4. BASI DI BIOINFORMATICA PER LO STUDIO DELLA REGOLAZIONE GENICA

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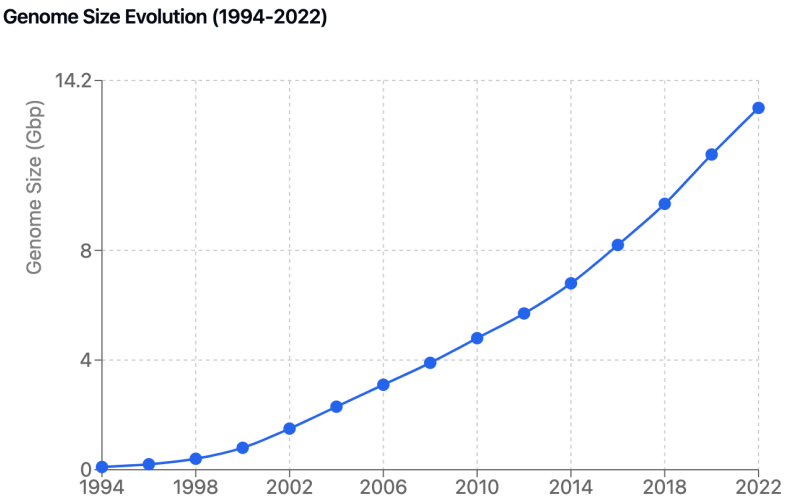
La sfida dei genome browsers

aumentare sempre di più le informazioni disponibili sulle sequenze



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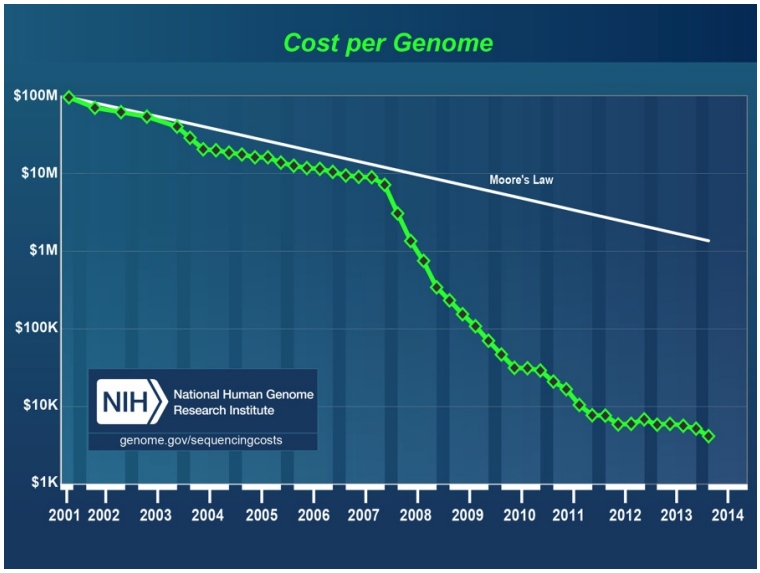

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Genome Browsers Oggi

- Ensembl Genome browser
  http://www.ensembl.org
- NCBI Map Viewer
  http://www.ncbi.nlm.nih.gov/mapview/
- UCSC Genome Browser
  http://genome.ucsc.edu

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Differenze tra Ensembl, UCSC ed NCBI?

	UCSC	Ensembl	NCBI
Presentation	Genome in horizontal orientation Main page contains a single graphic displaying annotation ('tracks') Clicking on annotation element presents web page of detailed information and links to other resources	Genome in horizontal orientation Main ContigView page contains three graphics displaying annotations at different resolutions Clicking on annotation element presents box with links to other resources or Views with more detailed information	Genome in vertical orientation Annotations graphically presented in columns ('maps') Clicking on annotation elements or links in columns provides quick access to other, primarily NCBI, resources
Content	13 vertebrate, 15 invertebrate Many cross-species annotations including conservation across eight species ENCODE Project annotations	13 vertebrate, six invertebrate Heavy focus on gene annotations such as Ensembl genes and VEGA HapMap project-related Views	11 vertebrate, five invertebrate, one protozoan, 12 plant, eight fungi Annotations primarily from NCBI resources
Functionality	Text search, BLAT sequence search, isPCR primer search Advanced annotation extraction using Table Browser Ability to upload and view own	Text search, BLAST and SSAHA sequence search, e-PCR primer search Advanced annotation extraction using BioMart Ability to upload and view own annotations	Text search, BLAST sequence search, e-PCR primer search Basic annotation extraction

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Genome Reference Consortium

- Wellcome Sanger Institute
- The McDonnell Genome Institute at Washington University
- The European Bioinformatics Institute
- The National Center for Biotechnology Information
- The Zebrafish Model Organism Database
- Rat Genome Database

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Human genome assemblies

- GRCh38 (aka hg38)
  - No gaps
  - www.ensembl.org
  - Most up-to-date and supported
- GRCh37 (aka hg19)
  - 250 gaps
  - grch37.ensembl.org
  - Limited data and software updates
- NCBI36 (aka hg18)
  - 150,000 gaps
  - ncbi36.ensembl.org
  - No longer updated

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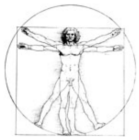

Human

The human genome assembly was produced as part of the Human Genome Project (HGP). The previous assembly (NCBI36) was the last one produced by the HGP and was described in 2004 (PMID: 15496913); this was the starting point for the GRC. The assembly is based largely on assembling overlapping clone sequences.

Human assembly information

Current major assembly	GRCh38
Regions with alternate loci	178
Assembly N50	67,794,873 bp
Remaining gaps	875
Patch release version	p14
Patches released	FIX: 164, NOVEL: 90

Mouse

The GRC has produced an updated assembly (GRCm38). This is an update of the last MGSC assembly (MGSCv37) which was described in 2009 (PMID: 19468303). The primary assembly is based on assembling overlapping BAC clones derived from the C57BL/6J strain and several loci have sequence available from other strains.

Mouse assembly information

Current major assembly	GRCm39
Regions with alternate loci	0
Assembly N50	106,145,001 bp
Remaining gaps	347
Patch release version	None

Zebrafish

The zebrafish genome assembly was produced at the Wellcome Sanger Institute. The last assembly produced from the original project was Zv9 and was described in 2013 (PMID: 23594743). This assembly is the starting point for the GRC. The assembly is based on assembling overlapping BAC clones and integrating these sequences with the whole genome shotgun assembly.

Zebrafish assembly information

Current major assembly	GRCz11
Regions with alternate loci	607
Assembly N50	7,379,053 bp
Remaining gaps	18,736

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Telomere-to-Telomere (T2T) Consortium

T2T-CHM13

STATISTICS	GRCH38	T2T-CHM13	DIFFERENCE (±%)
Summary			
Assembled bases (Gbp)	2.92	3.05	+4.5
Unplaced bases (Mbp)	11.42	0	−100.0
Gap bases (Mbp)	120.31	0	−100.0
Number of contigs	949	24	−97.5
Contig NG50 (Mbp)	56.41	154.26	+173.5
Number of issues	230	46	−80.0
Issues (Mbp)	230.43	8.18	−96.5
Gene annotation			
Number of genes	60,090	63,494	+5.7
Protein coding	19,890	19,969	+0.4
Number of exclusive genes	263	3,604	
Protein coding	63	140	
Number of transcripts	228,597	233,615	+2.2
Protein coding	84,277	86,245	+2.3
Number of exclusive transcripts	1,708	6,693	
Protein coding	829	2,780	
Segmental duplications			
Percentage of segmental duplications (%)	5.00	6.61	
Segmental duplication bases (Mbp)	151.71	201.93	+33.1
Number of segmental duplications	24097	41528	+72.3
RepeatMasker			
Percentage of repeats (%)	51.89	53.94	
Repeat bases (Mbp)	1,516.37	1,647.81	+8.7
Long interspersed nuclear elements	626.33	631.64	+0.8
Short interspersed nuclear elements	386.48	390.27	+1.0
Long terminal repeats	267.52	269.91	+0.9
Satellite	76.51	150.42	+96.6
DNA	108.53	109.35	+0.8
Simple repeat	36.5	77.69	+112.9
Low complexity	6.16	6.44	+4.6
Retroposon	4.51	4.65	+3.3
rRNA	0.21	1.71	+730.4

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Cosa impariamo da queste annotazioni?

- **All'interno di un genoma: elementi regolatori, ordine dei geni, struttura della cromatina…….**
- **Facendo studi comparativi: evoluzione, regioni conservate, riarrangiamenti…predizione di geni.**

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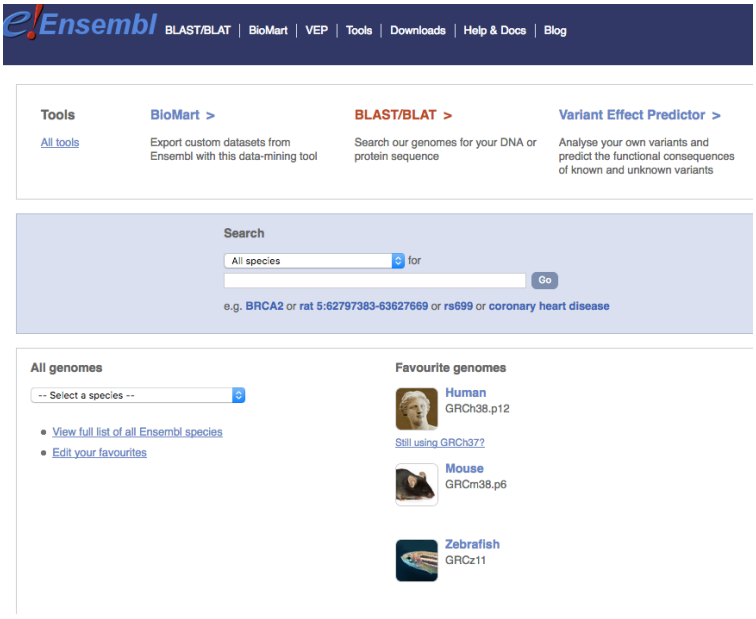
Studiare i genomi con Ensembl



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Nomenclatura in Ensembl

- **ENSG###** — **Ensembl Gene ID**
- **ENST###** — **Ensembl Transcript ID**
- **ENSP###** — **Ensembl Peptide ID**
- **ENSE###** — **Ensembl Exon ID**

- **Per specie diverse dall'uomo è aggiunto un suffisso**

MUS (*Mus musculus*) for mouse: ENSMUSG###
DAR (*Danio rerio*) for zebrafish: ENSDARG###, etc.

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Quali annotazioni sono disponibili?

- Gene/transcript/peptide models (coding and noncoding (ncRNAs))
- IDs in other database
- Mapped cDNAs, peptides, micro array probes, BAC clones etc.
- Cytogenetic bands, markers, repeats etc.
- Comparative data:
  orthologues and paralogues, protein families, whole genome alignments, syntenic regions
- Variation data:
  Single Nucleotide Polymorphisms (SNPs)
- Regulatory data:
  "best guess" set of regulatory elements from ENCODE
- Data from external sources (DAS)

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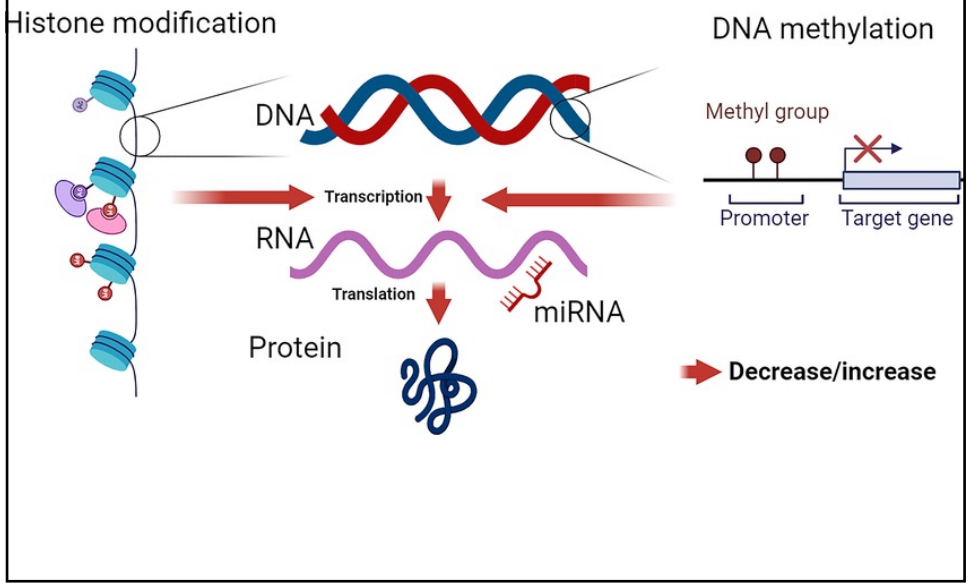

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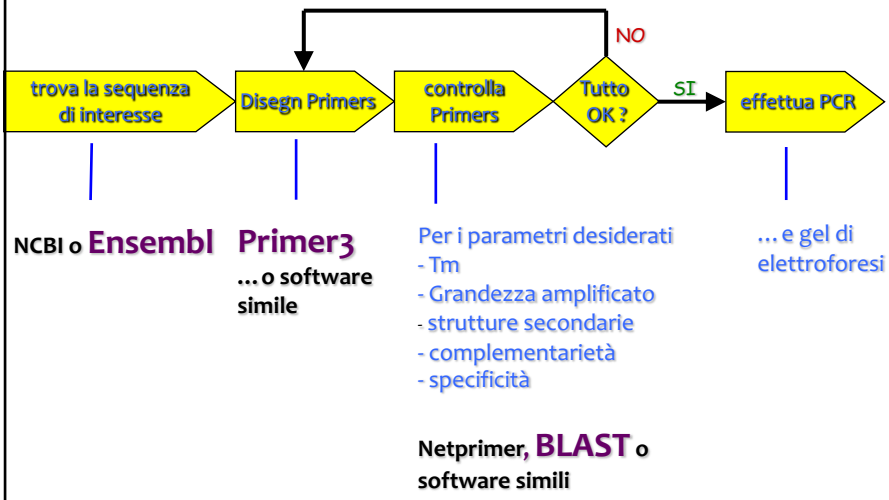
Primer design-come procedere



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disegno dei primers

Un buon disegno dei primers è la chiave di una PCR di successo !!

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Proprietà importanti di una buona coppia di primers

Ogni primers dovrà avere

- lunghezza basi compresa tra 18-24
- 40-60% G/C
- Distribuzione bilanciata di basi G/C e A/T
- T_m che permette un annealing tra 55-65° C
- NO strutture secondarie interne (hair-pins)

Le coppie di primers inoltre dovrebbero avere:

- T_m *simile* (*max* 2-3 ° C di differenza)
- **NO** complementarietà (> 2-3 bp) in particolare al 3'

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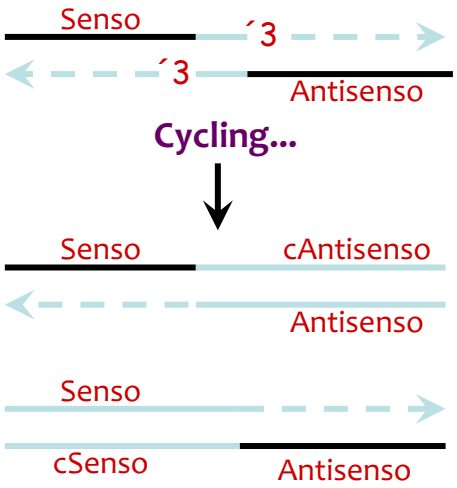
Il problema dei dimeri di primers

- Primers che interagiscono tra di loro sono AMPLIFICATI dalla PCR
- La formazione dei dimeri di primers compete con la PCR e può quindi compromettere l'efficienza della reazione.



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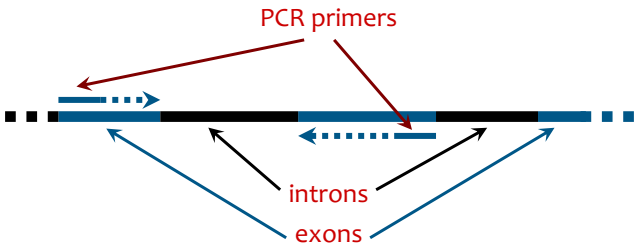
Considerazioni importanti

- Evitare di avere come bersaglio della qPCR delle **strutture secondarie**
- Evitare contaminazione genomica disegnando primers che **includono esoni diversi** e tagliano introni



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Links per disegno primers

- http://www.tataa.com/
- **http://www.ncbi.nlm.nih.gov/BLAST/**
- **www.premierbiosoft.com/netprimer/netprlaunch/netprlaunch.html**
- ***www.ensembl.org***
- **http://www-genome.wi.mit.edu/cgi-bin/primer/primer3_www.cgi**
- **http://www.bioinfo.rpi.edu/applications/mfold/dna/form1.cgi**
- http://primer3.ut.ee/ Primer3

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BLAST

Basic Local Alignment Search Tool

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BLAST Programs

Program	Database (Subject)	Query
BLASTN	Nucleotide	Nucleotide
BLASTP	Protein	Protein
BLASTX	Protein	Nt. → Protein
TBLASTN	Nt. → Protein	Protein
TBLASTX	Nt. → Protein	Nt. → Protein

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BLAST confronta le sequenze

- **usa** una sequenza ***"query"***
- **La confronta con** milioni di sequenze nei database ***GenBank*** ® costruendo local alignments
- **elenca** quelle che sembrano simili alla query
- **dice perchè sono eventualmente omologhe**

NB
– ***BLAST suggerisce***
– ***Il ricercatore trae le sue conclusioni***

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BLAST output

descrive in che modo le sequenze allineate sono simili

- *Quanto sono lunghi i segmenti allineati?*
- *BLAST ha dovuto introdurre degli spazi per allineare i segmenti?*
- *Quanto sono simili i segmenti allineati?*

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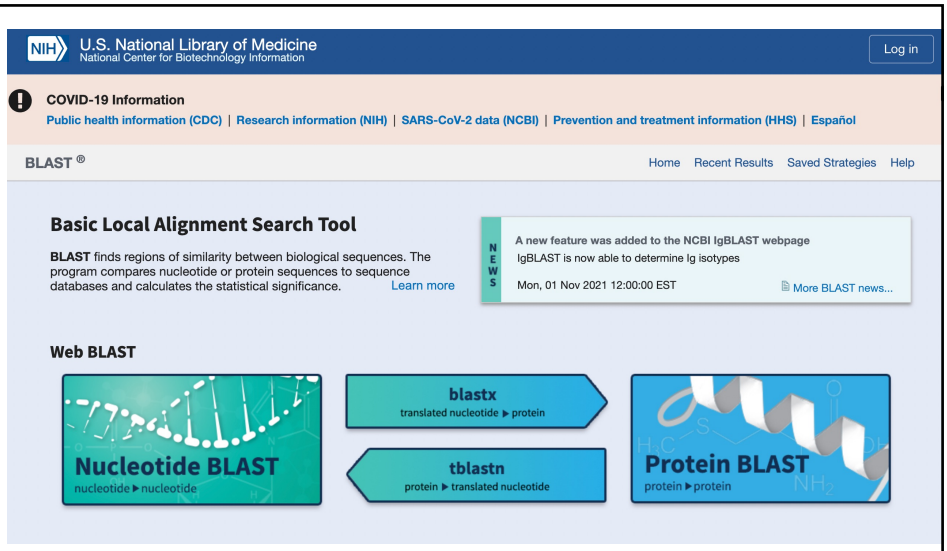
24



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

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Graphic Display

1. How good is the match?

- **Red = excellent!**
- Pink = pretty good
- **Green = OK, but look at other factors**
- **Blue = bad**
- **Black = really bad!**

2. How long are the matched segments?

Longer = better

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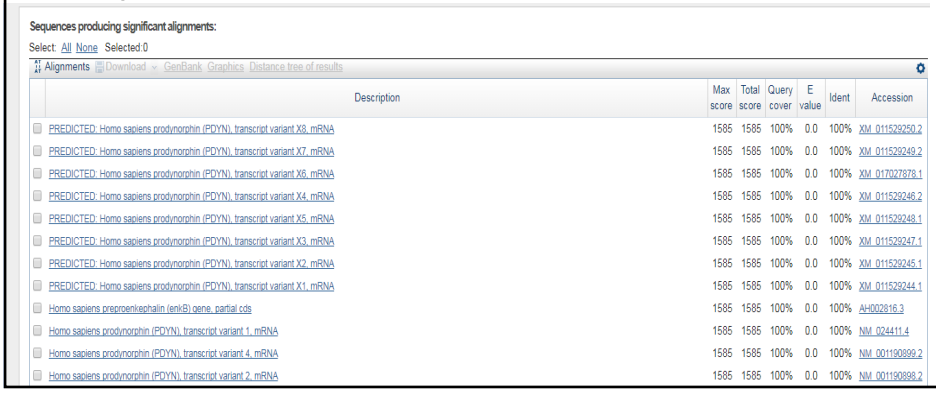
BLAST fa una lista dei migliori accoppiamenti (hits)

Per ogni accoppiamento fornisce:

- **Max Score: the highest alignment score calculated from the sum of matched nucleotides and penalities for mismatches and gaps.**
- **Tot Score: the sum of alignment scores of all segments**
- **Query Cover: the % of the query length included in the aligned segments.**
- **E[xpect] Value: the number of alignments expected by chance with the calculated score or better. for significant alignments the E value should be very close to zero.**
- **Ident[ity]: the highest % identity for a set of aligned segments to the same subject sequence.**



Sequences producing significant alignments:

Select: All None Selected:0

Alignments Download GenBank Graphics Distance tree of results

Description	Max score	Total score	Query cover	E value	Ident	Accession
PREDICTED: Homo sapiens prodynorphin (PDYN), transcript variant X8, mRNA	1585	1585	100%	0.0	100%	XM_011529250.2
PREDICTED: Homo sapiens prodynorphin (PDYN), transcript variant X7, mRNA	1585	1585	100%	0.0	100%	XM_011529249.2
PREDICTED: Homo sapiens prodynorphin (PDYN), transcript variant X6, mRNA	1585	1585	100%	0.0	100%	XM_017027878.1
PREDICTED: Homo sapiens prodynorphin (PDYN), transcript variant X4, mRNA	1585	1585	100%	0.0	100%	XM_011529246.2
PREDICTED: Homo sapiens prodynorphin (PDYN), transcript variant X5, mRNA	1585	1585	100%	0.0	100%	XM_011529248.1
PREDICTED: Homo sapiens prodynorphin (PDYN), transcript variant X3, mRNA	1585	1585	100%	0.0	100%	XM_011529247.1
PREDICTED: Homo sapiens prodynorphin (PDYN), transcript variant X2, mRNA	1585	1585	100%	0.0	100%	XM_011529245.1
PREDICTED: Homo sapiens prodynorphin (PDYN), transcript variant X1, mRNA	1585	1585	100%	0.0	100%	XM_011529244.1
Homo sapiens preproenkephalin (enkB) gene, partial cds	1585	1585	100%	0.0	100%	AH002816.3
Homo sapiens prodynorphin (PDYN), transcript variant 1, mRNA	1585	1585	100%	0.0	100%	NM_024411.4
Homo sapiens prodynorphin (PDYN), transcript variant 4, mRNA	1585	1585	100%	0.0	100%	NM_001190899.2
Homo sapiens prodynorphin (PDYN), transcript variant 2, mRNA	1585	1585	100%	0.0	100%	NM_001190898.2

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Che cos'è l'E-value?

- **E-value**

  La probabilità che quel determinato accoppiamento non è casuale

  + basso è l'E-value, + significativo è l'accoppiamento

  - **E = 10^{-4}** è considerato il **cutoff point**
  - **E = 0** significa che le due sequenze sono statisticamente **identiche**

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Software to predict CpG islands?

MethPrimer is an online platform which provides a number of tools and databases to facilitate the study of DNA methylation and epigenetics, including tools for designing prim

http://www.urogene.org/cgi-bin/methprimer/methprimer.cgi

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Software to predict miRNA binding ??

http://mirdb.org/index.html

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growing evidence suggest the importance of ***both environmental and genetic factors*** *in the* ***influence of DNA methylation****.*

DNA methylation can be influenced by *cis*-acting DNA sequence variation located on the same chromosome.

- *Mill et al., Am J Hum Genet 2008*
- *Zhang et al., Am J Hum Genet 2010*
- *Milani et al., Genome Res 2009*
- *Docherty et al., Behav and Brain Func 2012*
- *Ball et al., Genome Biol. 2011*

new models have to be developed to integrate genetic variants and DNA methylation*.*

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miR*dSNP*

a database of disease-associated SNPs and microRNA target sites on 3'UTRs of human genes

http://mirdsnp.ccr.buffalo.edu/

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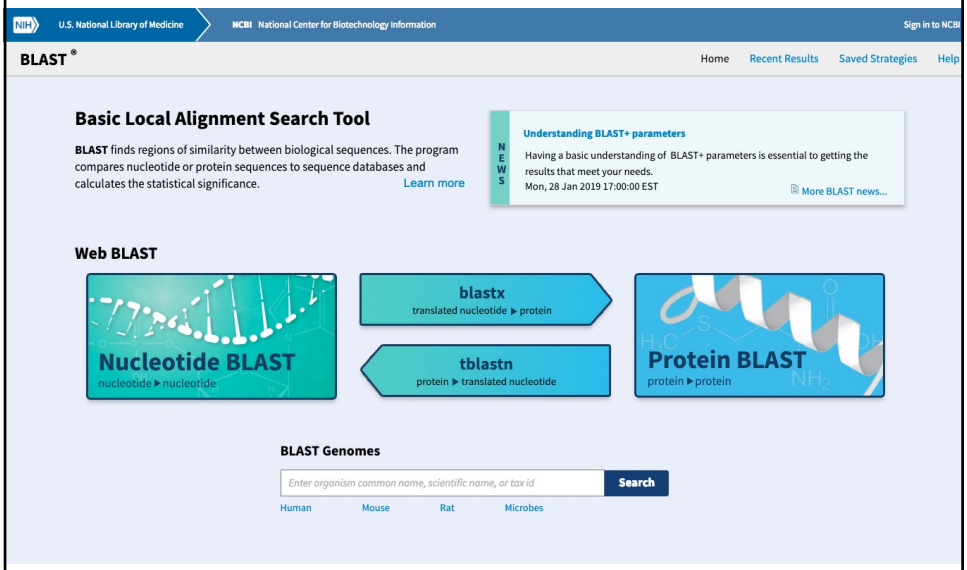
https://blast.ncbi.nlm.nih.gov/Blast.cgi



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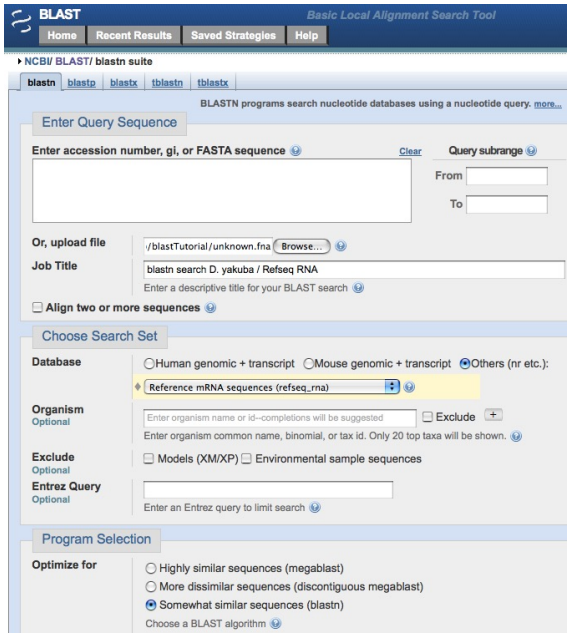

STEP 1

Setting up our blastn search of our unknown sequence against the NCBI Refseq RNA database

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When the NCBI web server is busy, the search may take 5 minutes or more

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BLAST report

Sequences producing significant alignments:		Score (bits)	E value	Source DB	NCBI Entrez	Cath Prot/Chain
pdbsa|1LBG_A	TRANSCRIPTION/DNA Lactose Operon Repressor Bo...	688	0	SDB	NCBI	CATH Prot
pdbsa|1LBH_A	TRANSCRIPTION REGULATION Intact Lactose Opero...	688	0	SDB	NCBI	CATH Prot
pdbsa|1JYF_A	TRANSCRIPTION Structure Of The Dimeric Lac Re...	669	0	SDB	NCBI	CATH Prot
pdbsa|1JYE_A	TRANSCRIPTION Structure Of A Dimeric Lac Repr...	666	0	SDB	NCBI	CATH Prot
pdbsa|1JWL_A	TRANSCRIPTION/DNA Structure Of The Dimeric La...	640	0	SDB	NCBI	CATH Prot
pdbsa|1EFA_A	TRANSCRIPTION/DNA Crystal Structure Of The La...	640	0	SDB	NCBI	CATH Prot
pdbsa|1EFA_C	TRANSCRIPTION/DNA Crystal Structure Of The La...	640	0	SDB	NCBI	CATH Prot
pdbsa|1JWL_C	TRANSCRIPTION/DNA Structure Of The Dimeric La...	640	0	SDB	NCBI	CATH Prot
pdbsa|1EFA_B	TRANSCRIPTION/DNA Crystal Structure Of The La...	640	0	SDB	NCBI	CATH Prot
pdbsa|1TLF_A	TRANSCRIPTION REGULATION Unprecedented Quater...	575	1e-164	SDB	NCBI	CATH Prot

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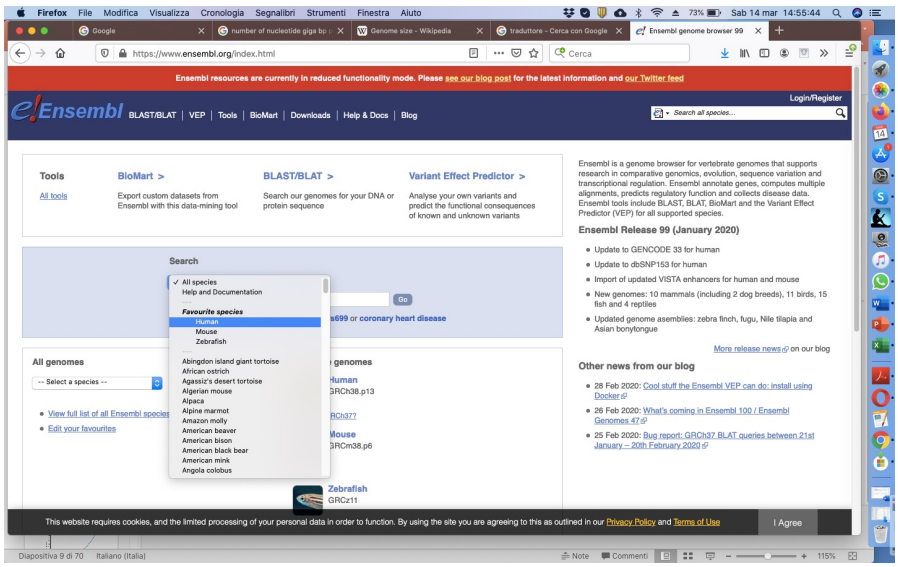
Ensembl resources are currently in reduced functionality mode. Please see our blog post for the latest information and our Twitter feed
Ensembl
BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog
Login/Register
Tools
BioMart >
BLAST/BLAT >
Variant Effect Predictor >
Ensembl Release 99 (January 2020)
Other news from our blog
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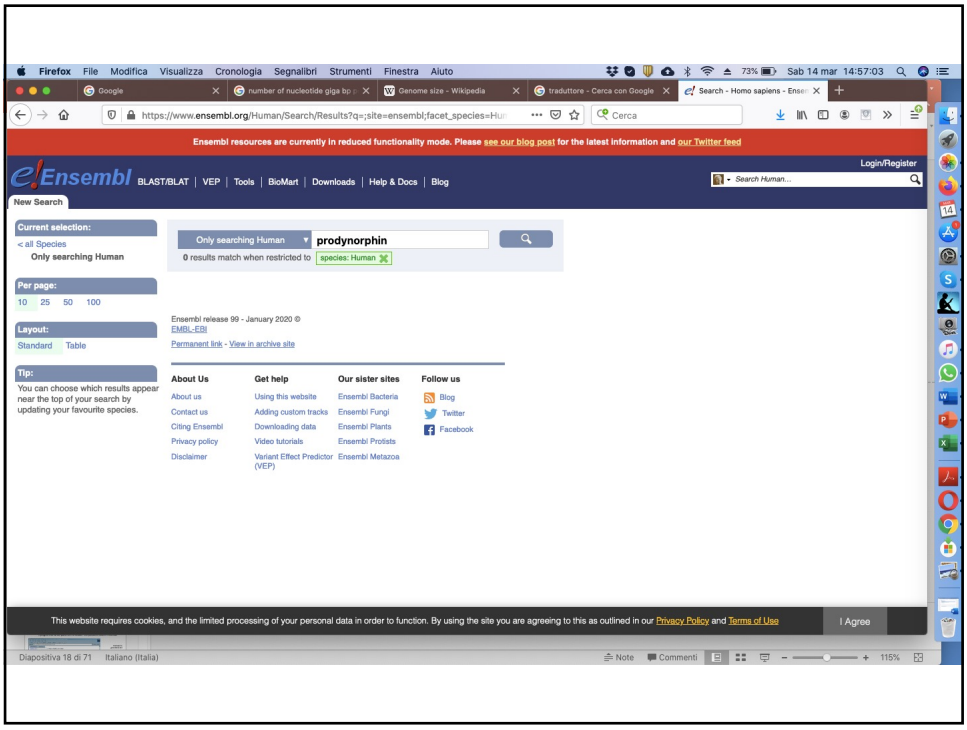
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Ensembl
BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog
Login/Register
New Search
Current selection:
Only searching Human
prodynorphin
0 results match when restricted to species: Human
Per page:
Layout:
Tip:
You can choose which results appear near the top of your search by updating your favourite species.
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I Agree

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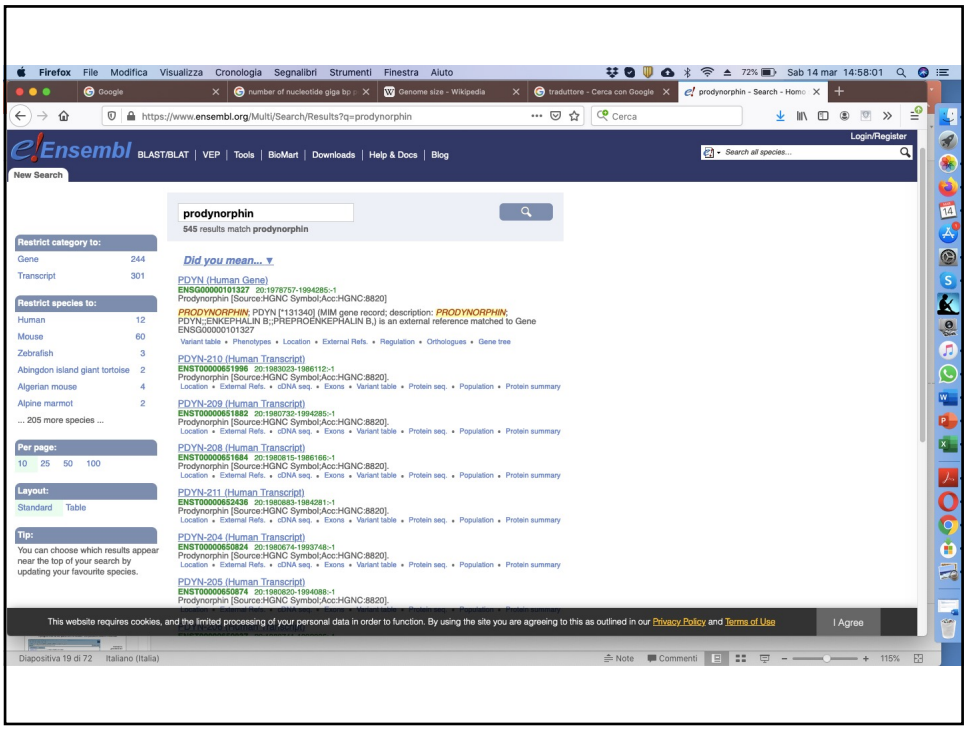
https://www.ensembl.org/Multi/Search/Results?q=prodynorphin
prodynorphin
545 results match prodynorphin
PDYN (Human Gene)
PDYN-210 (Human Transcript)
PDYN-209 (Human Transcript)
PDYN-208 (Human Transcript)
PDYN-211 (Human Transcript)
PDYN-204 (Human Transcript)
PDYN-205 (Human Transcript)

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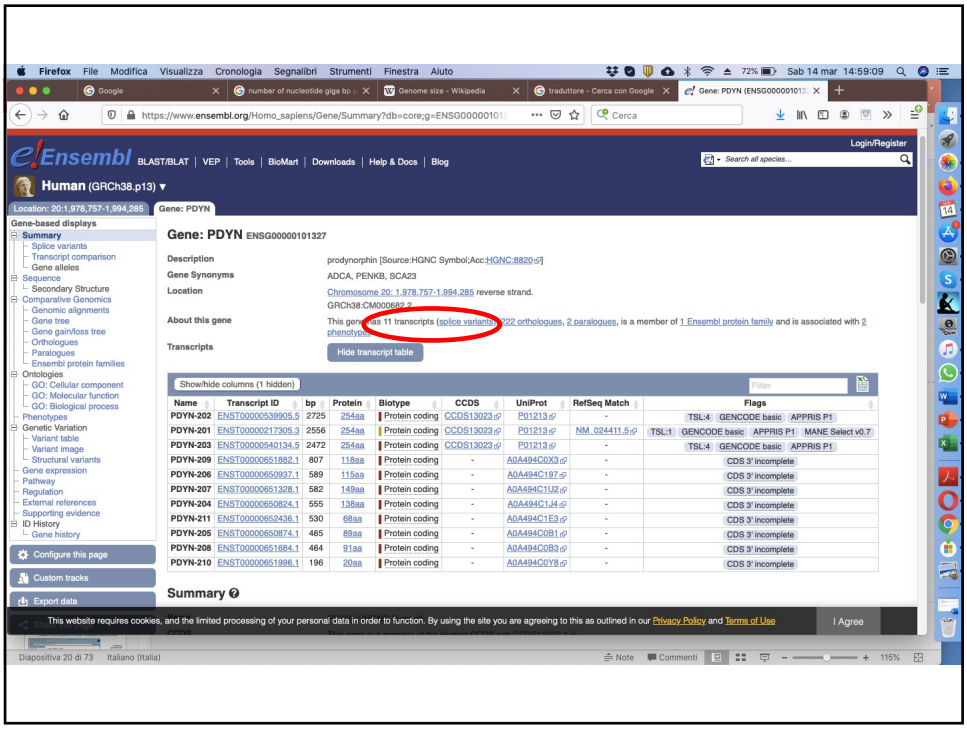
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Gene: PDYN ENSG00000101327
Description
Gene Synonyms
Location
About this gene
Transcripts
Hide transcript table
Summary

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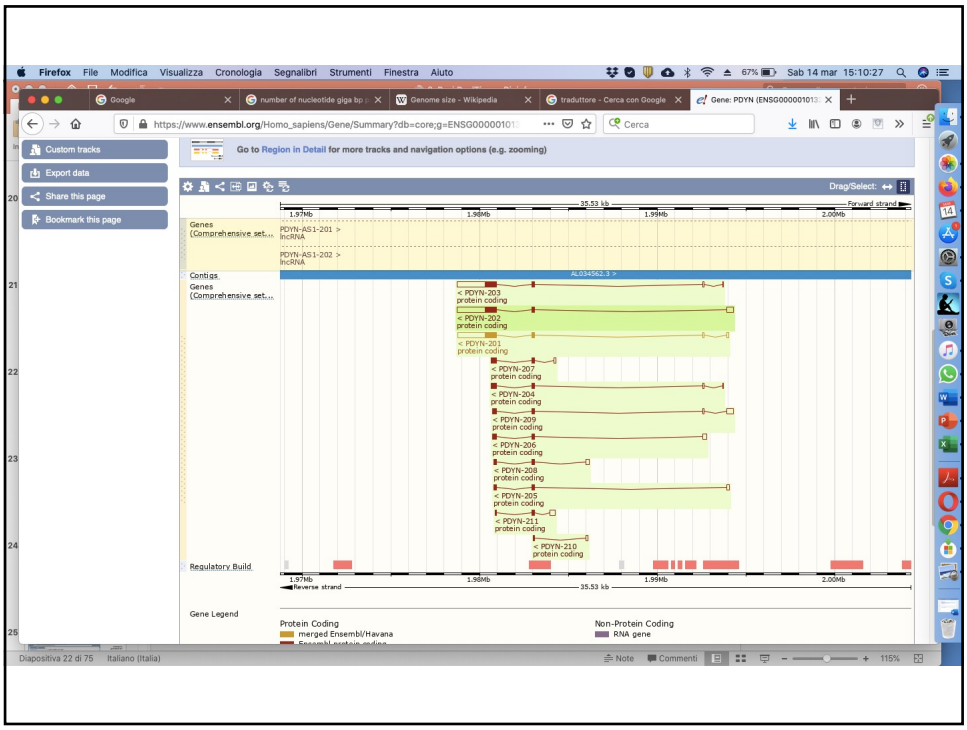
Custom tracks
Export data
Share this page
Bookmark this page
Go to Region in Detail for more tracks and navigation options (e.g. zooming)
Genes (Comprehensive set...
PDYN-AS1-201 > lncRNA
PDYN-AS1-202 > lncRNA
Contigs
Genes (Comprehensive set...
< PDYN-203 protein coding
< PDYN-202 protein coding
< PDYN-201 protein coding
< PDYN-207 protein coding
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< PDYN-209 protein coding
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< PDYN-205 protein coding
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Regulatory Build
Gene Legend
Protein Coding
merged Ensembl/Havana
Non-Protein Coding
RNA gene

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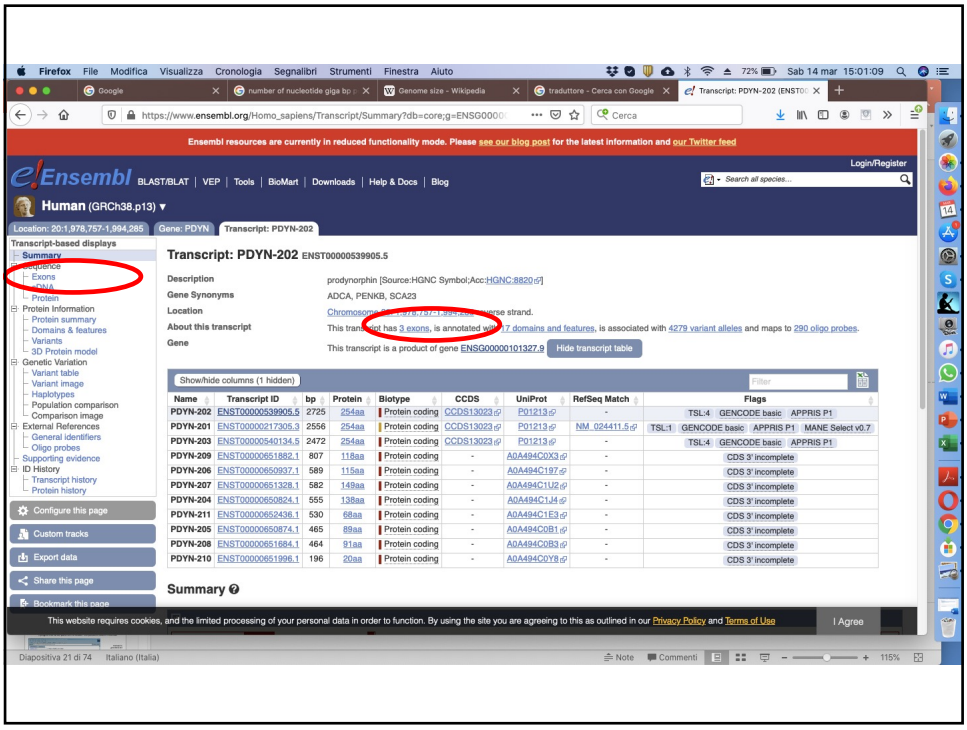
Ensembl resources are currently in reduced functionality mode. Please see our blog post for the latest information and our Twitter feed
Ensembl BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog
Human (GRCh38.p13)
Location: 20:1,978,757-1,994,285
Gene: PDYN
Transcript: PDYN-202
Transcript-based displays
Summary
Sequence
Exons
cDNA
Protein
Protein Information
Protein summary
Domains & features
Variants
3D Protein model
Genetic Variation
Variant table
Variant image
Haplotypes
Population comparison
Comparison image
External References
General identifiers
Oligo probes
Supporting evidence
ID History
Transcript history
Protein history
Configure this page
Custom tracks
Export data
Share this page
Transcript: PDYN-202 ENST00000539905.5
Description
prodynorphin [Source:HGNC Symbol;Acc:HGNC:8820]
Gene Synonyms
ADCA, PENKB, SCA23
Location
About this transcript
This transcript has 3 exons, is annotated with 17 domains and features, is associated with 4279 variant alleles and maps to 290 oligo probes.
Gene
This transcript is a product of gene ENSG00000101327.9
Hide transcript table
Show/hide columns (1 hidden)
Name | Transcript ID | bp | Protein | Biotype | CCDS | UniProt | RefSeq Match | Flags
PDYN-202 | ENST00000539905.5 | 2725 | 254aa | Protein coding | CCDS13023 | P01213 | - | TSL:4 GENCODE basic APPRIS P1
PDYN-201 | ENST00000217305.3 | 2556 | 254aa | Protein coding | CCDS13023 | P01213 | NM_024411.5 | TSL:1 GENCODE basic APPRIS P1 MANE Select v0.7
PDYN-203 | ENST00000540134.5 | 2472 | 254aa | Protein coding | CCDS13023 | P01213 | - | TSL:4 GENCODE basic APPRIS P1
PDYN-209 | ENST00000651882.1 | 807 | 118aa | Protein coding | - | A0A494C0X3 | - | CDS 3' incomplete
PDYN-206 | ENST00000650937.1 | 589 | 115aa | Protein coding | - | A0A494C197 | - | CDS 3' incomplete
PDYN-207 | ENST00000651328.1 | 582 | 149aa | Protein coding | - | A0A494C1U2 | - | CDS 3' incomplete
PDYN-204 | ENST00000650824.1 | 555 | 138aa | Protein coding | - | A0A494C1J4 | - | CDS 3' incomplete
PDYN-211 | ENST00000652436.1 | 530 | 68aa | Protein coding | - | A0A494C1E3 | - | CDS 3' incomplete
PDYN-205 | ENST00000650874.1 | 465 | 89aa | Protein coding | - | A0A494C0B1 | - | CDS 3' incomplete
PDYN-208 | ENST00000651684.1 | 464 | 91aa | Protein coding | - | A0A494C0B3 | - | CDS 3' incomplete
PDYN-210 | ENST00000651996.1 | 196 | 20aa | Protein coding | - | A0A494C0Y8 | - | CDS 3' incomplete
Summary
This website requires cookies, and the limited processing of your personal data in order to function. By using the site you are agreeing to this as outlined in our Privacy Policy and Terms of Use
I Agree

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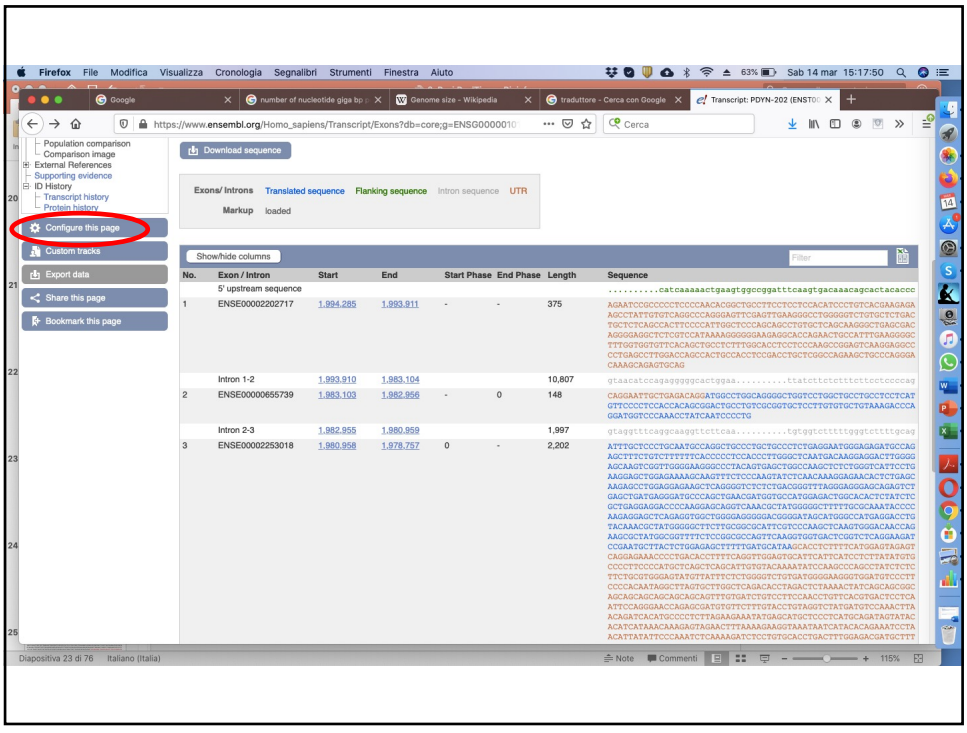
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Custom tracks
Export data
Share this page
Bookmark this page
Download sequence
Exons/ Introns
Translated sequence
Flanking sequence
Intron sequence
UTR
Markup
loaded
Show/hide columns

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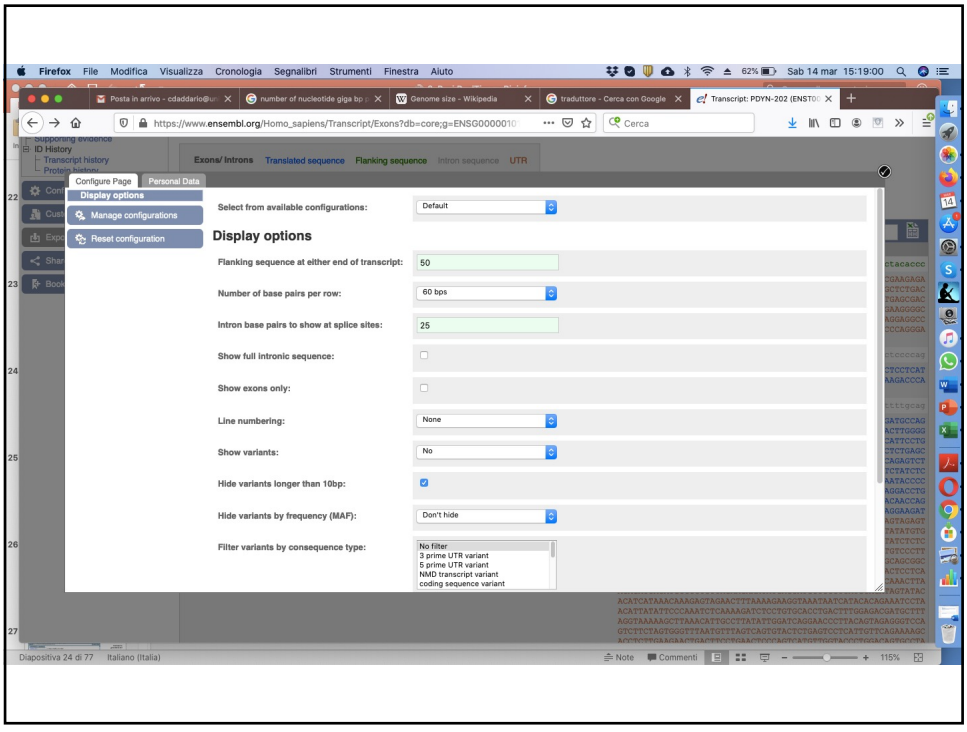
Configure Page
Personal Data
Display options
Manage configurations
Reset configuration
Select from available configurations:
Default
Flanking sequence at either end of transcript:
50
Number of base pairs per row:
60 bps
Intron base pairs to show at splice sites:
25
Show full intronic sequence:
Show exons only:
Line numbering:
None
Show variants:
No
Hide variants longer than 10bp:
Hide variants by frequency (MAF):
Don't hide
Filter variants by consequence type:
No filter
3 prime UTR variant
5 prime UTR variant
NMD transcript variant
coding sequence variant

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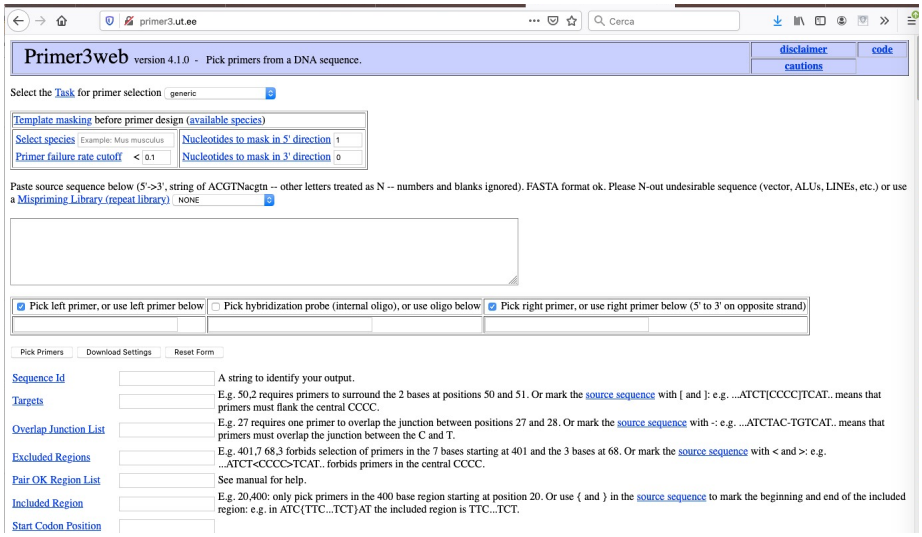
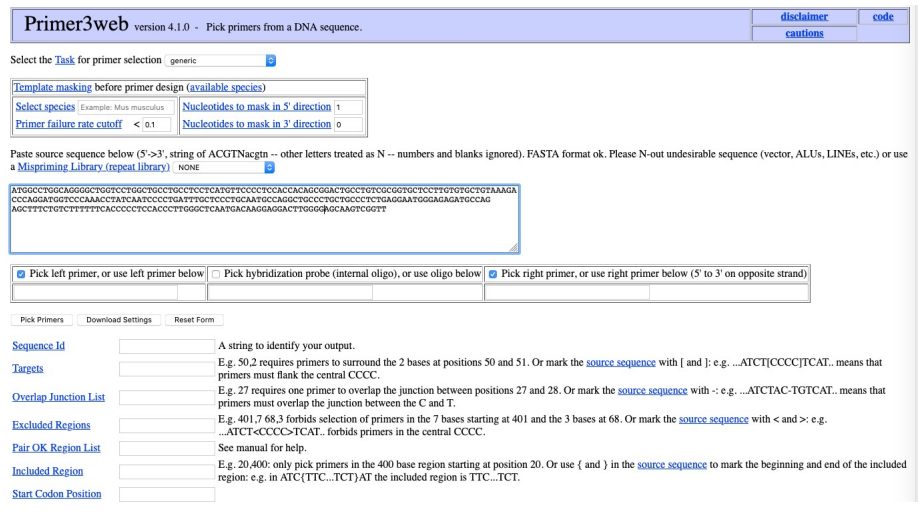
Primer 3
http://primer3.ut.ee/

Step 1 – copia la sequenza di interesse nella finestra



45



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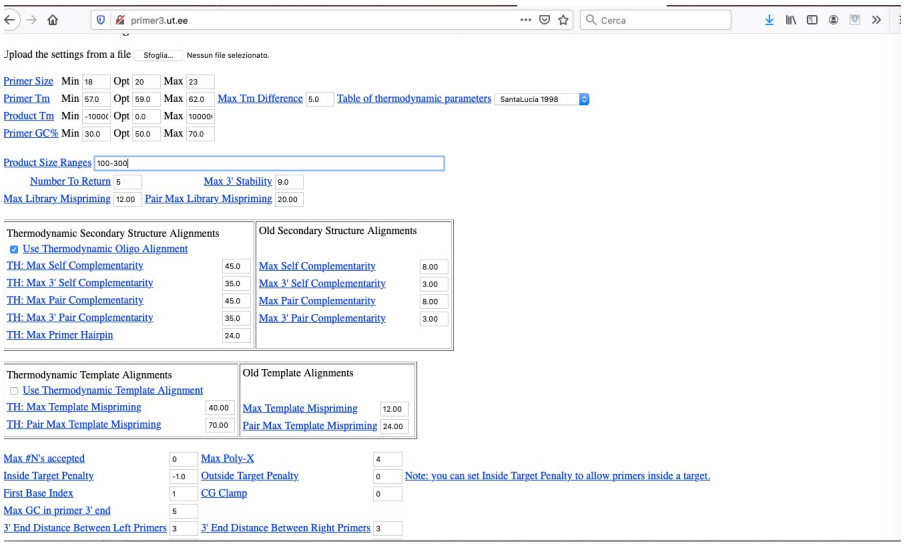
Step 3 – setting parametri
Il programma ha dei parametri di default
che possono essere modificati



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Step 4 –
Scegli i primers

Primer3 Output

```
PRIMER PICKING RESULTS FOR

Template masking not selected
No mispriming library specified
Using 1-based sequence positions
OLIGO              start  len       tm      gc%  any th  3' th  hairpin  seq
LEFT PRIMER           85   20    58.57    50.00    0.00   0.00     0.00 TGTGCTGTAAAGACCCAGGA
RIGHT PRIMER         187   20    58.86    55.00    0.00   0.00     0.00 GGCATCTCTCCCATTCCTCA
SEQUENCE SIZE: 261
INCLUDED REGION SIZE: 261

PRODUCT SIZE: 103, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00

    1 ATGGCCTGGCAGGGGCTGGTCCTGGCTGCCTGCCTCCTCATGTTCCCCTCCACCACAGCG


   61 GACTGCCTGTCGCGGTGCTCCTTGTGTGCTGTAAAGACCCAGGATGGTCCCAAACCTATC
                              >>>>>>>>>>>>>>>>>>>

  121 AATCCCCTGATTTGCTCCCTGCAATGCCAGGCTGCCCTGCTGCCCTCTGAGGAATGGGAG
                                                 <<<<<<<<<<<<

  181 AGATGCCAGAGCTTTCTGTCTTTTTTCACCCCCTCCACCCTTGGGCTCAATGACAAGGAG
      <<<<<<<

  241 GACTTGGGGAGCAAGTCGGTT


KEYS (in order of precedence):
>>>>>>> left primer
<<<<<< right primer

ADDITIONAL OLIGOS
                   start  len       tm      gc%  any th  3' th  hairpin  seq

 1 LEFT PRIMER         34   20    59.46    60.00    0.00   0.00     0.00 CTCCTCATGTTCCCCTCCAC
   RIGHT PRIMER       190   20    58.86    55.00    0.00   0.00     0.00 TCTGGCATCTCTCCCATTCC
   PRODUCT SIZE: 157, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00

 2 LEFT PRIMER        122   20    59.45    55.00    0.00   0.00     0.00 ATCCCCTGATTTGCTCCCTG
   RIGHT PRIMER       242   20    59.38    55.00    0.00   0.00     0.00 TCCTCCTTGTCATTGAGCCC
   PRODUCT SIZE: 121, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00

 3 LEFT PRIMER         37   20    60.04    60.00    0.00   0.00     0.00 CTCATGTTCCCCTCCACCAC
   RIGHT PRIMER       141   19    59.00    57.89    0.00   0.00     0.00 CAGGGAGCAAATCAGGGGA
   PRODUCT SIZE: 105, PAIR ANY_TH COMPL: 0.00, PAIR 3'_TH COMPL: 0.00

 4 LEFT PRIMER         80   21    59.12    52.38    0.00   0.00     0.00 CCTTGTGTGCTGTAAAGACCC
```

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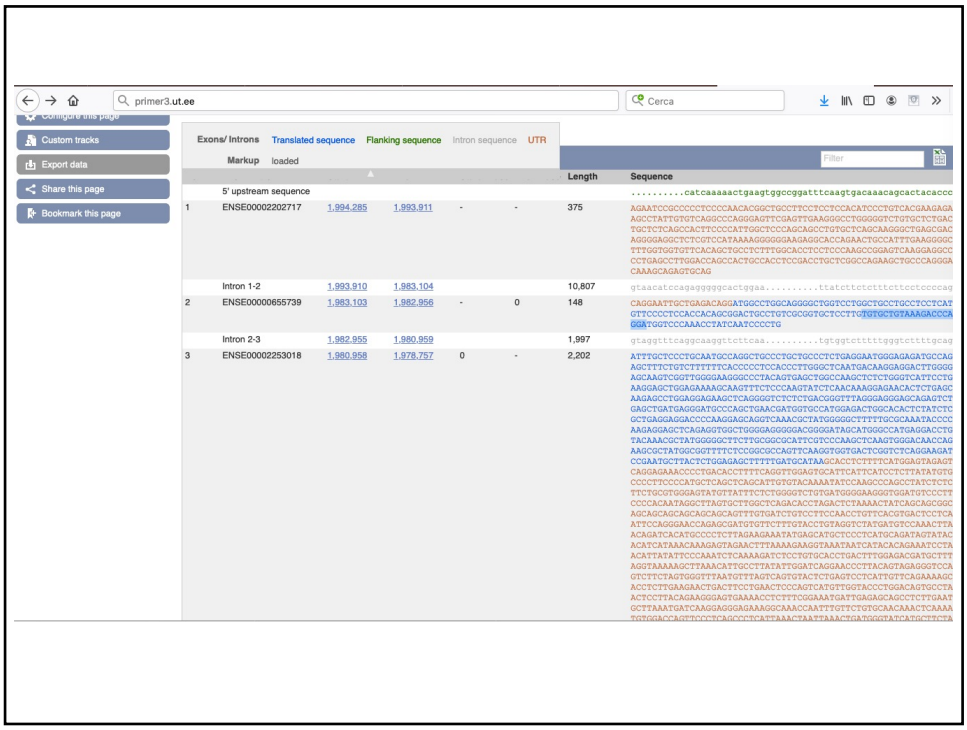
primer3.ut.ee
Cerca
Custom tracks
Export data
Share this page
Bookmark this page
Exons/ Introns
Translated sequence
Flanking sequence
Intron sequence
UTR
Markup
loaded
Filter
Length
Sequence
5' upstream sequence
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375
Intron 1-2
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1,983,104
10,807
2
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1,982,956
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3
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2,202

49