Les Arbres

Par Joel Sandé

Les arbres

- Il y a 3 groupes d'arbres: L'arbre des distances, l'arbre de parcimonie, et l'arbre des vraissemblances (Likelihood). Ils ont chacuns leurs forces et faiblesse.
- L'arbre des distances est le plus facile et rapide à rouler...
- Toutefois, les arbres de parcimonie et de vraissemblance son en théorie, les plus précis, mais prennent plus de temps à rouler.

Arbre des distances

- Quand on décide d'utilise l'arbre des distances, on doit tenir compte de 4 choses, don't 2 majeurs :
 - L'algorithme de reconstruction (UPGA, NJ, Fitch, Kitsch)
 - Le type d'arbre qu'on veut construire.
 - Arbre sans distances (Cladogram)
 - Arbre avec distances (Phenogram)
 - Arbre enraciné ou non-enraciné

Afficher un arbre sur l'ordinateur

 Philip est le nom du Package qui permet de construire les arbres philogéniques (petit détail).

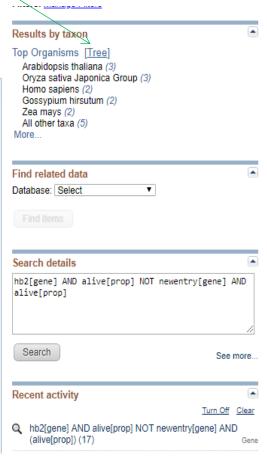
Construisons l'arbre de l'hémoglobine HB2

Vous pouvez construire un cladogram directement via NCBI en clikant Tree

https://www.ncbi.nlm.nih.gov/gene?term=hb2[gene]%20AND%20alive[prop]%20NO T%20newentry[gene]%20&sort=weight

Items: 17 Showing Current items. Name/Gene ID Description Location Aliases MIM SCN5A sodium voltage-gated Chromosome 3, CDCD2, CMD1E, CMPD2, HB1, HB2, HBBD, HH1, 600163 ID: 6331 channel alpha subunit 5 NC 000003.12 ICCD, IVF, LQT3, Nav1.5, PFHB1, SSS1, VF1 [Homo sapiens (human)] (38548061..38649673. complement) homeobox protein 2 Chromosome 4. AT4G16780, ARABIDOPSIS THALIANA HOMEOBOX HB-2 ID: 827384 [Arabidopsis thaliana (thale NC_003075.7 PROTEIN 2, ATHB-2, ATHB2, DL4415W, FCAALL.101, (9449114..9450905) cress)] HAT4, homeobox protein 2 hemoglobin 2 [Arabidopsis AT3G10520, AHB2, ARABIDOPSIS HEMOGLOBIN 2. HB2 Chromosome 3. ID: 820216 thaliana (thale cress)] NC 003074.8 ARATH GLB2. ATGLB2. GLB2. HEMOGLOBIN. (3276163..3277930. HEMOGLOBIN 2. NON-SYMBIOTIC HAEMOGLOBIN 2. NSHB2, haemoglobin 2 complement) KRT82 keratin 82 [Homo sapiens Chromosome 12, HB2. Hb-2. KRTHB2 601078 ID: 3888 (human)] NC_000012.12 (52393951..52406392. complement) HB21 homeobox protein 21 Chromosome 2, AT2G18550, ATHB21, F24H14.10, F24H14.10, HB-2, ID: 816370 NC 003071.7 [Arabidopsis thaliana (thale homeobox protein 21, homeobox-2 cress)] (8049371..8051316, complement) Hb2 Glb2 non-symbiotic hemoglobin Chromosome 3. ID: 543822 class 2 [Solanum NC 015440.2 (18328609..18330350, lycopersicum (tomato)] complement) <u>hb2</u> globin [Ciona intestinalis

Search results



Search results

Items: 17

Showing Current items.

Name/Gene ID	Description	Location	Aliase
SCN5A ID: 6331	sodium voltage- gated channel alpha subunit 5 [<i>Homo sapiens</i> (human)]	Chromosome 3, NC_000003.12 (3854806138649673, complement)	CDCI HB2, LQT3 VF1
☐ <u>HB-2</u> ID: 827384	homeobox protein 2 [<i>Arabidopsis</i> <i>thaliana</i> (thale cress)]	Chromosome 4, NC_003075.7 (94491149450905)	AT4G THAL PRO1 DL44 home
☐ <u>HB2</u> ID: 820216	hemoglobin 2 [<i>Arabidopsis</i> <i>thaliana</i> (thale	Chromosome 3, NC_003074.8 (32761633277930,	AT3G ARAE 2, AR

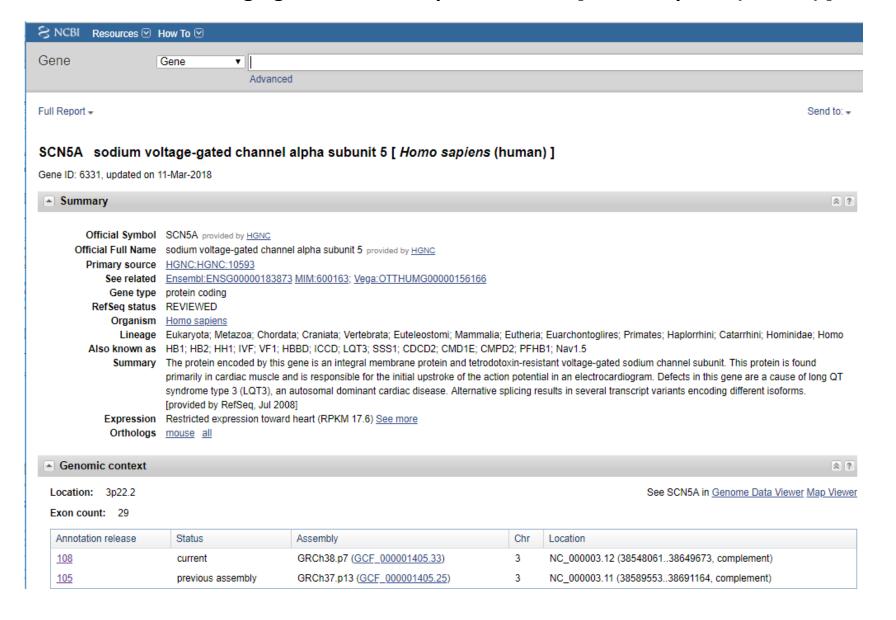
Results by taxon Taxonomic Groups [List] = eukaryotes (17) green plants (14) eudicots (9) Brassicales (5) Arabidopsis (4) Brassica (1) Solanum (1) -Nicotiana (1) -Malvales (2) imonocots (5) -Oryza *(3)* ^LZea *(2)* i animals (3) vertebrates (2) tunicates (1)

Pour l'arbre référez-vous à ClustalW

www.ebi.ac.uk/clustalw/ Ou http://www.genome.jp/tools-bin/clustalw

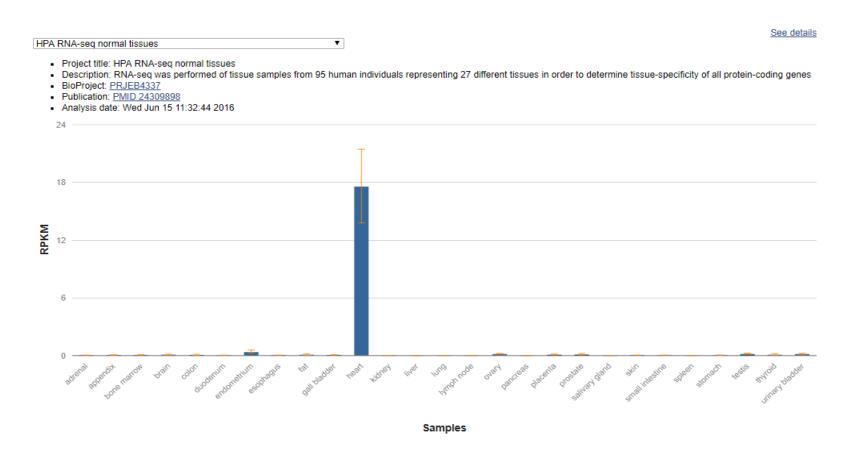
Je vous le montre dans les prochaines slides

SCN5A sodium voltage-gated channel alpha subunit 5 [Homo sapiens (human)]



SCN5A sodium voltage-gated channel alpha subunit 5 [Homo sapiens (human)]

Si vous descendez plus bas, vous verrez les tissus sujets d'études de ce gènes. Dans cet exemple-ci, le tissus cardiaque est le plus concerné



Ainsi que la Bibliographie à ce gène

Bibliography

☆ ?

Related articles in PubMed

 Genotype-Phenotype Correlation of SCN5A Mutation for the Clinical and Electrocardiographic Characteristics of Probands With Brugada Syndrome: A Japanese Multicenter Registry.

Yamagata K, et al. Circulation, 2017 Jun 6. PMID 28341781

Electrocardiogram changes and atrial arrhythmias in individuals carrying sodium channel SCN5A D1275N mutation.

Vanninen SUM, et al. Ann Med, 2017 Sep. PMID 28294644

Gain-of-function mutation in SCN5A causes ventricular arrhythmias and early onset atrial fibrillation.

Lieve KV, et al. Int J Cardiol, 2017 Jun 1. PMID 28262340

A Common Variant in SCN5A and the Risk of Ventricular Fibrillation Caused by First ST-Segment Elevation Myocardial Infarction.

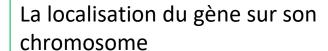
Jabbari R, et al. PLoS One, 2017. PMID 28085969, Free PMC Article

Multilevel analyses of SCN5A mutations in arrhythmogenic right ventricular dysplasia/cardiomyopathy suggest non-canonical mechanisms for disease pathogenesis.

Te Riele AS, et al. Cardiovasc Res, 2017 Jan. PMID 28069705, Free PMC Article

See all (539) citations in PubMed

See citations in PubMed for homologs of this gene provided by HomoloGene



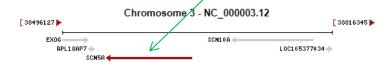
Location

Location: 3p22.2 Exon count: 29 See SCN5A in Genome Data Viewer Map Viewer

Annotation release	Status	Assembly	
<u>108</u>	current	GRCh38.p7 (GCF_000001405.33)	
<u>105</u>	previous assembly	GRCh37.p13 (<u>GCF_000001405.25</u>)	

NC_000003.12 (38548061..38649673, complement)

3 NC_000003.11 (38589553..38691164, complement)



Genomic regions, transcripts, and products

Go to reference sequence details

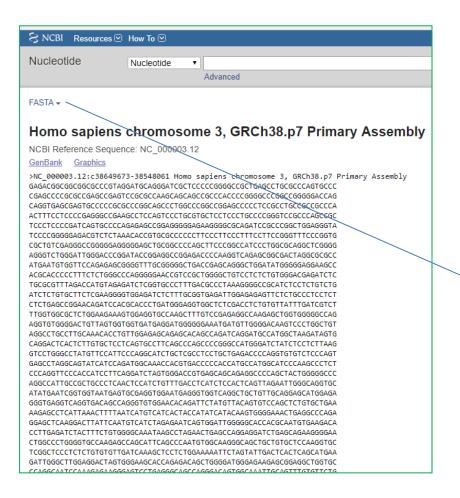
Go to nucleotide: Graphics FASTA GenBank

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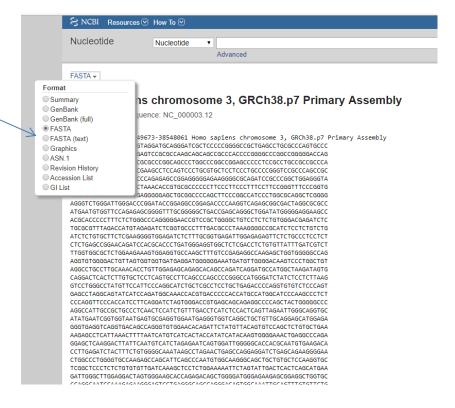
Genomic Sequence: NC_000003.12 Chromosome 3 Reference GRCh38.p7 Primary Assembly ▼

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NM_198056.2	-	\rightarrow	\rightarrow	>	\rightarrow		4	\rightarrow		\rightarrow	-	\rightarrow		\rightarrow	\rightarrow	>-	> 111	->-	NP_932173.1	
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Le format Fasta



Choisissez le format .text pour pouvoir le copier-coller dans clustalW. Faites-en autant pour tous les organismes qui vous interessent.



 Copier-coller le format .txt à soumettre sur ClustalW.

 Faite en de même pour toutes les espèces qui vous interessent.

 Bone pratique.. N'hésitez pas à me contacter en cas de problèmes techniques.