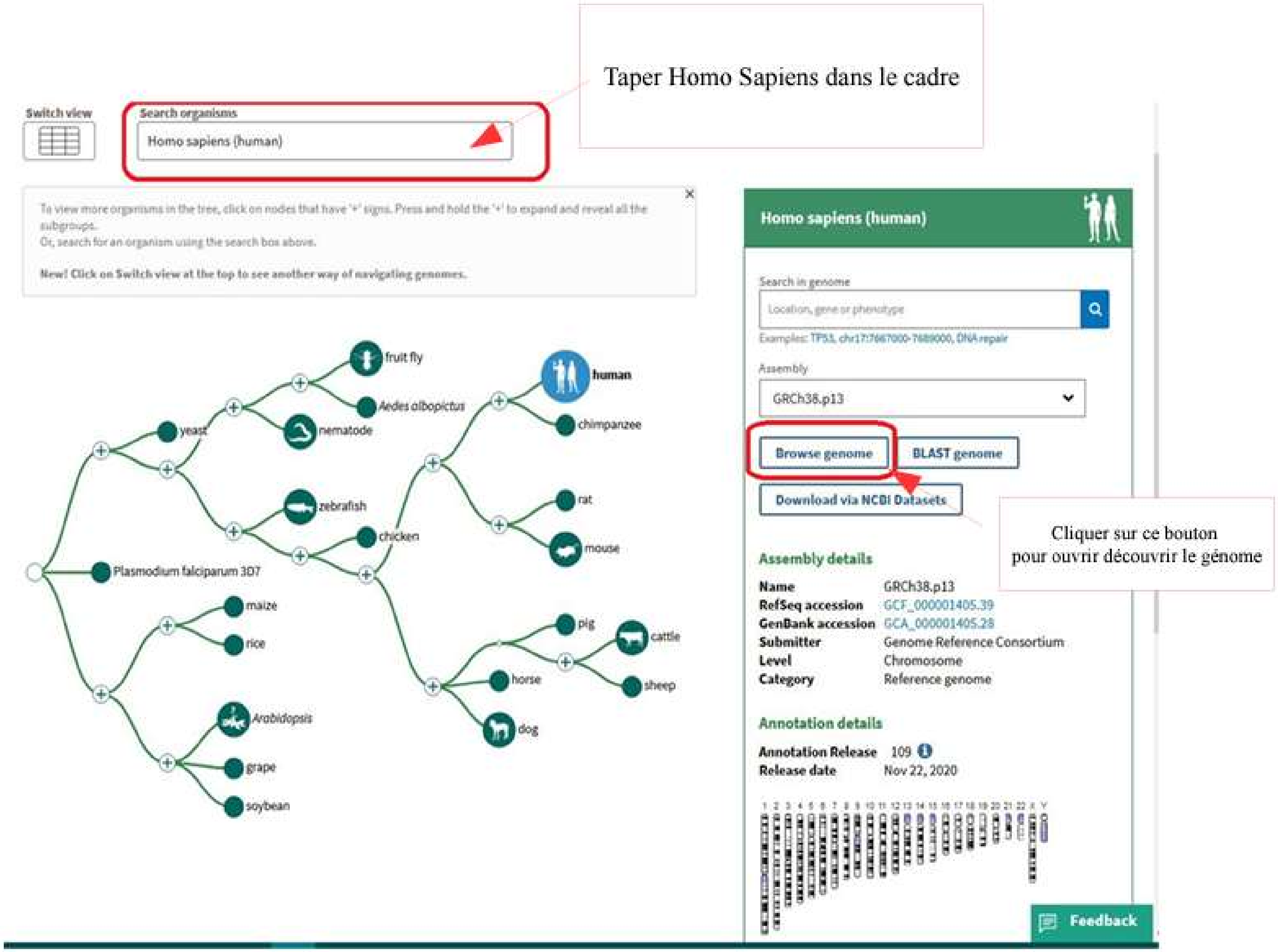
A la découverte des informations relatives au génome d’une espèce (*Homo sapiens*)
Fiche technique

Aller sur le site https://www.ncbi.nlm.nih.gov/genome/gdv/



Taper Homo Sapiens dans le cadre

Cliquer sur ce bouton pour ouvrir découvrir le génome

Search organisms: Homo sapiens (human)

To view more organisms in the tree, click on nodes that have '+' signs. Press and hold the '+' to expand and reveal all the subgroups.
Or, search for an organism using the search box above.

New! Click on Switch view at the top to see another way of navigating genomes.

Homo sapiens (human)

Search in genome: Location, gene or phenotype

Examples: TP53, chr17:7667000-7689000, DNA repair

Assembly: GRCh38.p13

Assembly details

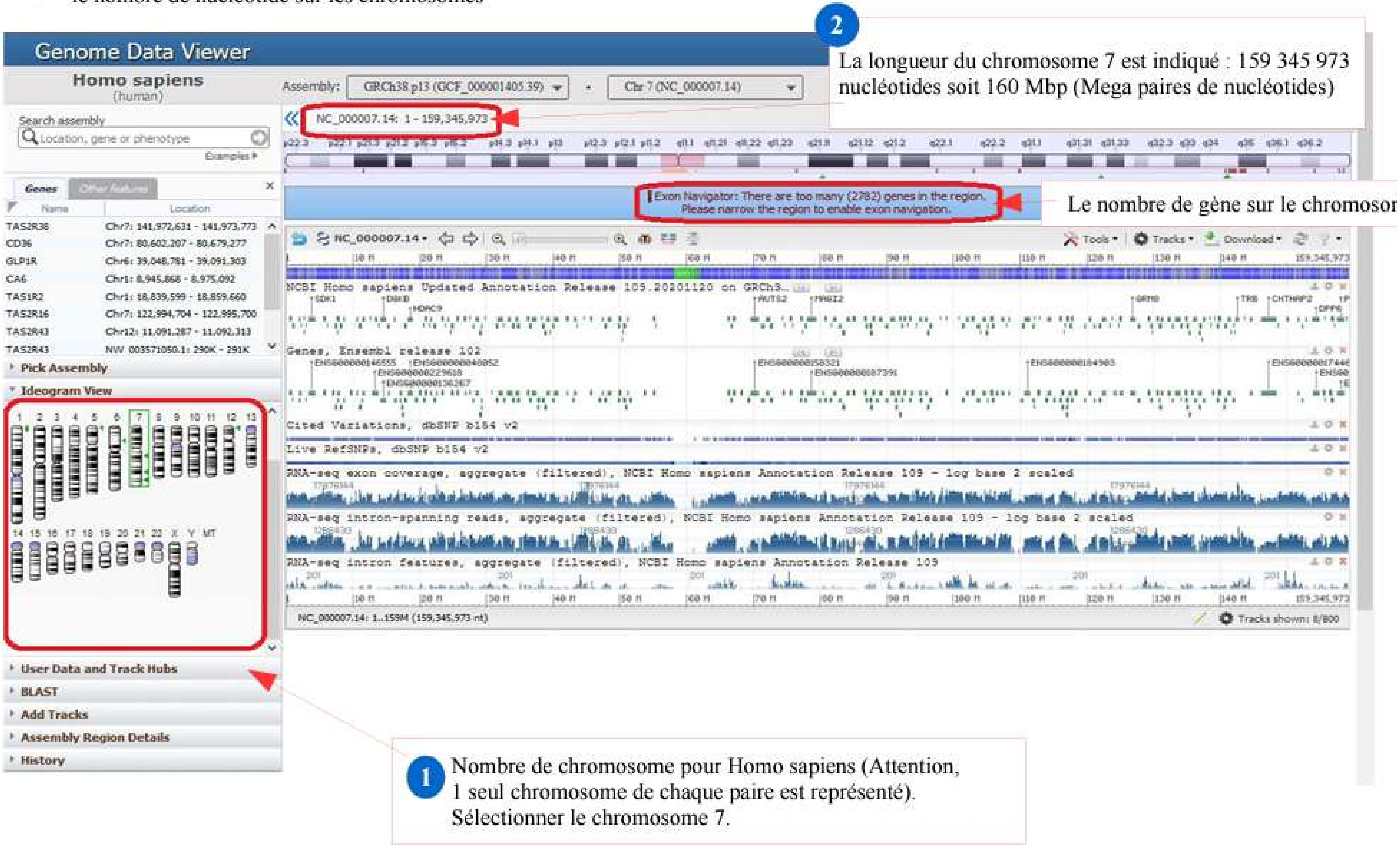
Name	GRCh38.p13
RefSeq accession	GCF_000001405.39
GenBank accession	GCA_000001405.28
Submitter	Genome Reference Consortium
Level	Chromosome
Category	Reference genome

Annotation details

Annotation Release	109
Release date	Nov 22, 2020

La fenêtre ci-dessous apparaît. Nous pouvons connaître :

- le caryotype d'un Homo sapiens
- le nombre de nucléotide sur les chromosomes



Name	Location
TAS2R38	Chr7: 141,972,631 - 141,973,773
CD36	Chr7: 80,602,207 - 80,679,277
GLP1R	Chr6: 39,048,781 - 39,091,303
CA6	Chr1: 8,945,868 - 8,975,092
TAS1R2	Chr1: 18,839,599 - 18,859,660
TAS2R16	Chr7: 122,994,704 - 122,995,700
TAS2R43	Chr12: 11,091,287 - 11,092,313
TAS2R43	NW_003571050.1: 290K - 291K

Exon Navigator: There are too many (2782) genes in the region. Please narrow the region to enable exon navigation.

La longueur du chromosome 7 est indiqué : 159 345 973 nucléotides soit 160 Mbp (Mega paires de nucléotides)

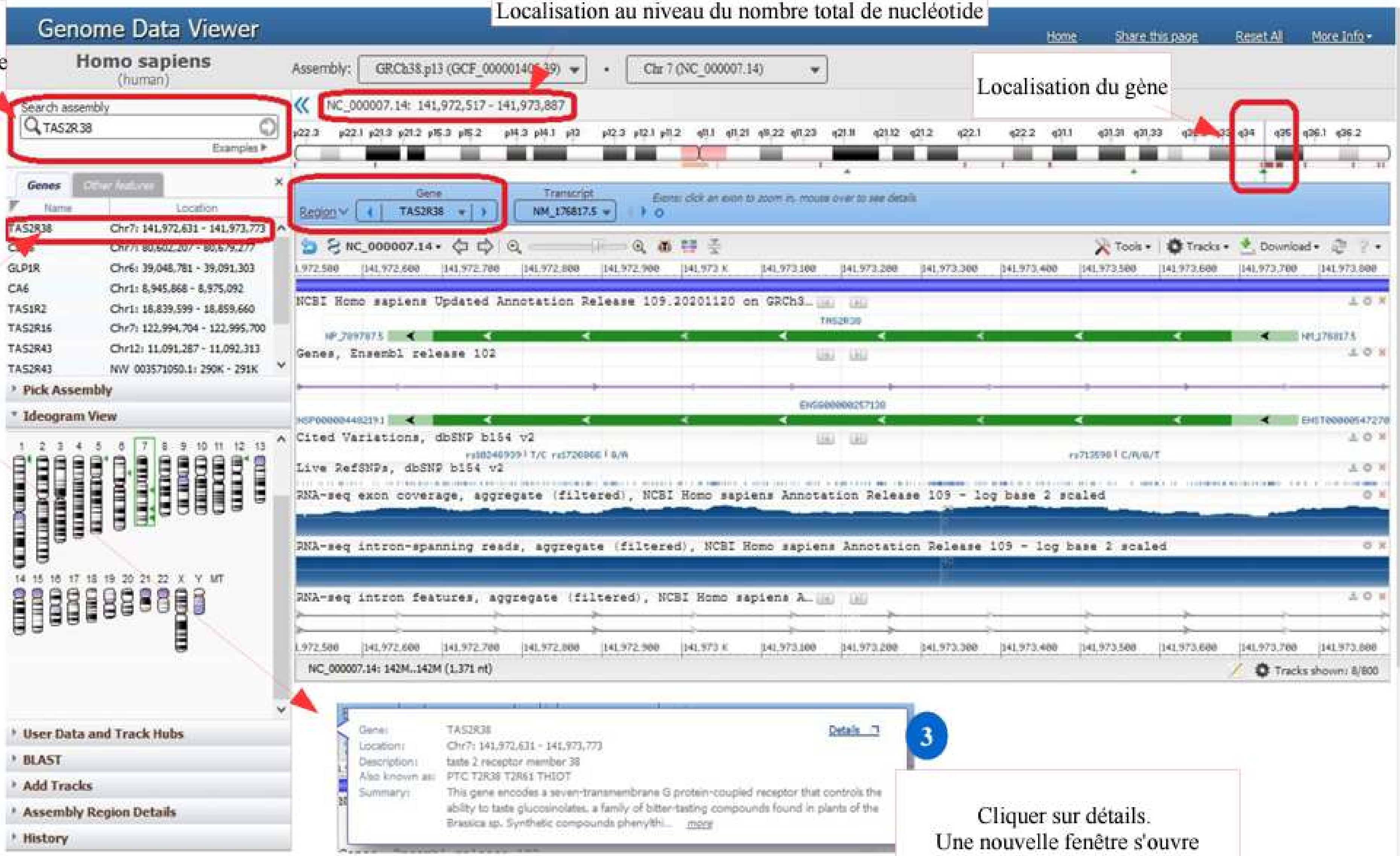
Le nombre de gène sur le chromoso

Nombre de chromosome pour Homo sapiens (Attention, 1 seul chromosome de chaque paire est représenté). Sélectionner le chromosome 7.

1

Cet outil permet de connaître de découvrir un gène en particulier.

Entrer le nom du gène



Localisation au niveau du nombre total de nucléotide

Localisation du gène

Name	Location
TAS2R38	Chr7: 141,972,631 - 141,973,773
[illegible]	Chr7: 80,602,207 - 80,679,277
GLP1R	Chr6: 39,048,781 - 39,091,303
CA6	Chr1: 8,945,868 - 8,975,092
TAS1R2	Chr1: 18,839,599 - 18,859,660
TAS2R16	Chr7: 122,994,704 - 122,996,700
TAS2R43	Chr12: 11,091,287 - 11,092,313
TAS2R43	NW_003571050.1: 290K - 291K

2

Cliquer sur le gène.

Une fenetre s'ouvre

Gene: TAS2R38

Location: Chr7: 141,972,631 - 141,973,773

Description: taste 2 receptor member 38

Also known as: PTC T2R38 T2R61 THIOT

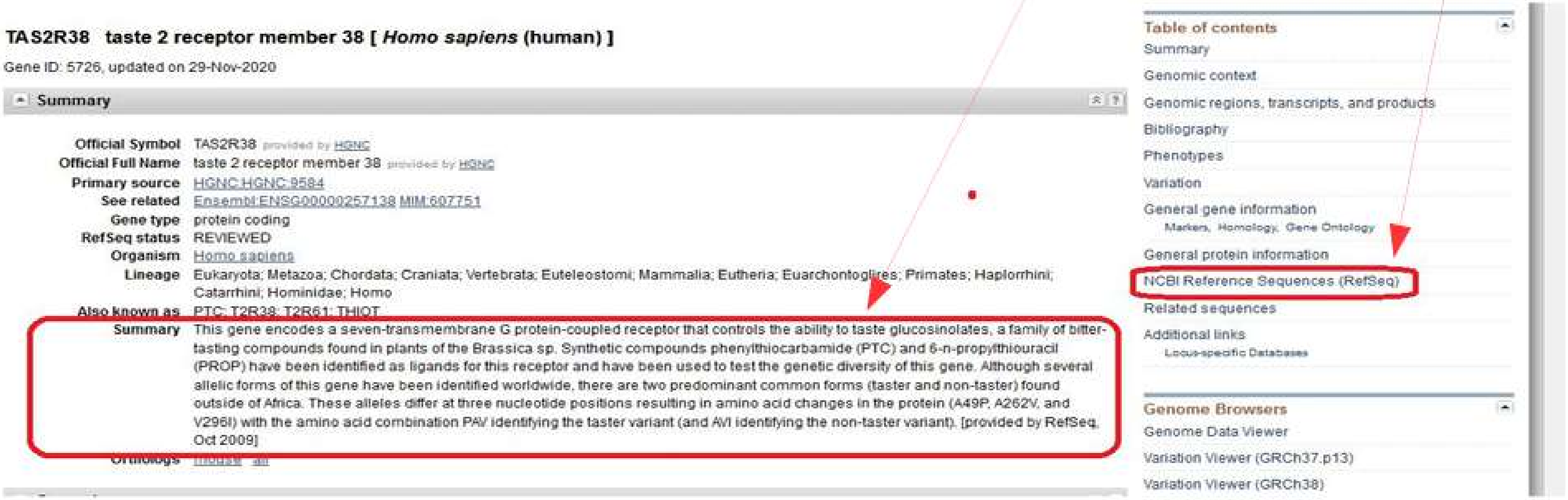
Summary: This gene encodes a seven-transmembrane G protein-coupled receptor that controls the ability to taste glucosinolates, a family of bitter-tasting compounds found in plants of the Brassica sp. Synthetic compounds phenylthi... more

Details

3

Cliquer sur détails.
Une nouvelle fenêtre s'ouvre

Sur la page qui s'ouvre, une multitude d'informations s'affiche, compréhensible par des post-doc. Lire les particularités de ce gène . Puis cliquer sur NCBI reference sequences.



TAS2R38 taste 2 receptor member 38 [*Homo sapiens* (human)]

Gene ID: 5726, updated on 29-Nov-2020

Summary

Official Symbol	TAS2R38 provided by HGNC
Official Full Name	taste 2 receptor member 38 provided by HGNC
Primary source	HGNC:HGNC:9584
See related	Ensembl:ENSG00000257138 MIM:607751
Gene type	protein coding
RefSeq status	REVIEWED
Organism	Homo sapiens
Lineage	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Homo
Also known as	PTC; T2R38; T2R61; THIOT
Summary	This gene encodes a seven-transmembrane G protein-coupled receptor that controls the ability to taste glucosinolates, a family of bitter-tasting compounds found in plants of the Brassica sp. Synthetic compounds phenylthiocarbamide (PTC) and 6-n-propylthiouracil (PROP) have been identified as ligands for this receptor and have been used to test the genetic diversity of this gene. Although several allelic forms of this gene have been identified worldwide, there are two predominant common forms (taster and non-taster) found outside of Africa. These alleles differ at three nucleotide positions resulting in amino acid changes in the protein (A49P, A262V, and V296I) with the amino acid combination PAV identifying the taster variant (and AVI identifying the non-taster variant). [provided by RefSeq, Oct 2009]
Orthologs	mouse all

Cet onglet apparaît. Cliquer sur FASTA. Votre séquences complètes du gène TA S2R38 apparaît. Copier la séquence.

NCBI Reference Sequences (RefSeq)

RefSeqs maintained independently of Annotated Genomes

These reference sequences exist independently of genome builds. Explain

Genomic

1. **NG_016141.1 RefSeqGene**

Range	6001..614
Download	GenBank, FASTA, Sequence Viewer (Graphics)

mRNA and Protein(s)

1. **NM_176817.5 → NP_789787.5 taste receptor type 2 member 38**

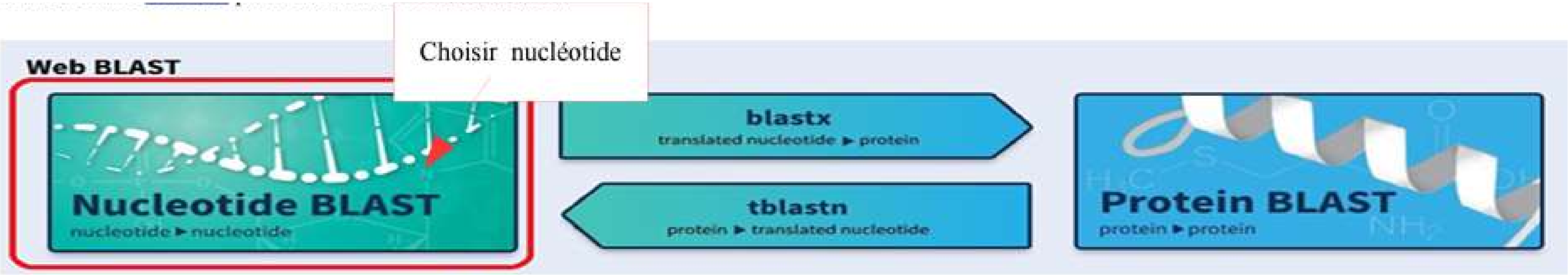
Status: REVIEWED

Source sequence(s)	AC073647
Consensus CDS	CCDS34766.1
Related	ENSP00000448219.1, ENST00000547270.1

Conserved Domains (1) summary

cd15025 Location:16 → 309	7tm_TAS2R38; mammalian taste receptor 2, subtype 38, member of the seven-transmembrane G protein-coupled receptor superfamily

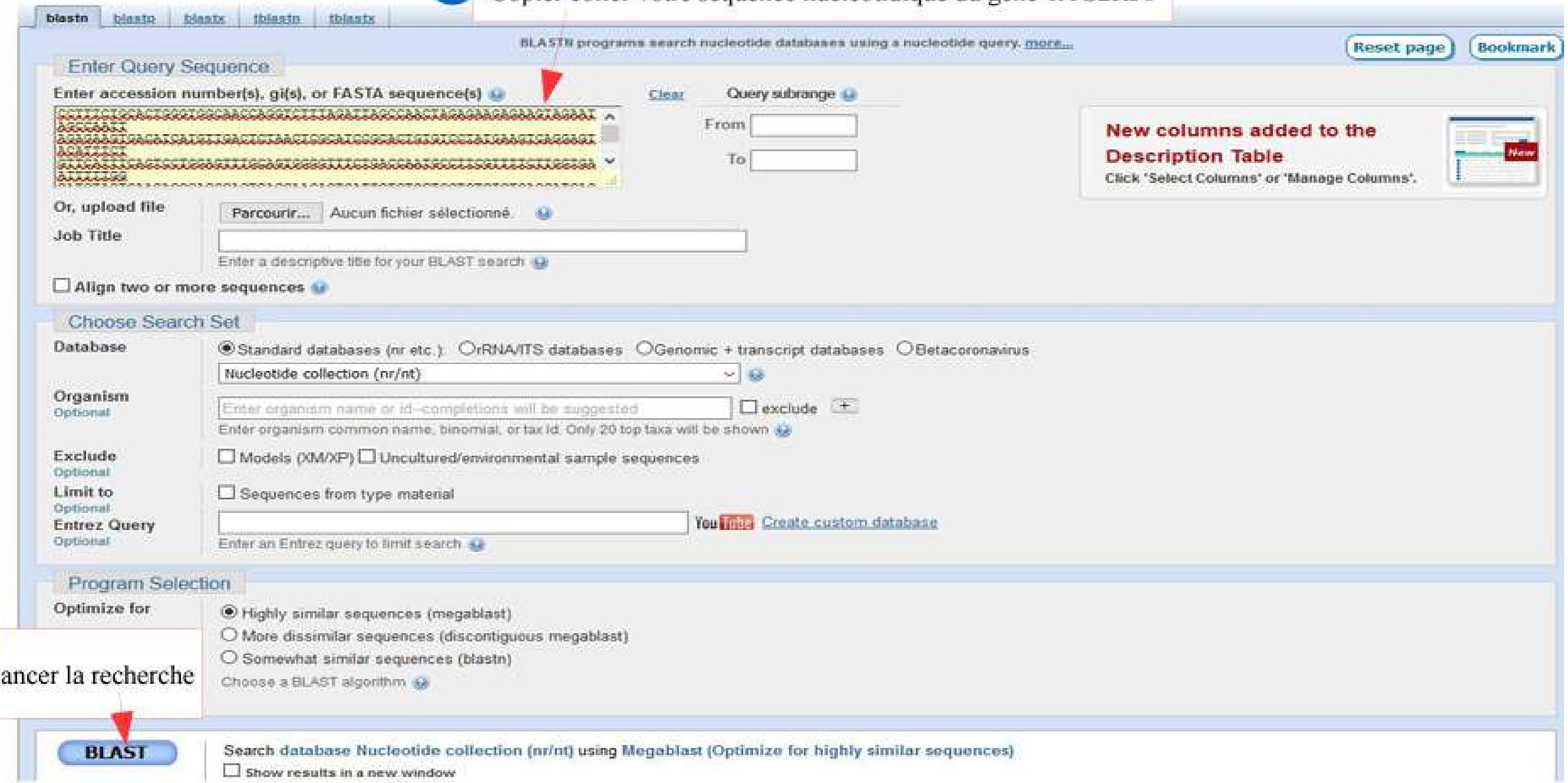
Ouvrir l'outil BLAST pour construire une phylogénie : https://blast.ncbi.nlm.nih.gov/Blast.cgi



Choisir nucléotide

Cette fenêtre s'ouvre :

1 Copier coller votre séquence nucléotidique du gène TA S2R38



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

Enter Query Sequence

Enter accession number(s), gi(s), or FASTA sequence(s)

Query subrange

From

To

Or, upload file: Parcourir... Aucun fichier sélectionné.

Job Title

Enter a descriptive title for your BLAST search

☐ Align two or more sequences

New columns added to the Description Table

Click 'Select Columns' or 'Manage Columns'.

Choose Search Set

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

Nucleotide collection (nr/nt)

Organism (Optional): Enter organism name or id--completions will be suggested ☐ exclude

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): 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)

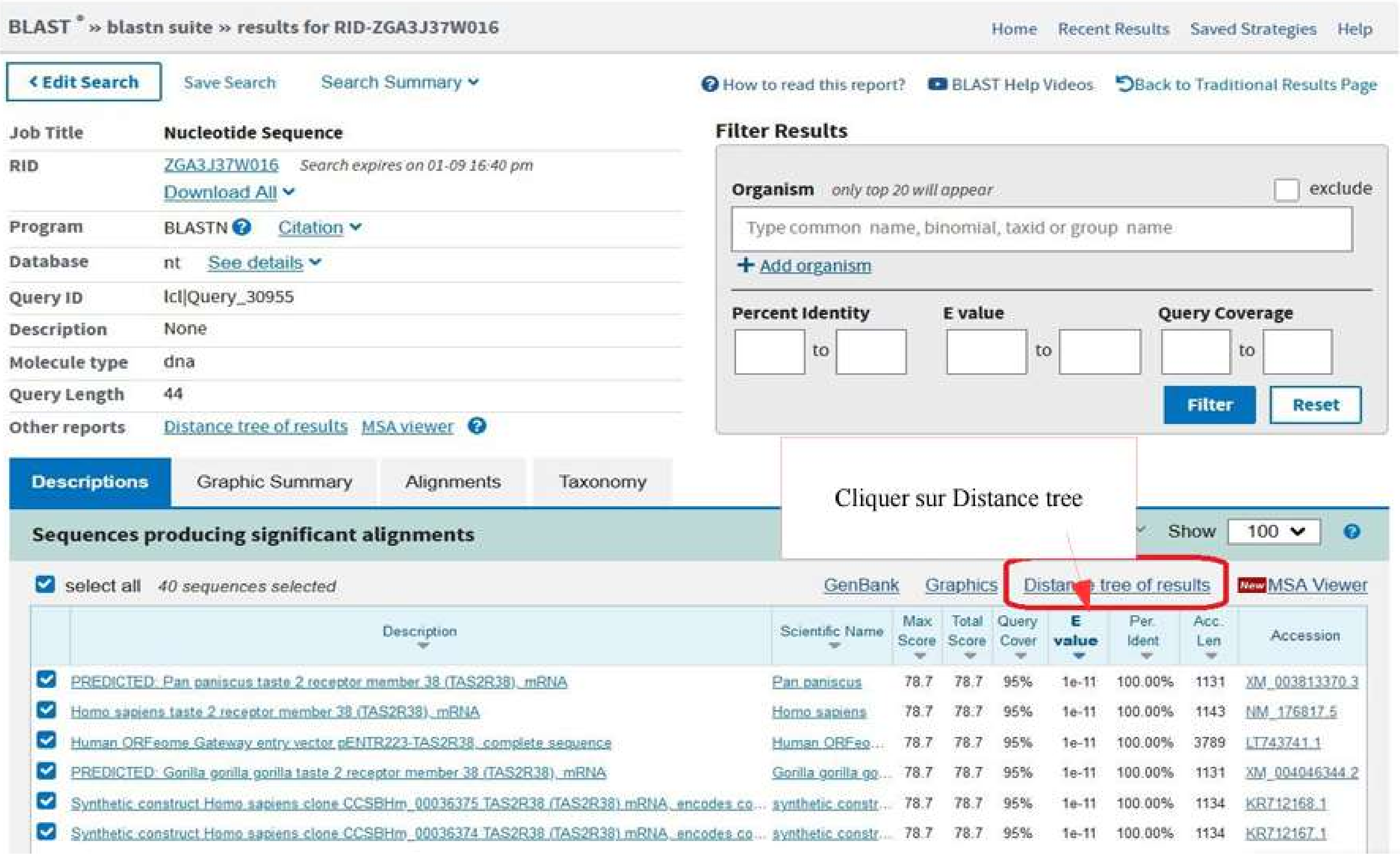
Choose a BLAST algorithm

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

☐ Show results in a new window

Lancer la recherche

Cette fenêtre apparaît : toutes les séquences chez toutes les espèces qui sont proches de la séquence recherchée sont affichées. Le pourcentage de ressemblance est indiqué dans cette colonne. Cliquer sur « Distance tree of results » pour afficher l'arbre phylogénétique correspondant.



Cliquer sur Distance tree

BLAST® » blastn suite » results for RID-ZGA3J37W016

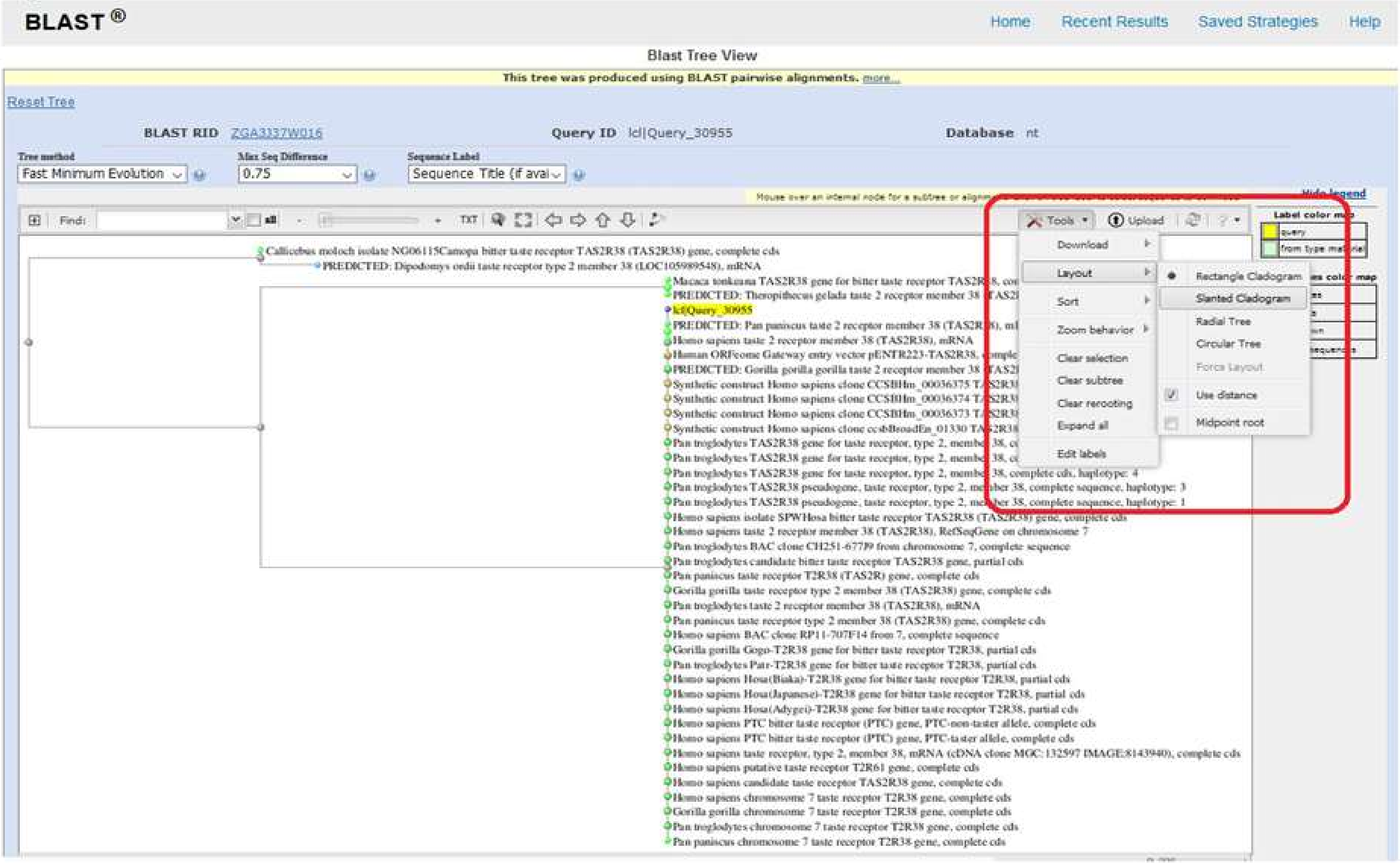
Job Title	**Nucleotide Sequence**
RID	ZGA3J37W016 *Search expires on 01-09 16:40 pm* Download All
Program	BLASTN Citation
Database	nt See details
Query ID	lcl|Query_30955
Description	None
Molecule type	dna
Query Length	44
Other reports	Distance tree of results MSA viewer

Sequences producing significant alignments

☑ select all *40 sequences selected*

	Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Per. Ident	Acc. Len	Accession
☑	PREDICTED: Pan paniscus taste 2 receptor member 38 (TAS2R38), mRNA	Pan paniscus	78.7	78.7	95%	1e-11	100.00%	1131	XM_003813370.3
☑	Homo sapiens taste 2 receptor member 38 (TAS2R38), mRNA	Homo sapiens	78.7	78.7	95%	1e-11	100.00%	1143	NM_176817.5
☑	Human ORFeome Gateway entry vector pENTR223-TAS2R38, complete sequence	Human ORFeo...	78.7	78.7	95%	1e-11	100.00%	3789	LT743741.1
☑	PREDICTED: Gorilla gorilla gorilla taste 2 receptor member 38 (TAS2R38), mRNA	Gorilla gorilla go...	78.7	78.7	95%	1e-11	100.00%	1131	XM_004046344.2
☑	Synthetic construct Homo sapiens clone CCSBHm_00036375 TAS2R38 (TAS2R38) mRNA, encodes co...	synthetic constr...	78.7	78.7	95%	1e-11	100.00%	1134	KR712168.1
☑	Synthetic construct Homo sapiens clone CCSBHm_00036374 TAS2R38 (TAS2R38) mRNA, encodes co...	synthetic constr...	78.7	78.7	95%	1e-11	100.00%	1134	KR712167.1

L'arbre affiché traduit la parenté entre les espèces pour le gène TA S2R38. Pour modifier l'affichage, cliquer sur « tools », « Layout », « slanted cladogram »



Blast Tree View

This tree was produced using BLAST pairwise alignments. more...

BLAST RID ZGA3337W016 **Query ID** lcl|Query_30955 **Database** nt

Tree method: Fast Minimum Evolution
Max Seq Difference: 0.75
Sequence Label: Sequence Title (if avai

Callicebus moloch isolate NG06115Camopu bitter taste receptor TAS2R38 (TAS2R38) gene, complete cds
PREDICTED: Dipodomys ordii taste receptor type 2 member 38 (LOC105989548), mRNA
Macaca tonkeana TAS2R38 gene for bitter taste receptor TAS2R 8, co
PREDICTED: Theropithecus gelada taste 2 receptor member 38 TAS2
lcl|Query_30955
PREDICTED: Pan paniscus taste 2 receptor member 38 (TAS2R 8), ml
Homo sapiens taste 2 receptor member 38 (TAS2R38), mRNA
Human ORFeome Gateway entry vector pENTR223-TAS2R38, comple
PREDICTED: Gorilla gorilla gorilla taste 2 receptor member 38 TAS2
Synthetic construct Homo sapiens clone CCSBHm_00036375 TAS2R3
Synthetic construct Homo sapiens clone CCSBHm_00036374 TAS2R3
Synthetic construct Homo sapiens clone CCSBHm_00036373 TAS2R3
Synthetic construct Homo sapiens clone ccsbBroadEn_01330 TAS2R38
Pan troglodytes TAS2R38 gene for taste receptor, type 2, member 38, c
Pan troglodytes TAS2R38 gene for taste receptor, type 2, member 38, c
Pan troglodytes TAS2R38 gene for taste receptor, type 2, member 38, complete cds, haplotype: 4
Pan troglodytes TAS2R38 pseudogene, taste receptor, type 2, member 38, complete sequence, haplotype: 3
Pan troglodytes TAS2R38 pseudogene, taste receptor, type 2, member 38, complete sequence, haplotype: 1
Homo sapiens isolate SPWHosa bitter taste receptor TAS2R38 (TAS2R38) gene, complete cds
Homo sapiens taste 2 receptor member 38 (TAS2R38), RefSeqGene on chromosome 7
Pan troglodytes BAC clone CH251-677J9 from chromosome 7, complete sequence
Pan troglodytes candidate bitter taste receptor TAS2R38 gene, partial cds
Pan paniscus taste receptor T2R38 (TAS2R) gene, complete cds
Gorilla gorilla taste receptor type 2 member 38 (TAS2R38) gene, complete cds
Pan troglodytes taste 2 receptor member 38 (TAS2R38), mRNA
Pan paniscus taste receptor type 2 member 38 (TAS2R38) gene, complete cds
Homo sapiens BAC clone RP11-707F14 from 7, complete sequence
Gorilla gorilla Gogo-T2R38 gene for bitter taste receptor T2R38, partial cds
Pan troglodytes Patr-T2R38 gene for bitter taste receptor T2R38, partial cds
Homo sapiens Hosa(Biaka)-T2R38 gene for bitter taste receptor T2R38, partial cds
Homo sapiens Hosa(Japanese)-T2R38 gene for bitter taste receptor T2R38, partial cds
Homo sapiens Hosa(Adygei)-T2R38 gene for bitter taste receptor T2R38, partial cds
Homo sapiens PTC bitter taste receptor (PTC) gene, PTC-non-taster allele, complete cds
Homo sapiens PTC bitter taste receptor (PTC) gene, PTC-taster allele, complete cds
Homo sapiens taste receptor, type 2, member 38, mRNA (cDNA clone MGC:132597 IMAGE:8143940), complete cds
Homo sapiens putative taste receptor T2R61 gene, complete cds
Homo sapiens candidate taste receptor TAS2R38 gene, complete cds
Homo sapiens chromosome 7 taste receptor T2R38 gene, complete cds
Gorilla gorilla chromosome 7 taste receptor T2R38 gene, complete cds
Pan troglodytes chromosome 7 taste receptor T2R38 gene, complete cds
Pan paniscus chromosome 7 taste receptor T2R38 gene, complete cds