGGTGTGTGAAGTAAAAACATTTTAGGGCCATAC
GGTAGATAGTACCTGCCACATAGTTGTCTTGGTCAGCCCCGGCTGCCATG
ACAAAATACCATAAAGTGGGTGGCTTAGACACAGAAATGTTTCTCTCAC
AGTCCAGAGGCTTGGGATGCAAGATCAATGTTGGGAGGACACAAGT
AGCCCAACAACATAGTCTGTAAGTCAAGTATGAGTGATAATTGGGGACTGA
AGAAAATGAACACGTTAAGAACTAATATGTTCTCTGAAGTGTCTTACAAAC
TCTAACCTCGTTTATGAGCGTGAGCTTTGCTGTCTGGTGTGTGCTTGG
GCACTGGGAGGTGATGGTTGTCTCCACACAGCAACCTGAAGAGGGCTG
AACAGATCACTGCACAAATGTTTTTAAAGGGCTTAGTGAATCCGTTAATC
CAGATTTATCTAAACCTCTATGATTTAGCCTGTGCTGCTTCTGGAATAAT
GAGATCCATAATTACCACTGATGGGAAGTGAATAATACTTACGTTTCT
TCTGTATTGTTAGTGTGTCATTCTAGAGTTTGGTAACCAAGTCTGTCT
TTTTATCCCACTTATCCTGGTGGGAGGAAAAAGTGAGGAGATAGAAAGTT
TCAGGTGGCTTGGGGGTCTGGCAGATGGTTCAAATCCTGAGTTCAAGC
ACTTGCTGAGTGACCTTGGGCAAGTCATATAAGTTTACTGAGTCTCAGTT
TCTTTCTCTATAAAATAGAGCTTATAAAATACCACACAGGGTTTTGTG
GGGTTATCTGAAAACGGTTTGAACCATTAAGAACTGGCCATTTAACTA

Está lá para baixo.
Mas como foi achado?

ACACGGTGAACCCCGTCTCTACCAAAAAAAAAAAAACTGCTGGT
GGCGGGCACCTGTAGTCCCAGCTACTCGGGAGGCTTGAAGATGG
TGTGAACCCGGGAGGCGGAGCGTGCAGTGAGCCGATCACTGCA
CTCCAGCCTGGGCGACAGAGTGAGACTCTGTCTCGAATAAAAAA
AAGATAGGGACGTGTATGTTAACTTGCCTATCCAAGAGCTGTGC
TTATGGTCTCTGCTGTGCGTCATGATTTTCCAGGACAACGGGA
TAAAGTGAAGTAGCTTCGGCTTGTGAATGTGCATTGACGTGGGAG
AAGAAAGCTGCAAAAGTCATTATAAGCAACACCCTTGTAGGGGTGC
TGGTCTGTGAGAAGAGAGCTCTAAGCCTTTTGTAGAGTTAGAAAGGT
ATCGGAGCCACGGTGAATGCAGGGGAGATTGGGTTTTGGCTTTCCTG
GTCTGCATTCTGCTACAGCCGTTAAATGCCGCTAGATAGTGCGTGATT
CTGGTATGGCCTCACGTGGACCTGCTGCGAAGGATGGAGAACATGGTC
TCTGCTTCCAGAAAAAAGGAGAAATTTGGTAATAAGTGTGGAGACTGCT
CTTAAATAATGCTCCAGATTTCAAGCCACTTCTTCTGGACCATGAGAGA
GCTCCCTAATGTTGTATTTATTTTTCTAGGTCCATGGCTAATGAAACAC
AGAAGGTTGGTGCCATCCATTTTCTTTTCCCTTACACCCTATTCCATC

Aonde estão os Éxons? Onde começa este gene?



Localizando os éxons no texto do Genbank

mRNA

```
join(5016..5247,9546..9693,14969..15217,15739..15825,  
16125..16282,19094..19139,20200..20307,20559..20646,  
21042..21250,22875..23027,24002..24048,24401..24480,  
25746..25790,25911..25978,27497..27535,27793..27901,  
28015..28146,29041..29153,31791..31863,32183..32286,  
32989..33138,33399..33467,33583..33683,34092..34176,  
34473..34551,34733..34887,34963..35955)  
/gene="DDX11"  
/gene_synonym="CHL1; CHLR1; KRG2; WABS"  
/product="DEAD/H-box helicase 11, transcript variant 1"  
/transcript_id="NM_030653.4"  
/db_xref="GeneID:1663"  
/db_xref="HGNC:HGNC:2736"  
/db_xref="MIM:601150"
```

exon

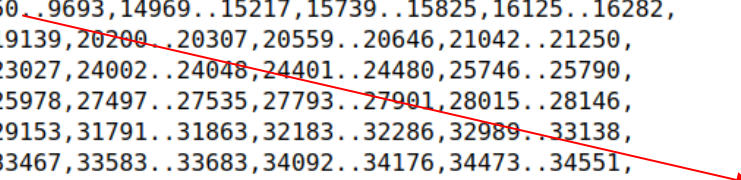
```
5016..5247  
/gene="DDX11"  
/gene_synonym="CHL1; CHLR1; KRG2; WABS"  
/inference="alignment:Splign:2.1.0"  
/number=1
```

exon

```
9546..9693  
/gene="DDX11"  
/gene_synonym="CHL1; CHLR1; KRG2; WABS"  
/inference="alignment:Splign:2.1.0"  
/number=2
```

CDS

```
join(9550..9693,14969..15217,15739..15825,16125..16282,  
19094..19139,20200..20307,20559..20646,21042..21250,  
22875..23027,24002..24048,24401..24480,25746..25790,  
25911..25978,27497..27535,27793..27901,28015..28146,  
29041..29153,31791..31863,32183..32286,32989..33138,  
33399..33467,33583..33683,34092..34176,34473..34551,  
34733..34887,34963..34992)  
/gene="DDX11"  
/gene_synonym="CHL1; CHLR1; KRG2; WABS"  
/EC_number="3.6.4.12"
```



```
9541 cctaggtcca tggctaata aacacagaag gttggtgcca tccattttcc ttttccttc  
9601 acaccctatt ccatccagga agacttcatg gcagagctgt accgggtttt ggaggctggc  
9661 aagattggga tatttgagag tccaactggc actgtgagta tgaacagtga gagatactga  
9721 aaaggacaac ttaacagcag ccgtactagc ttttcctgtt tgcctatcca gagattttca
```


Parte do registro do Genbank refere-se a anotações

```
/EC_number="3.6.4.12"  
/note="isoform 1 is encoded by transcript variant 1;  
DEAD/H (Asp-Glu-Ala-Asp/His) box polypeptide 11 (CHL1-like  
helicase homolog, S. cerevisiae); probable ATP-dependent  
RNA helicase DDX11; CHL1-related helicase gene-1; DEAD/H  
(Asp-Glu-Ala-Asp/His) box helicase 11; KRG-2; hCHLR1;  
DEAD/H box protein 11; CHL1-related protein 1;  
keratinocyte growth factor-regulated gene 2 protein;  
probable ATP-dependent DNA helicase DDX11"  
/codon_start=1  
/product="ATP-dependent DNA helicase DDX11 isoform 1"  
/protein_id="NP_085911.2"  
/db_xref="CCDS:CCDS41767.1"  
/db_xref="GeneID:1663"  
/db_xref="HGNC:HGNC:2736"  
/db_xref="MIM:601150"  
/translation="MANETQKVGAIHFPPFTPYSIQEDFMAELYRVLEAGKIGIFES  
PTGTGKSLSLICGALSWLRDFEQKKREEEARLLETGTGPLHDEKDESLCLSSSCEGAA  
GTPRPAGEPAWVTQFVQKKEERDLVDRLKAEQARRKQREERLQQLQHRVQLKYAAKRL  
RQEEEEERENLLRLSRELETGPEAERLEQLESCEEELVLAYESDEEKKVASRVEDE  
DDLEEEHITKIYYCSRTHSQLAQFVHEVKKSPFGKDVRLVSLGSRQNLVNEDEVKSLG  
SVQLINDRCVDMQRSRHEKKKGAEKKPKRRRQEKQAACPFYNHEQMGLLRDEALAEV  
KDMEQLLALGKEARACPYYSRLAIPAAQLVVLPHYQMLLHAATRQAAGIRLQDQVVII  
DEAHNLIDTITGMHSEVSGSQLCQAHSQLLQYVERYGKRLKAKNLMYKQILYLLEK  
FVAVLGGNIKQNPNTQSLSQGTGTELKTINDFLFQSQIDNINLFKVQRYCEKSMISRL  
FGFTERYGAVFSSREQPKLAGFQQFLQSLQPRTEALAAPADESQASTLRPASPLMHI  
QGFLAALTANQDGRVILSRQGSLSQSTLKFLLLNPAVHFAQVVKECRAVVIAGGTMQ  
PVSDFRQQLACAGVEAERVVEFSCGHVIPPDNILPLVICSGISNQPLEFTFQKREL  
QMMDEVGRILCNLCGVVPGGVVCFPPSYEYLRQVHAHWEKGGLLGRLAARKKIFQEPK  
SAHQVEQVLLAYSRCIQACGQERGQVTGALLLSVVGGMSEGINFSDNLGRCVVMVGM  
PPFNIRSAELQEKMAYLDQTLPRAPGQAPP GKALVENLCMKAVNQSIGRAIRHQKDF  
SVVLLDQRYARPPVLAKLPWIRARVEVKATFGPAIAAVQKFHREKSASS"
```

outras bases
do NCBI

Protein
CDS
HGNC (Hugo)
MIM



clique aqui para
ir para as anotações
da proteína

clique aqui também
para ver o coding
segment CDS

Salvar a proteína em fasta no site

GenPept ▾

Send to: ▾

ATP-dependent DNA helicase DDX11 isoform 1 [Homo sapiens]

NCBI Reference Sequence: NP_085911.2

[Identical Proteins](#) [FASTA](#) [Graphics](#)

Go to: ☐

LOCUS NP_085911 906 aa linear PRI 12-MAR-2023
DEFINITION ATP-dependent DNA helicase DDX11 isoform 1 [Homo sapiens].
ACCESSION NP_085911
VERSION NP_085911.2
DBSOURCE REFSEQ: accession [NM_030653.4](#)
KEYWORDS RefSeq; MANE Select.
SOURCE Homo sapiens (human)
ORGANISM [Homo sapiens](#)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
Catarrhini; Hominidae; Homo.
REFERENCE 1 (residues 1 to 906)
AUTHORS Saeed M, Ibanez-Costa A, Patino-Trives AM, Munoz-Barrera L,
Collantes Estevez E, Aguirre MA and Lopez-Pedrerera C.
TITLE Expression of DDX11 and DNMT1L at the 12p11 Locus Modulates Systemic
Lupus Erythematosus Susceptibility
JOURNAL Int J Mol Sci 22 (14), 7624 (2021)
PUBMED [34299244](#)
REMARK GeneRIF: Expression of DDX11 and DNMT1L at the 12p11 Locus Modulates
Systemic Lupus Erythematosus Susceptibility.

Export:
File
Fasta



<https://www.ncbi.nlm.nih.gov/protein/100913202>

Copie as sequências CDS no conversor do EMBOSS

<https://www.ebi.ac.uk/>

<https://www.embl.org/>

EMBL

The European
Molecular
Biology
Laboratory

EMBOSS Transeq

Input form

Web services

Help & Documentation

Bioinformatics Tools FAQ

Feedback

Tools > Sequence Translation > EMBOSS Transeq

Service Announcement

The new Job Dispatcher Services beta website is now available at <https://www.dev.ebi.ac.uk/Tools/jdispatcher>. We'd love to hear your [feedback](#) about the new webpages!

EMBOSS Transeq

EMBOSS Transeq translates nucleic acid sequences to their corresponding peptide sequences. It can translate to the three forward and three reverse frames, and output multiple frame translations at once.

STEP 1 - Enter your input sequence

Enter or paste a DNA/RNA sequence in any supported [format](#):

ATGGCTAATGAAACACAGAAGGTTGGTGCCATCCATTTTCCTTTCCCTTCACACCCTATTCCATCCAGG
AAGACTTCATGGCAGAGCTGTACCGGTTTTGGAGGCTGGCAAGATTGGGATATTTGAGAGTCCAAGTGG
CACTGGGAAGTCCTTAAGTCTTATTTGTGGGGCCCTCTCTTGGCTCCGTGACTTTGAACAGAAGAAGCGT
GAAGAAGAGGGCACGACTCCTTGAAACTGGAAGTGGCCCCCTACATGATGAGAAAAGATGAATCCCTGTGTC
TGTCTTCTTCTCGAAGGGGCTGCAGGCACCCGAGGCCTGCTGGAGAACC GGCTGGGTACTCAGTT
TGTGCAGAAGAAAGAAGAGAGGGGACCTGGTGGACCGACTAAAGGCGGAGCAGGCCAGGAGGAAGCAGCGA
GAAGAACGCCTGCAGCAGCTGCAGCACAGGGTGACAGCTCAAGTATGCAGCCAAGCGCCTGAGGCAGGAAG
AAGAGAAACAGACAAATCTCTCTGGGCTGAGGAGGAGATGCTAGACAGAGCGGGGAGCGCTGAGCGGCT

Or, upload a file: No file chosen

[Use an example sequence](#) | [Clear sequence](#) | [See more example input](#)

STEP 2 - Select Parameters

FRAME

1

CODON TABLE

Standard Code

Copie o CDS
aqui

https://www.ebi.ac.uk/Tools/st/emboss_transeq/

Resultado do conversor do EMBOSS

<https://www.ebi.ac.uk/Tools/emboss/>

EMBL

The European
Molecular
Biology
Open Source
Software

Results for job emboss_transeq-l20230518-184221-0857-82638710-p2m

Tool Output

Submission Details

Download

Show Colors

```
>EMBOSS_001_1
MANETQKVGAIHFPPFTPYSIQEDFMAELYRVLEAGKIGIFESPTGTGKSLSLICGALS
WLRDFEQKKREEEARLLETGTGPLHDEKDESLCLSSSCEGAAGTPRPAGEPAWVTQFVQK
KEERDLVDRLKAEQARRKQREERLQQLQHRVQLKYAAKRLRQEEEEERENLLRLSREMLET
GPEAERLEQLESGEEELVLAYESDEEKKVASRVDEDEDDLEEEHITKIYYCSRTHSQA
QFVHEVKKSPFGKDVRLVSLGSRQNL CVNEDVKSLSVQLINDRCVDMQRSRHEKKKGAE
EEKPKRRRQEKQAACPFYNHEQMGLLRDEALAEVKDMEQLLAGKEARACPYYSRLAIP
AAQLVVLPHYQMLLHAATRQAAGIRLQDQVVIIDEAHNLIDTITGMHSVEVSGSQLCQHS
QLLQYVERYGKRLKAKNLMYLKQILYLLEKFVAVLGGNIKQNPNTQSLSQTGTELKTIND
FLFQSQIDNINLFKVQRYCEKSMISRLFGFTERYGAVFSSREQPKLAGFQQFLQSLQPR
TTEALAAPADESQASTLRPASPLMHIQGFALAALTANQDGRVILSRQGSLSQSTLKFLLL
NPAVHFAQVVKECRAVVIAGGTMQPVSDFRQQLACAGVEAERVVEFSCGHVIPPDNILP
LVICSGISNQPLEFTFQKRELQMMDEVGRILCNLCGVVPGGVVCFFPSYEYLRQVHAHW
EKGGLLGRLAARKKIFQEPKSAHQVEQVLLAYSRCIQACGQERGQVTGALLSVVGGKMS
EGINFSDNLGRCVVMVGMPFPNIRSAELQEKMAYLDQTLPRAPGQAPPKALVENLCMKA
VNQSIGRAIRHQKDFASVLLDQRYARPPVLAKLPWIRARVEVKATFGPAIAAVQKFHR
EKSASS*
```

exercício

Exercício fazer um BLAST de amino ácidos

Pegue os 30 primeiros aa de DDX11 e faça um BLAST



<https://blast.ncbi.nlm.nih.gov/Blast.cgi>

Mas, na verdade eu gosto do Seaview



PRABI-Doua
Pôle Rhône-Alpes de Bioinformatique Site Doua

Download

<https://doua.prabi.fr/software/seaview>

Presentation

Online Services

Databases

Software and packages

Miscellaneous

Legacy

Partners



Use Linux,
por favor

SeaView - Multiplatform GUI for molecular phylogeny

Version 5.0.5

NEW: seaview performs reconciliation between gene and species trees using **Treerecs** version 1.2
NEW: bootstrap support optionally with the "Transfer Bootstrap Expectation" method
NEW: trimming-rule to shorten long sequence names in phylogenetic trees
NEW: 64-bit version for the MS Windows platform
NEW: multiple-tree windows
NEW: seaview uses **PHYMLIP v3.696** to compute parsimony trees
NEW: seaview can be run without GUI using a command line
NEW: seaview drives the **PhyML v3.1** program to compute maximum likelihood phylogenetic trees.
NEW: seaview drives the **Gblocks** program to select blocks of conserved sites.

SeaView is a multiplatform, graphical user interface for multiple sequence alignment and molecular phylogeny.

- SeaView reads and writes various file formats ([NEXUS](#), MSF, CLUSTAL, FASTA, PHYLIP, [MASE](#), Newick) of DNA and protein sequences and of phylogenetic trees.
- SeaView drives programs [muscle](#) or [Clustal Omega](#) for multiple sequence alignment, and also allows to use any external alignment algorithm able to read and write FASTA-formatted files.
- SeaView drives the [Gblocks](#) program to select blocks of evolutionarily conserved sites.
- SeaView computes phylogenetic trees by
 - parsimony, using PHYLIP's [dnapars/protpars](#) algorithm,
 - distance, with [NJ](#) or [BioNJ](#) algorithms on a variety of evolutionary distances,
 - maximum likelihood, driving program [PhyML](#) 3.1.
- SeaView can use the [Transfer Bootstrap Expectation](#) method to compute the bootstrap support of PhyML and distance trees.
- SeaView uses the [Treerecs](#) method to reconcile gene and species trees.
- SeaView prints and draws phylogenetic trees on screen, SVG, PDF or PostScript files.
- SeaView allows to download sequences from EMBL/GenBank/UniProt using the Internet.

Screen shots of the main [alignment](#) and [tree](#) windows. Dialog window to perform [Maximum-Likelihood](#) tree-building.
On-line [help](#) document.Old [seaview version 3.2](#)

Download SeaView



macOS X
ready for macOS 10.3 - 13.0



32-bit Linux on x86
[64-bit Linux on x86_64](#)



MS Windows 100% CLEAN
self-extractable archive



Solaris on SPARC

Bioinformática

Curso de Especialização na Área da Saúde – 2025/2026
Bases Técnicas em Vacinas e Biofármacos

PhD Flavio Lichtenstein

Bioinformatics, Systems Biology, and Biostatistics

dúvidas: flavio.lichtenstein@butantan.gov.br

abril/2025 e maio/2023