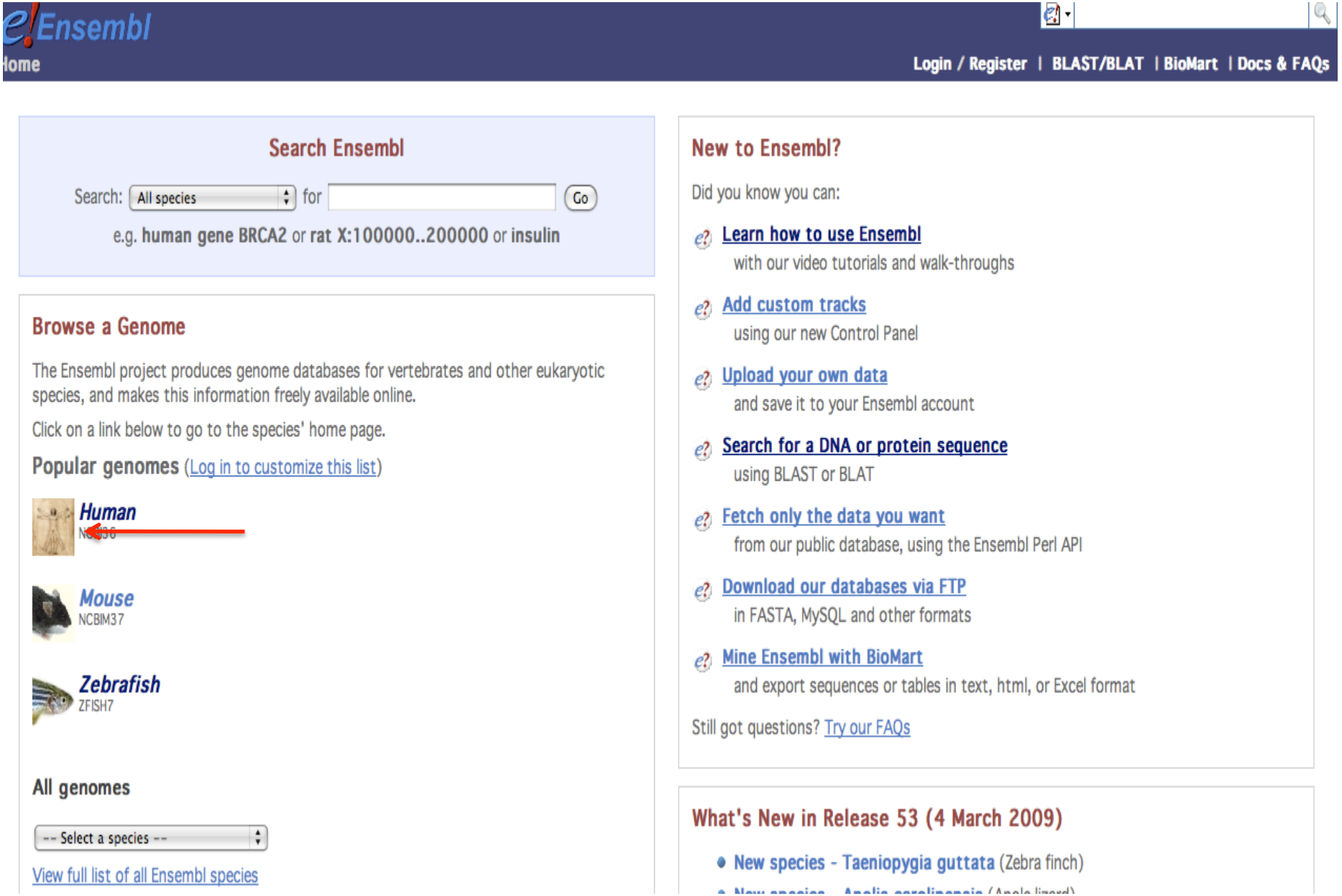
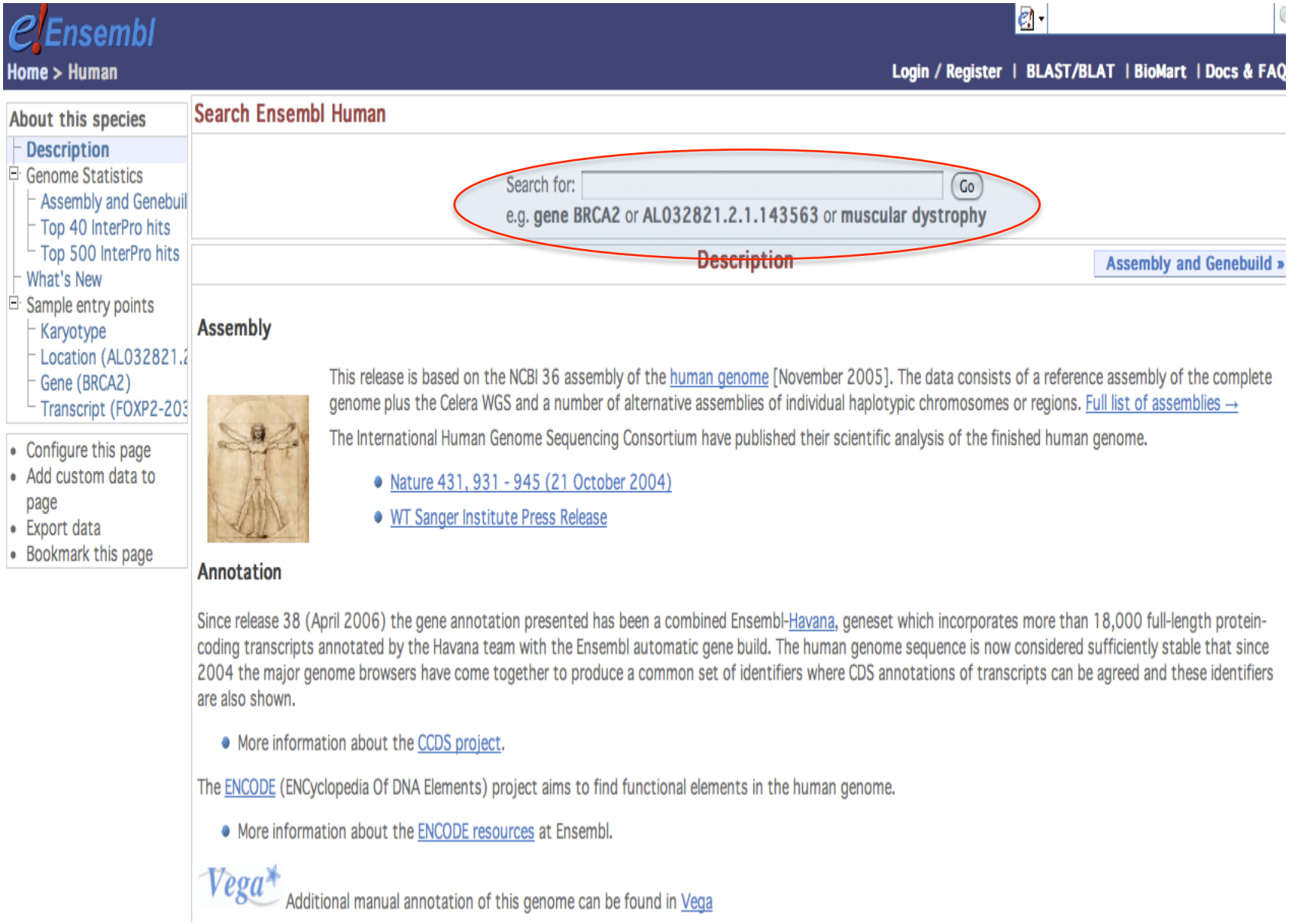
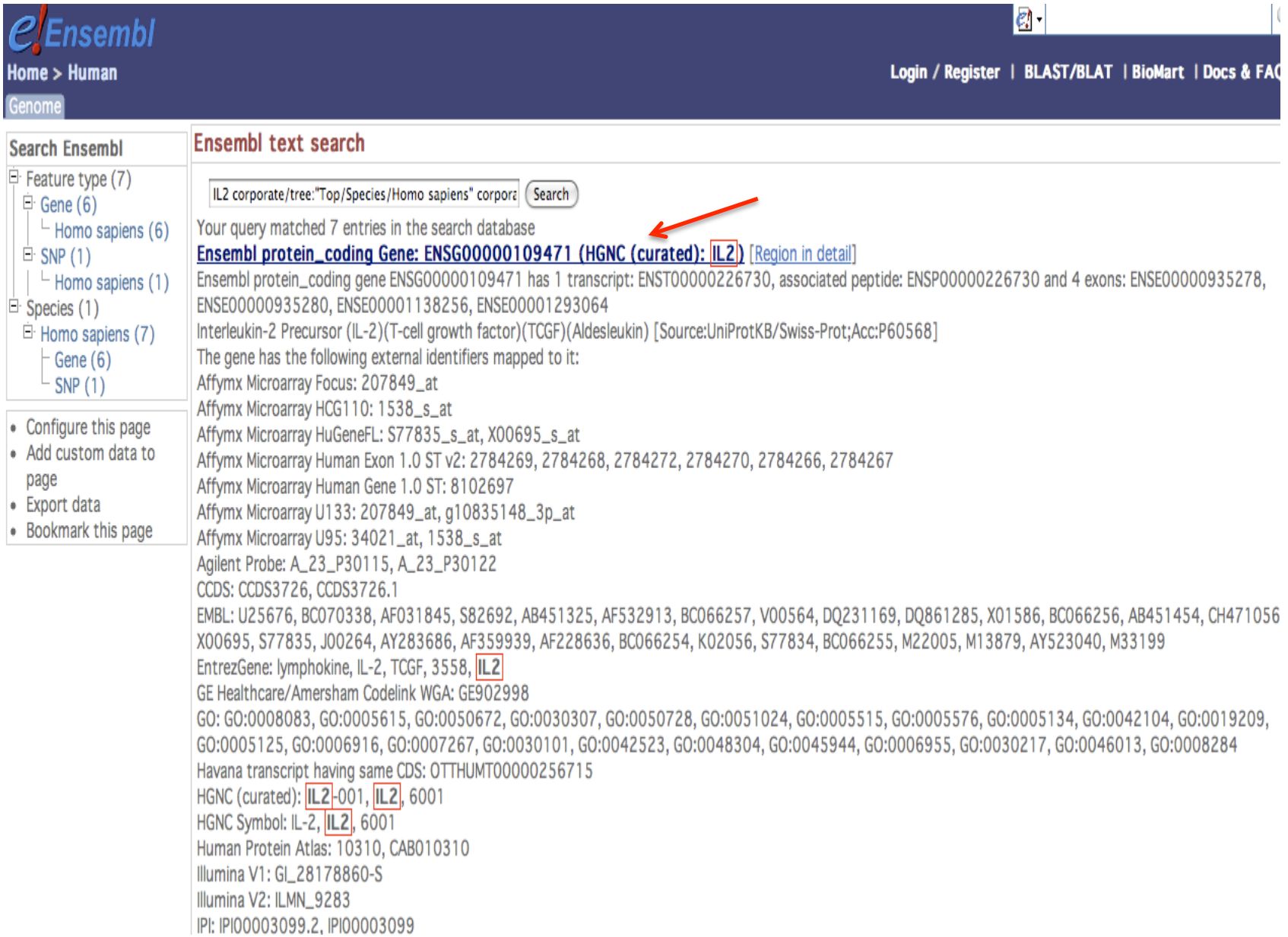
Start by going to **www.ensembl.org** or eBioKits Entry page



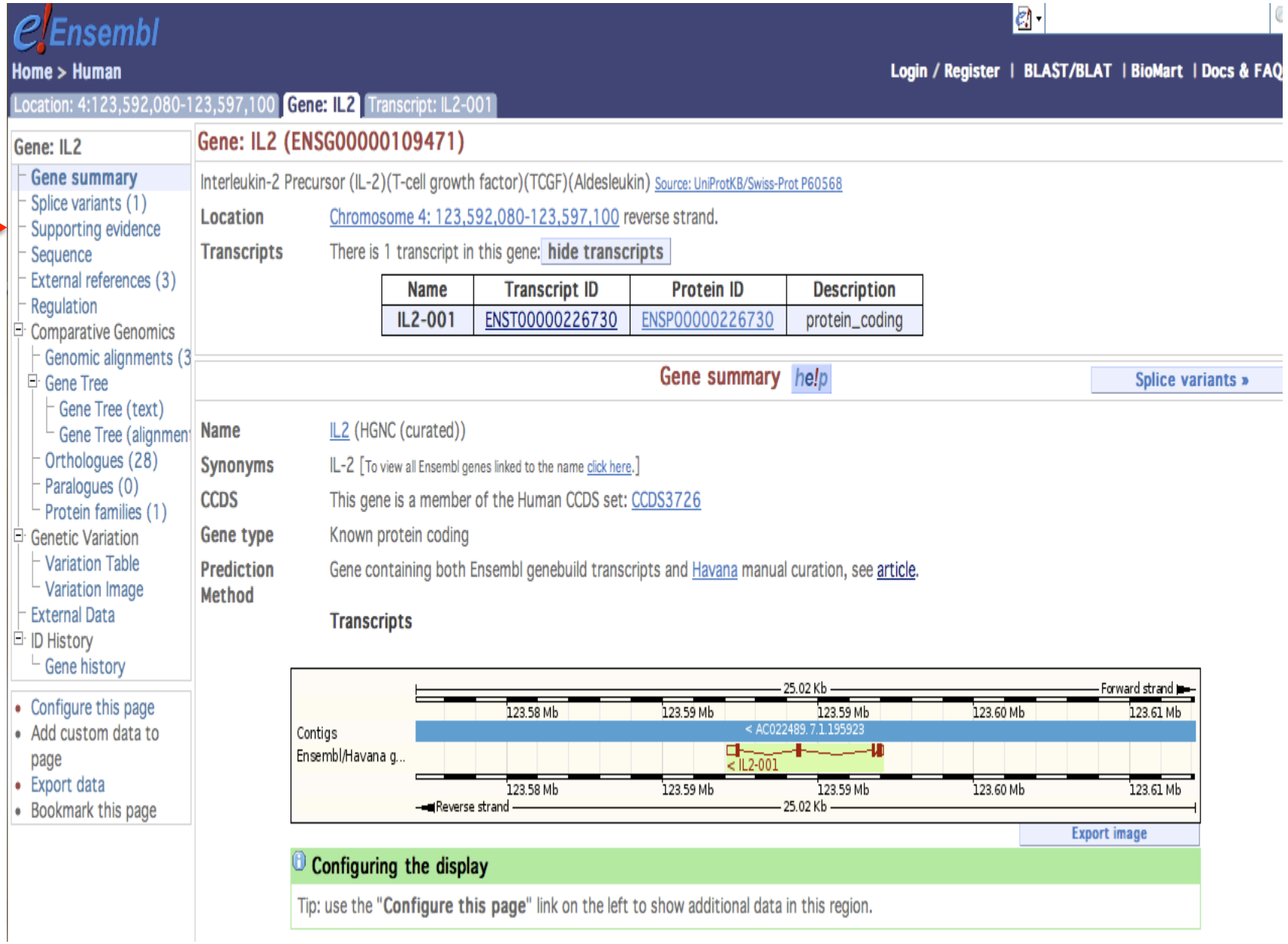
Type: **IL2** into the search bar circled below and click the **GO** button.



Select the Ensembl gene ENSG00000109471.



In the left hand navigation column click on **Supporting evidence** to show biological sequence records that have been used for the annotation.

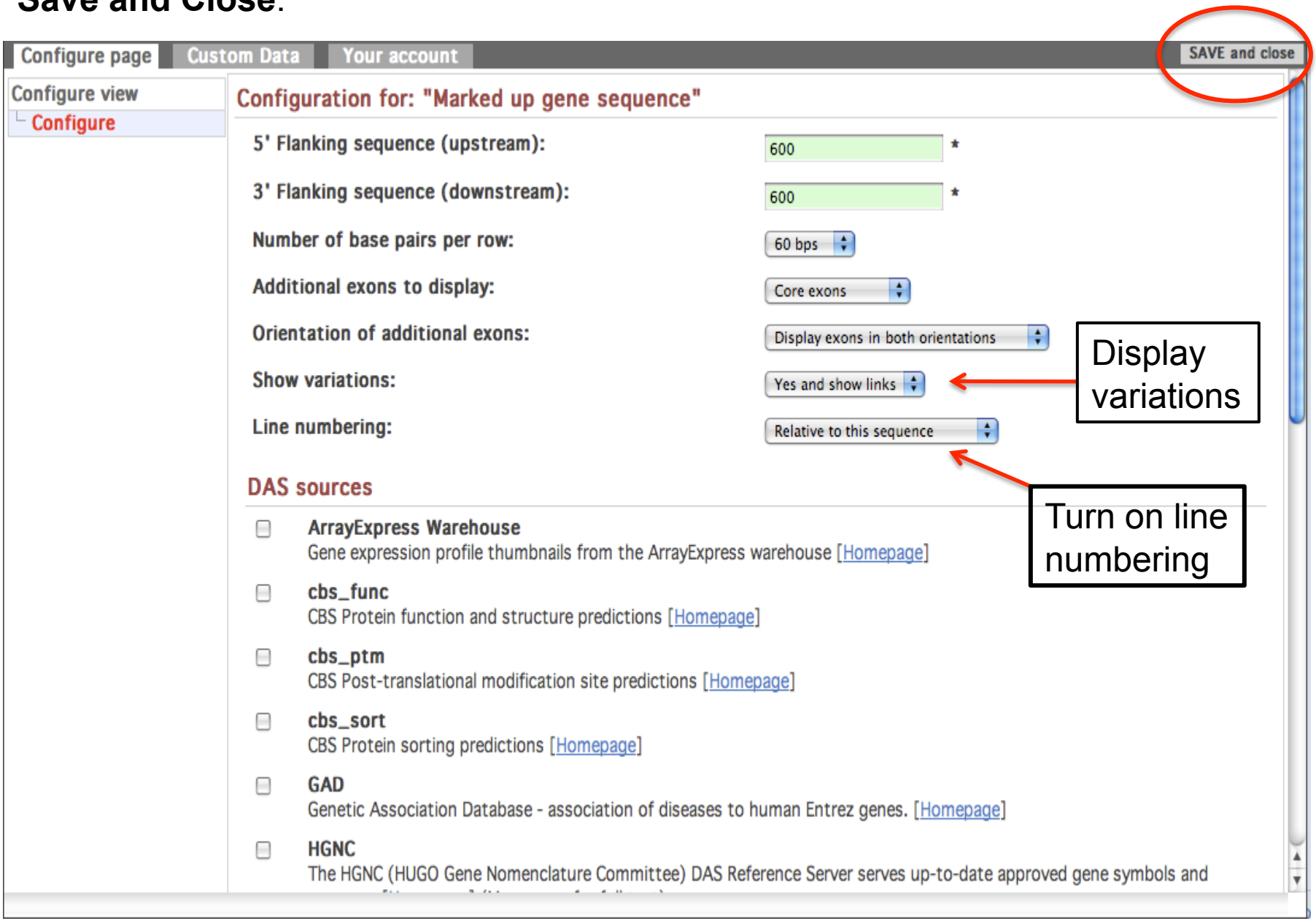


Now we would like to view the genomic sequence. Click **Sequence** at the left.

Exons are highlighted within the genomic sequence. Variations for this sequence can be added. Click on **Configure this page.**

THIS STYLE: Location of ENSG00000109471 exons
THIS STYLE: Location of Ensembl exons

In this example we display variations and show line numbers. Last click **Save and Close**.



THIS STYLE: Location of ENSG00000109471 exons
THIS STYLE: Location of Ensembl exons
THIS STYLE: Location of SNPs
THIS STYLE: Location of inserts
THIS STYLE: Location of deletes

```
>chromosome:NCBI36:4:123591480:123597700:-1
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     61 CTTAGTATTTCTCTAGCTGACATGTAAGAAGCAATCTATCTTATTGTATGCAATTAGCTC    120
    121 ATTGTGTGGATAAAAAGGTAAAACCATTCTSAAACAGGAAACCAATACACTTCCTGTTTW    180 151:G/C; 180:T/A;
    181 ATCAACAAATCTAAACATTTATTCTTTTCATCTGTTTACTCTTGCTCTTGTCCACCACAA    240 205:TTTTC/-;
    241 TATGCTATTCACATGTTCAGTGTAGTTTTAKGACAAAGAAAATTTTCTGAGTTACTTTTG    300 271:T/G; 286:TC/-;
    301 TATCYCCACCCCCTTAAAGAAAGGAGGAAAAACTGTTTCATACARAAGGCGTTAATTGCA    360 305:C/T; 345:G/A;
    361 TGAATTAGAGCTATCACCTAAGTGTGGGCTAATGTAACAAAGAGGGATTTCACCTACATC    420
    421 CATTCAGTCAGTCTTTGGGGGTTTAAAGAAATTCCAAAGAGTCATCAGAAGAGGAAAAAT    480
    481 GAAGGTAATGTTTTTTCAGACWGGTAAAGTCTTTGAAAATATGTGTAATATGTAAAACAT    540 502:A/T;
    541 TTTGACACCCCCATAATATTTTTCCAGAATTAACAGTATAAATTGCATCTCTTGTTCAAG    600
    601 AGTTCCCTATCACTCTCTTTAATCACTACTCACAGTAACCTCAACTCCTGCCACAATGTA    660
    661 CAGGATGCAACTCCTGTCTTGCATTGCACTAAGTCTTGCACTTGTCACAAACAGTGCACC    720
    721 TACTTCAAGTTCTACAAAGAAAACACAGCTACAACTGGAGCATTTACKKCTGGATTTACA    780 768:T/G; 769:G/T;
    781 GATGATTTTGAATGGAATTAATGTAAGTATATTTCCTTTCTTACTAAAATTATTACATTT    840
    841 AGTAATCTAGCTGGAGATCATTTCTTAATWACAATGCATTATACTTTCTTAGAATTACAA    900 870:A/T;
    901 GAATCCCAAACTCACCAGGATGCTCACATTTAAGTTTTACATGCCCAAGAAGGTAAGTAC    960
    961 AATATTTTAATGTTYAATTTCTGTTTTAATAAAATTCAAAGTAATATGAAAATTTGMACAG   1020 968:TA/-; 974:C/T; 1016:C/A;
   1021 ATGGGACTAATAGCAGCTCATCTGAGGTAAAGAGTAACTTTAATTTGTTTTTTTGAAAAC   1080
   1081 CCAAGTTTGATAATGAAGCCTCTATTAAAACAGTTTTACCTATATTTTTAATATATATTT   1140
   1141 GTGTGTTGGTGGGGGTGGGAAGAAAACATAAAAATAATATTCTCACTTTATCGATAAGAC   1200
   1201 AATTCTAAACAAAAATGTTCATTTATGGTTTCATTTAAAAATGTAAAACTCTAAAATATT   1260
   1261 TGATTATGTCATTTTAGTATGTAAWATACCAAAATCTATTTCCAAGGAGCCCACTTTTAA   1320 1285:A/T; 1319:A/-;
   1321 AAATCTTTTCTTGTTTTAGGAAAGGTTTCTAAGTGAGAGGCAGCATAACACTAATAGCAC   1380
   1381 AGAGTCTGGGGCCAGATATCTGAAGTGAAATCTCAGCTCTGCCATGTCCTAGCTTTCATG   1440
   1441 ATCTTTGGCAAATTACCYACTCTGTTTGTGATTCAGTTTCATGTCTACTTAAATGAATAA   1500 1458:T/C;
   1501 CTGTATATACTTAATATGGCTTTGTGAGAATTAGTAAGTAAATGTAAAGCACTCAGAACC   1560
   1561 GTGTCTGGCATAAGGTAAATACCATACAAGCATTAGCTATTATTAGTAGTATTAAAGATA   1620
   1621 AAATTTTCACTGAGAAATACAAAGTAAAATTTTGGACTTTATCTTTTTACCAAWAGAACT   1680 1674:T/A;
   1681 TGAGATTTATAATGCTATATGACTTATTTTCCAAGATTAAAAGCTTCATTAGGTTGTTTT   1740
   1741 TGGATTCAGATAGAGCATAAGCATAATCATCCAAGCTCCTAGGCTACATTAGGTGTGTAA   1800
   1801 AGCTACCTAGTAGYTGTGCCAGTTAAGAGAGAATGAACAAAATCTGGTGCCAGAAAGAGC   1860 1814:C/T;
   1861 TTGTGCCAGGGTGAATCCAAGCCCAGAAAATAATAGGATTTAAGGGGACACAGATGCAAT   1920
   1921 CCCATTGACTCAAATTCTATTAATTCAAGAGAAATCTGCTTCTAACTACCCTTCTGAAAG   1980
   1981 ATGTAAAGGAGACAGCTTACAGATGTTACTCTAGTTTAATCAGAGCCACATAATGCAACT   2040
   2041 CCARCAACATAAAGATACTAGATGCTGTTTTCTGAAGAAAATTTCTCCACATTGTTCAYG   2100 2044:G/A; 2099:T/C;
   2101 CCAAAAACTTAAACCYGAATTTGTAGAATTTGTAGTGGTGAATTGAAAGCGCAATAGATG   2160 2116:C/T;
   2161 GACATATCAGGGGATTGGTATTGTCTTGACCTACCTTTCCCACTAAAGAGTGTTAGAAAG   2220
   2221 ATGAGATTATGTGCATAATTTAGGGGGTGGTAGAATTCATGGAAATCTAAGTTTGAAACC   2280
   2281 AAAAGTAATGATAAACTCTATTCATTTGTTCATTTAACCCTCATTGCACATTTACAAAAG   2340
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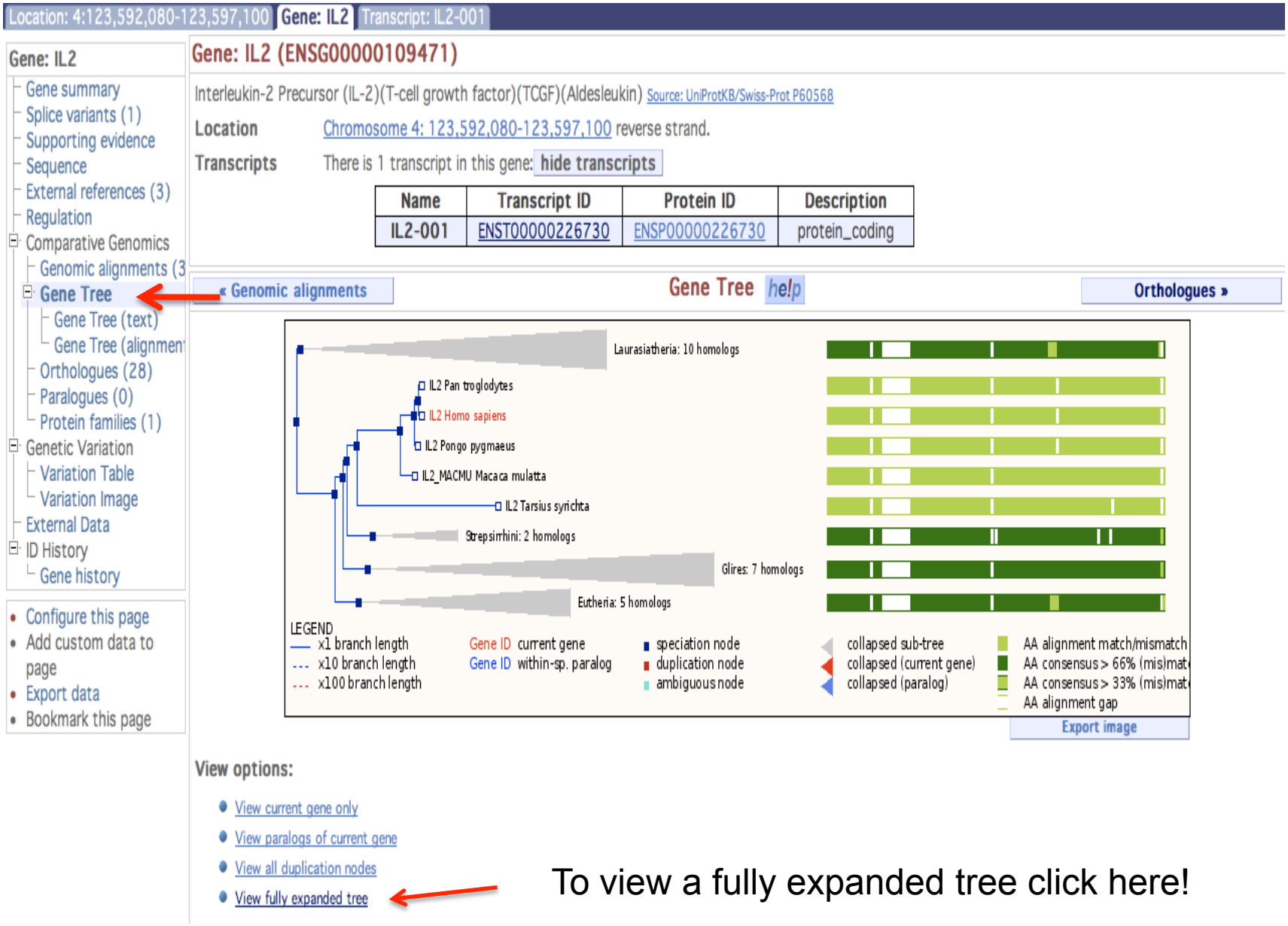
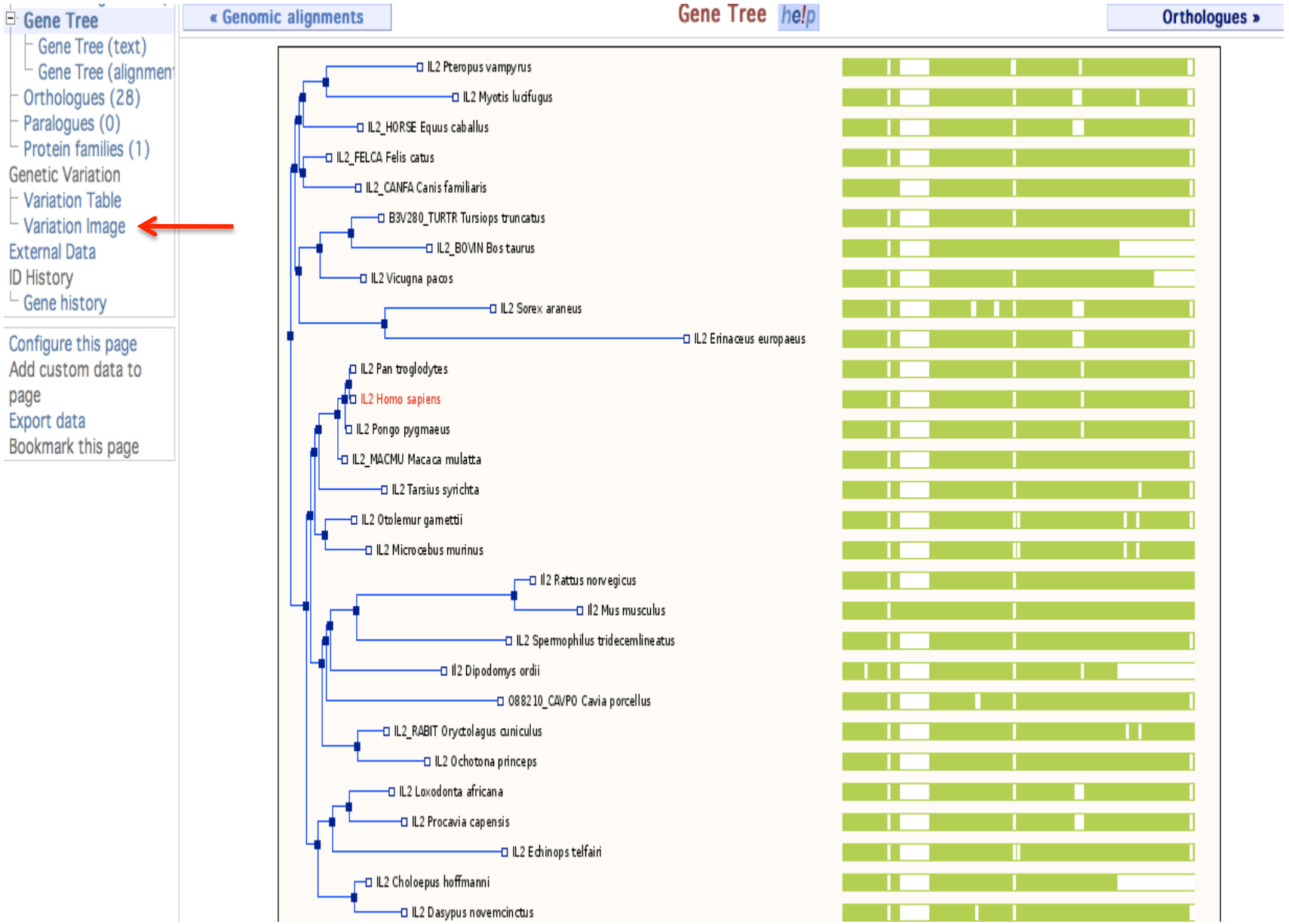
   2401 AAGAAATGAAATCTAATTCTGGCTCTACCTACTTATGTGGTCAAATTCTGAGATTTAGTG   2460
   2461 TGCTTATTTATAAAGTGGAGATGATACTTCACTGCCTACTTCAAAAGATGACTGTGAGAA   2520
   2521 GTAAATGGGCCTATTTTSGAGAAAATTCTTTTAAATTGTAATATACCATAGAAATATGAA   2580 2538:G/C;
   2581 ATATTATATATAATATAGAATCAAGAGGCCTGTCCAAAAGTCCTCCCAAAGTATTATAAT   2640
   2641 YTTTTATTTCACTGGGACAAACATTTTTAAAATGCATCTTAATGTAGTGATTGTAGAAAA   2700 2641:T/C; 2696:-/A;
```

Now let's click on **Gene Tree** which will display the current gene in the context of a phylogenetic tree of orthologues and paralogues genes.

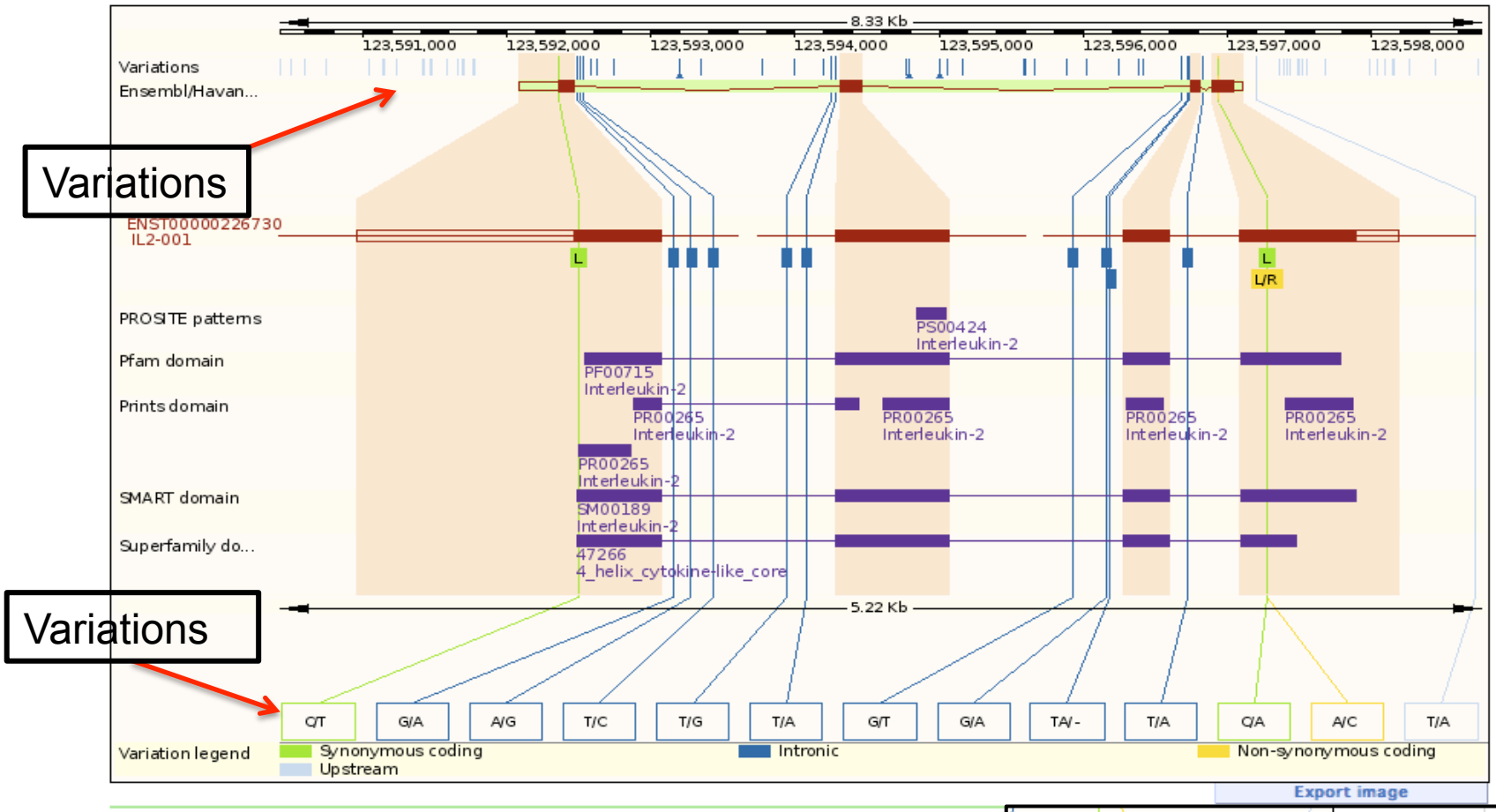


To view a fully expanded tree click here!

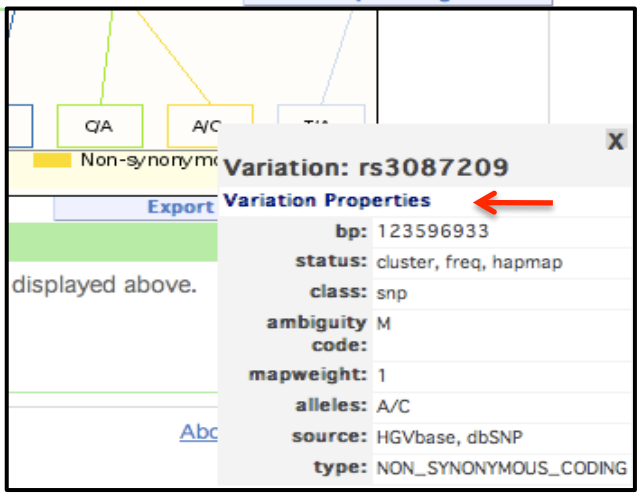
Now lets take another look at genetic variation. Click **Variation Image**.

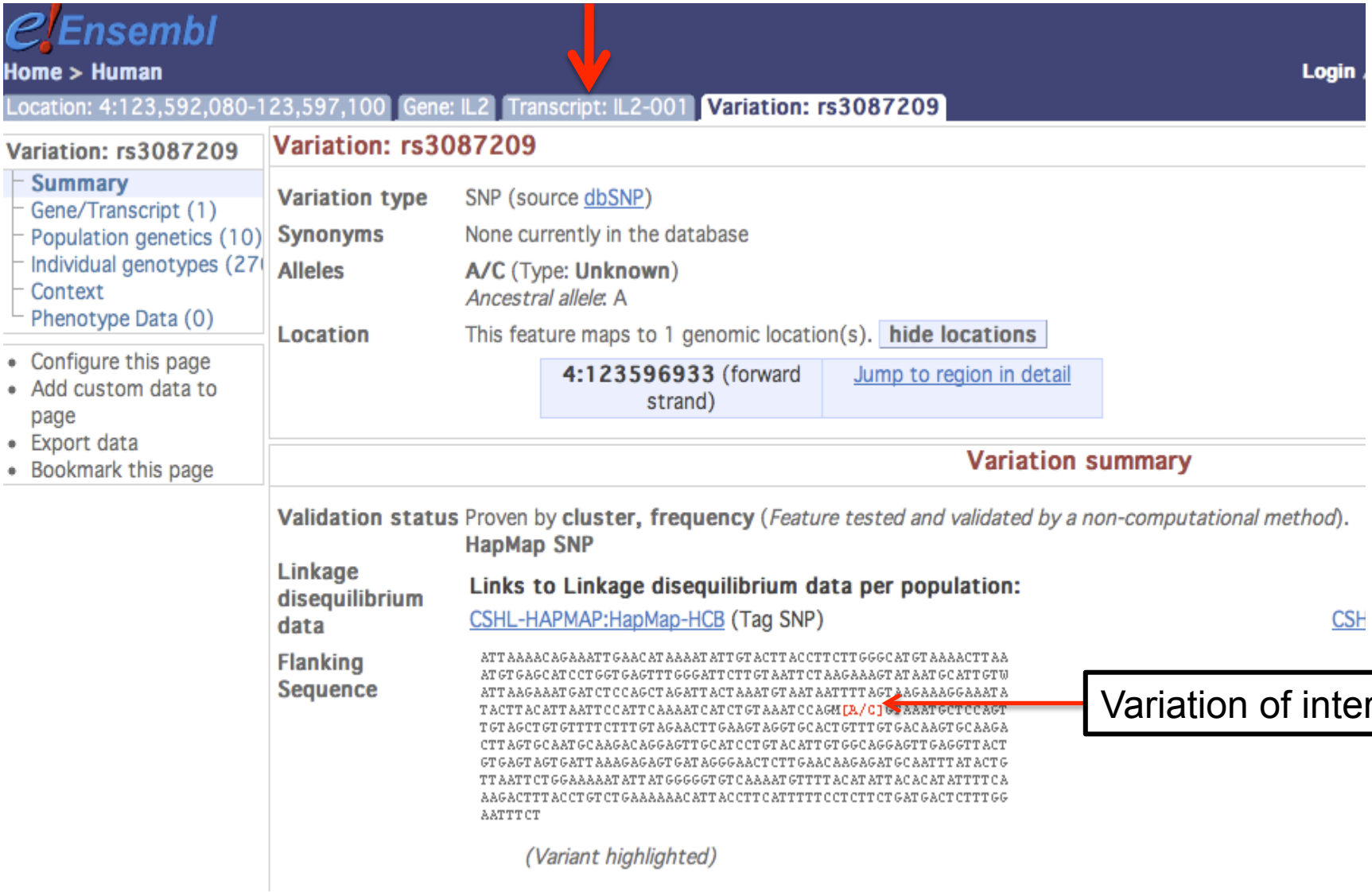


« Variation Table | Variation Image help | External Data »



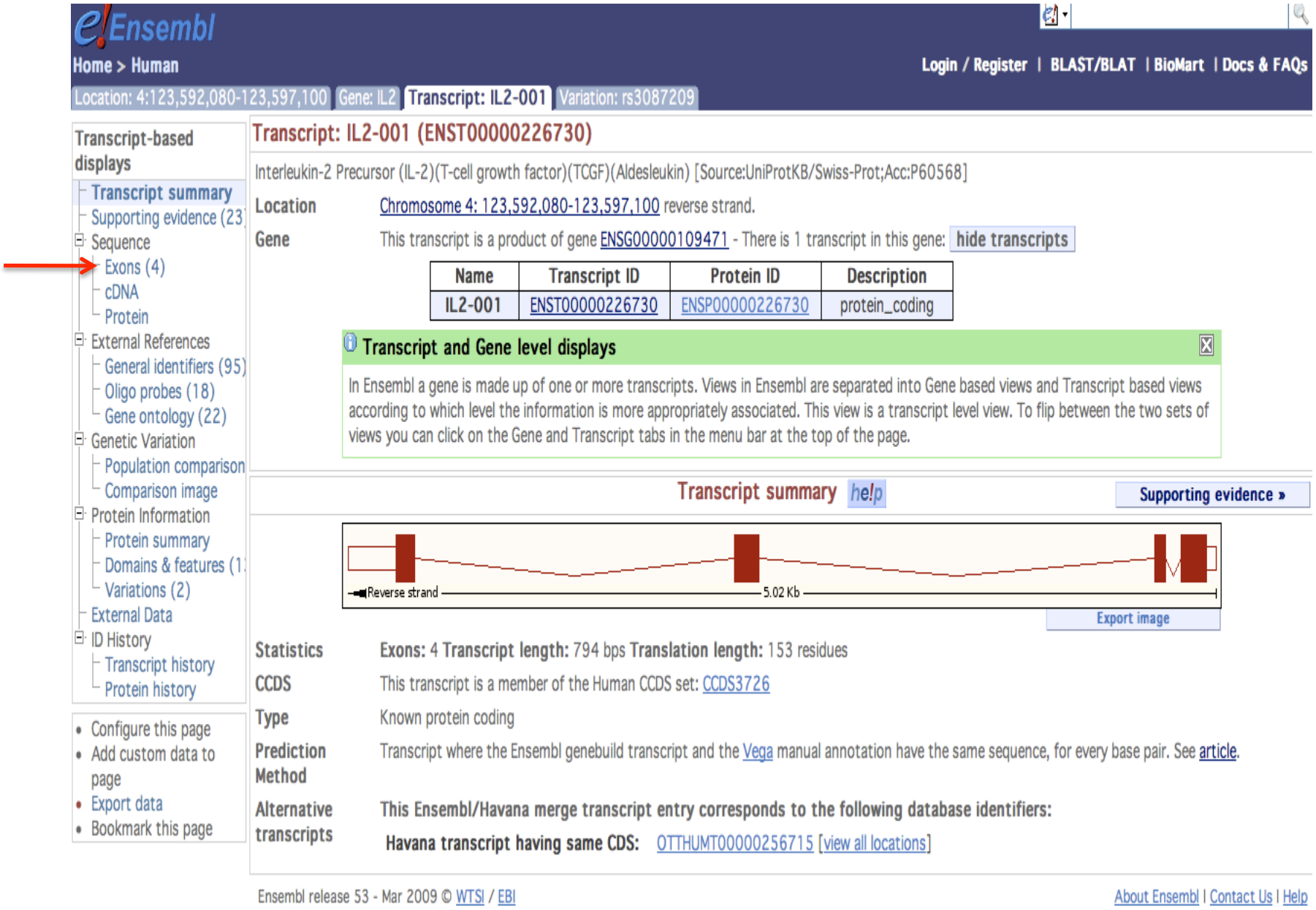
Click at the only non-synonymous coding SNP and then **Variation properties** to learn more about it.

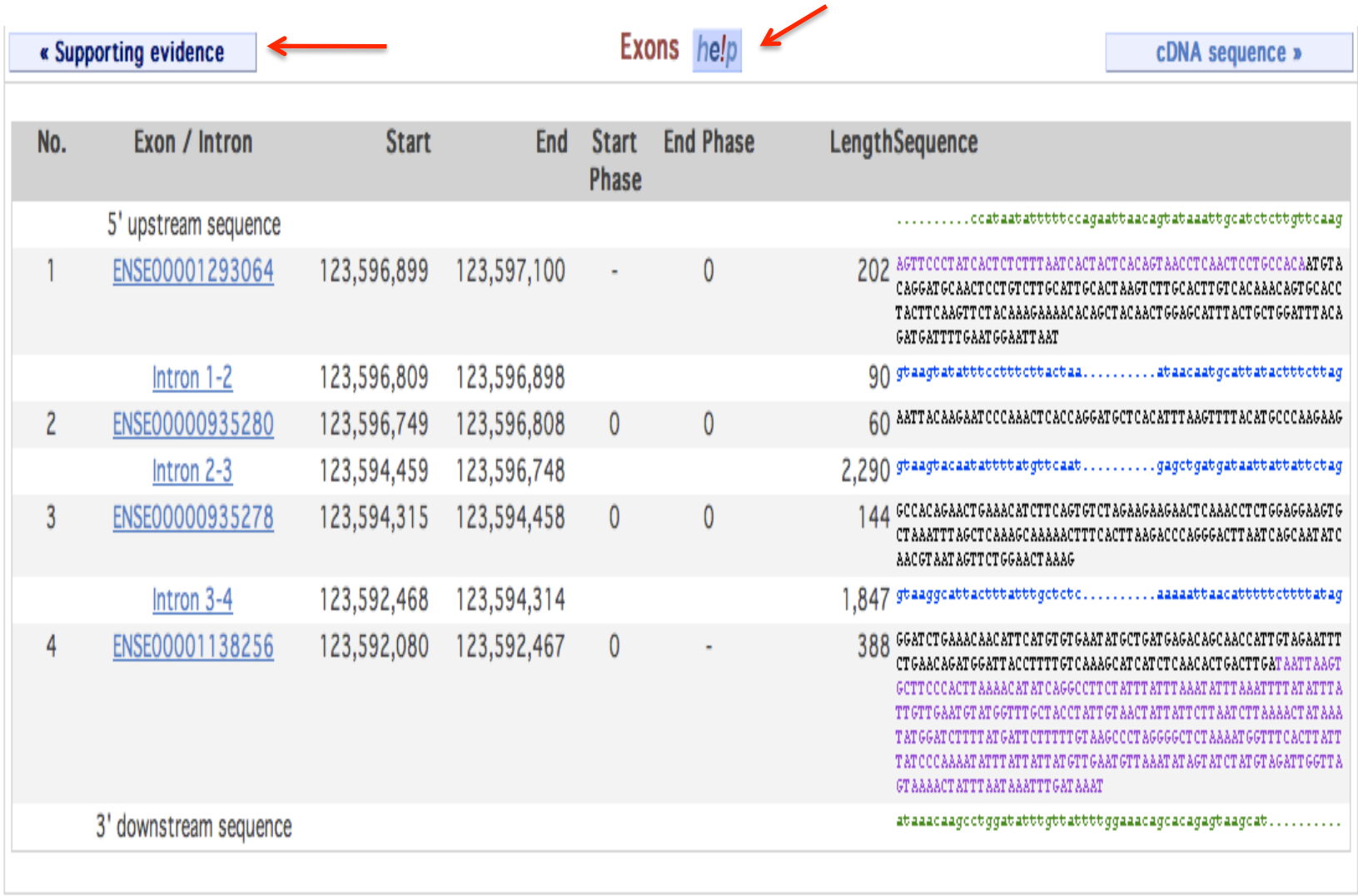




Next let's focus on one transcript. Select the transcript from the header section by clicking on the Transcript tab for IL2 marked with a red arrow above.

This is the transcript summary display. Now lets lock in more detail at the exons.



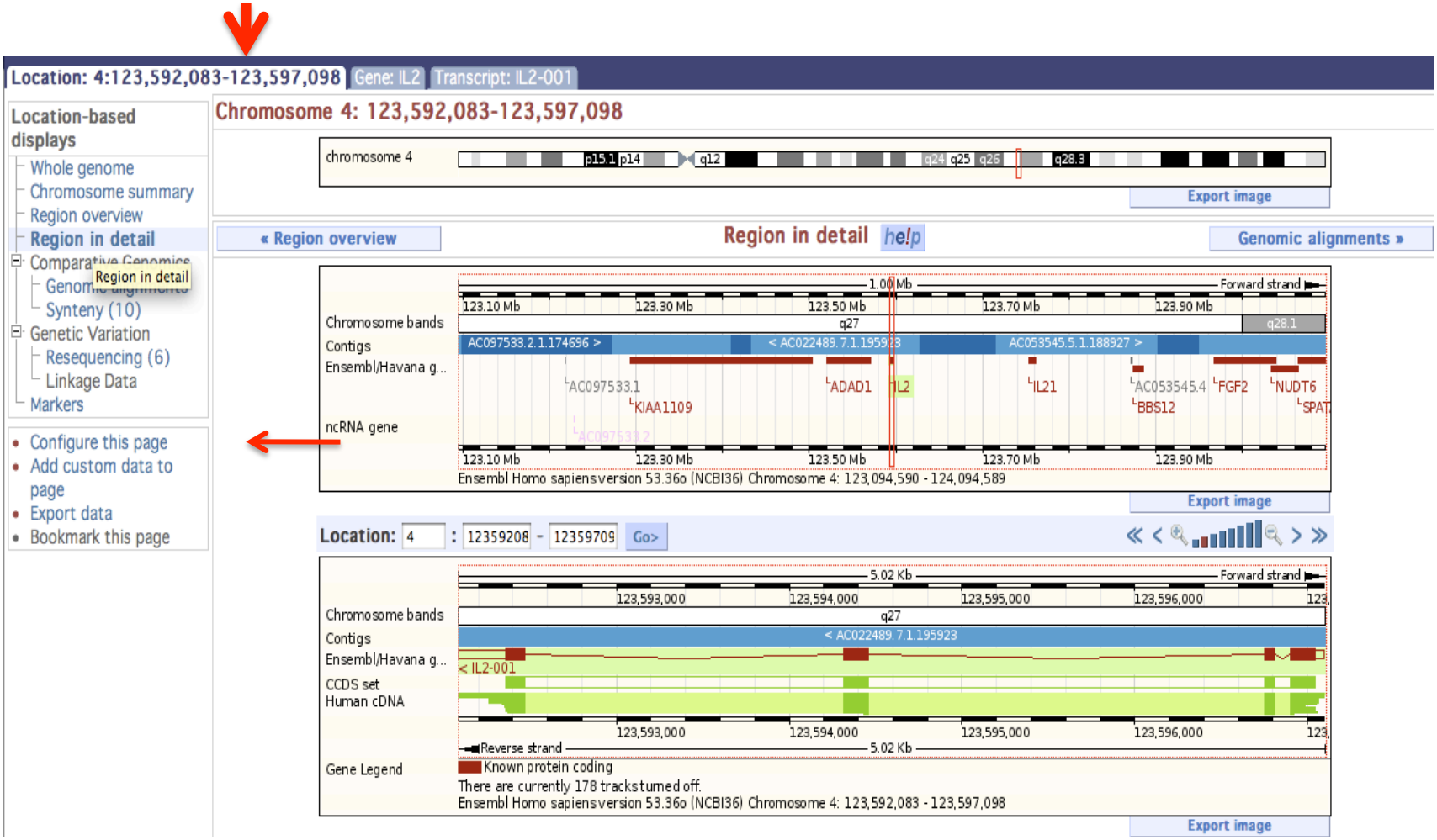


If you would like to see more of the introns and the flanking sequences you can use **Configure this page.** If you want to find out what the different colors mean click the **Help** button. Finally follow the link for **Supporting evidence.**

Red boxes:
Exons in the
Ensembl transcript

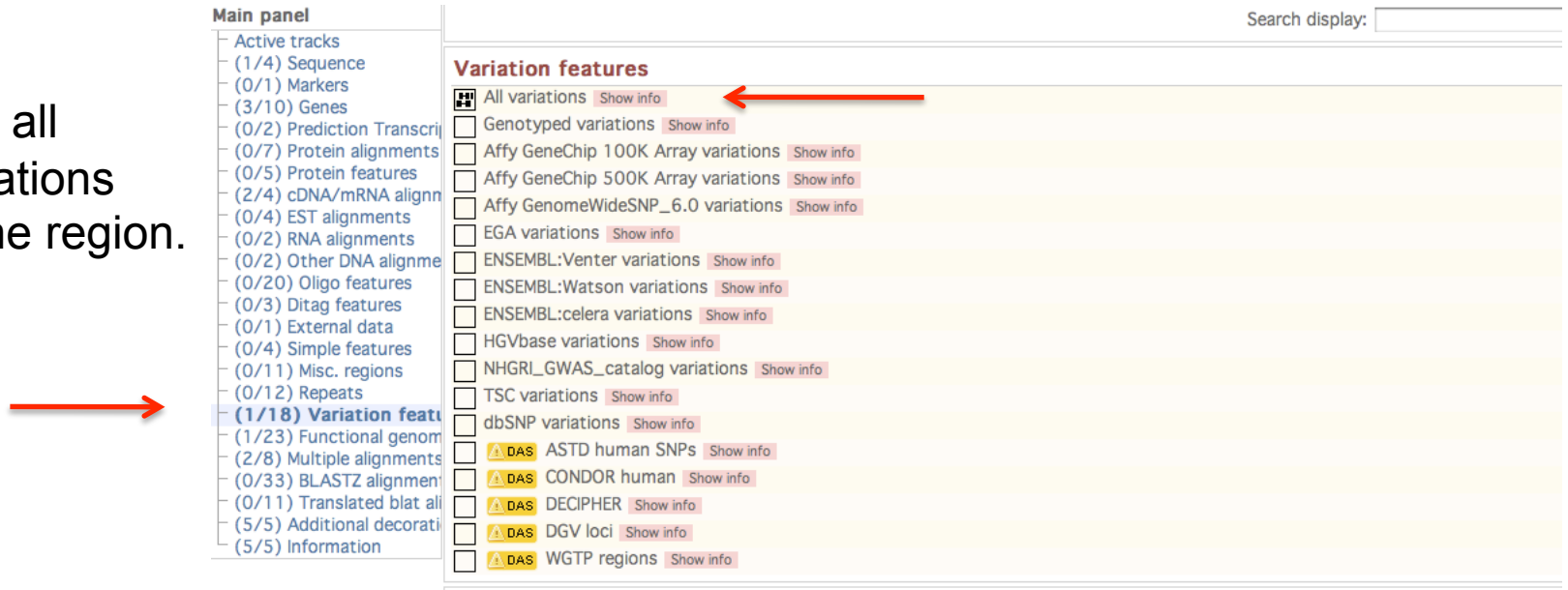
Alignment of cDNA
and proteins to the
Ensembl exons.

Let’s now look at the genomic region for this gene by clicking onto the **Location tab**

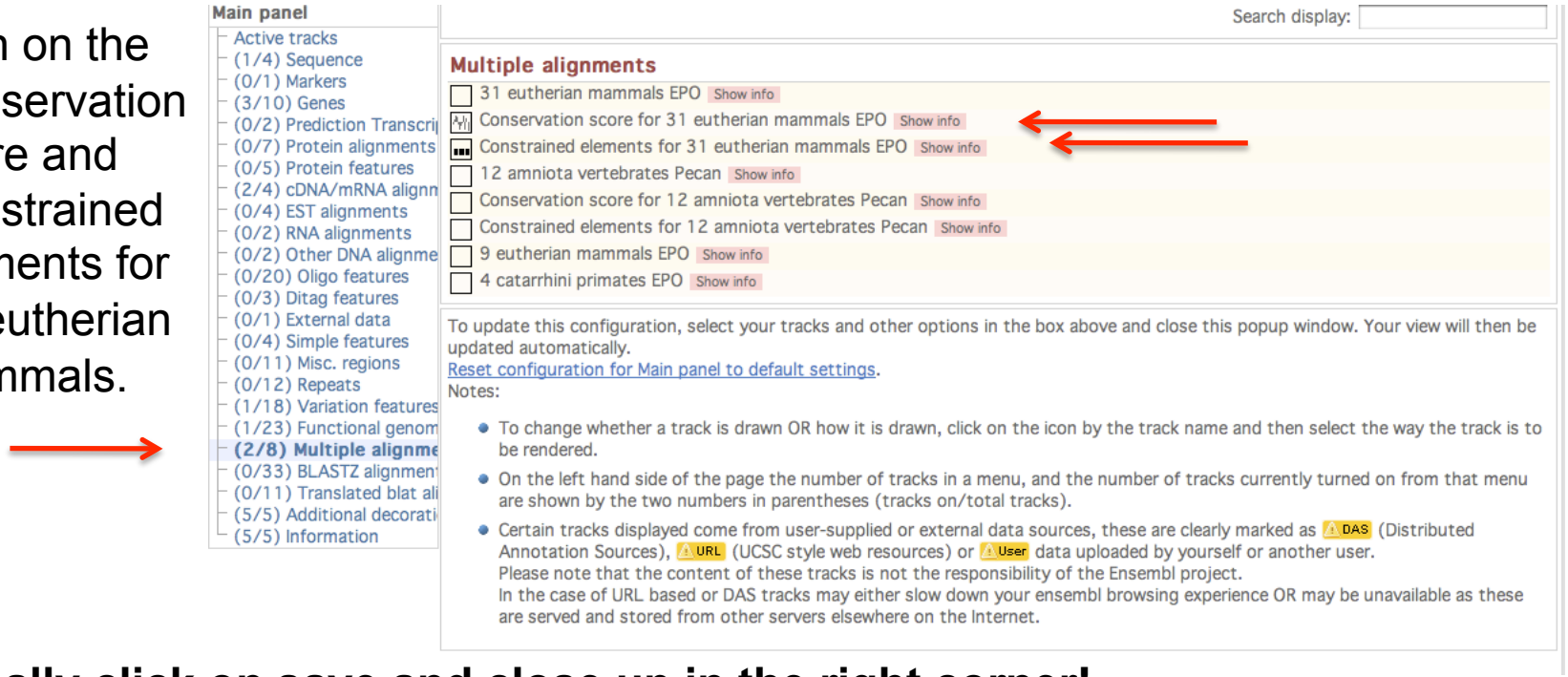


Ensembl Location displays are highly configurable. You can switch on additional tracks displaying various features. **Click Configure this page** now.

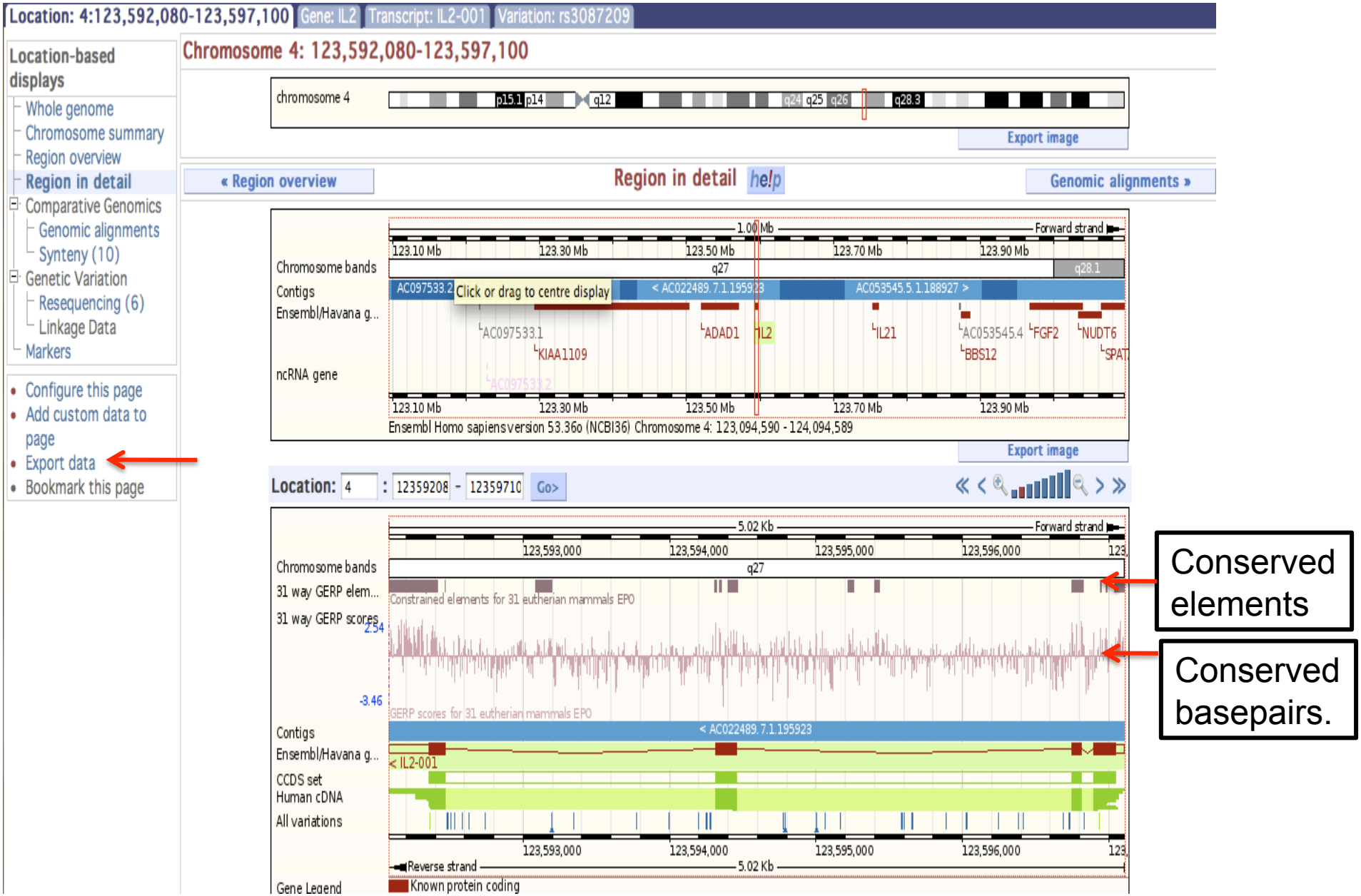
Add all variations to the region.

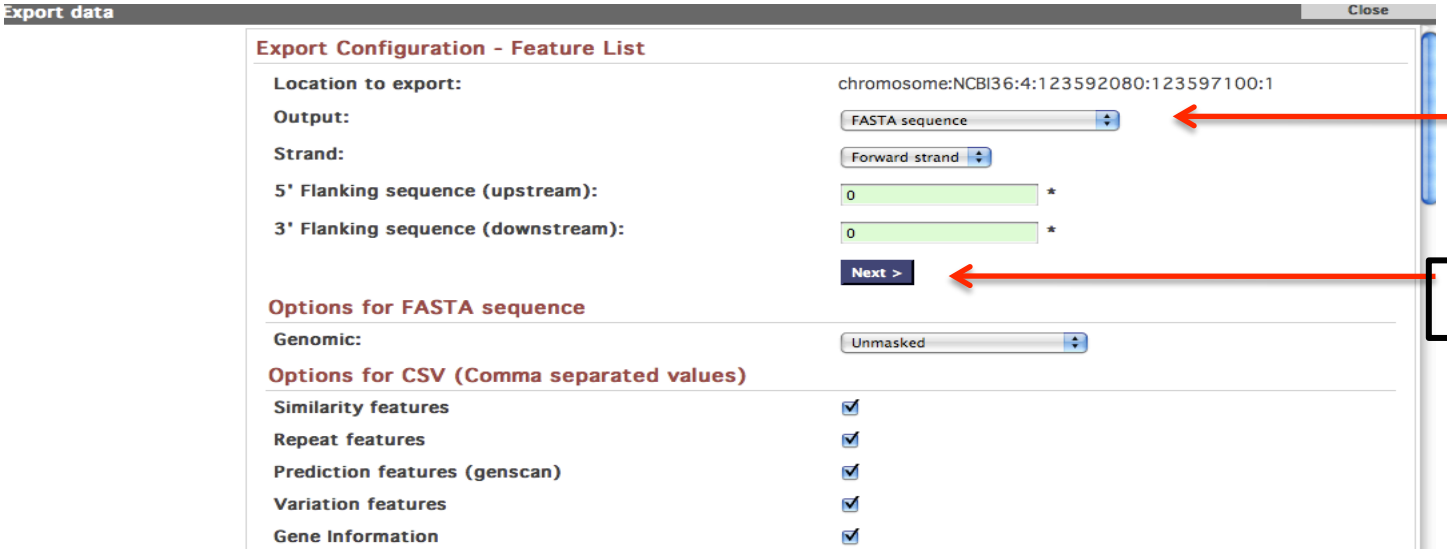


Turn on the Conservation score and Constrained elements for 31 eutherian mammals.



Finally click on save and close up in the right corner!


Location: 4:123,592,080-123,597,100
Gene: IL2
Transcript: IL2-001
Variation: rs3087209
Location-based displays
Whole genome
Chromosome summary
Region overview
Region in detail
Comparative Genomics
Genomic alignments
Synteny (10)
Genetic Variation
Resequencing (6)
Linkage Data
Markers
Configure this page
Add custom data to page
Export data
Bookmark this page
Chromosome 4: 123,592,080-123,597,100
chromosome 4
Export image
« Region overview
Region in detail help
Genomic alignments »
1.00 Mb
Forward strand
Chromosome bands
Contigs
Ensembl/Havana g...
ncRNA gene
Click or drag to centre display
Ensembl Homo sapiens version 53.36o (NCBI36) Chromosome 4: 123,094,590 - 124,094,589
Location: 4 : 12359208 - 12359710 Go>
5.02 Kb
31 way GERP elem...
31 way GERP scores
Constrained elements for 31 eutherian mammals EPO
GERP scores for 31 eutherian mammals EPO
CCDS set
Human cDNA
All variations
Reverse strand
Gene Legend
Known protein coding
Conserved elements
Conserved basepairs.



Select the FASTA sequence format

Click Next

Choose Text

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>4 dna:chromosome chromosome:NCBI36:4:123592080:123597100:1
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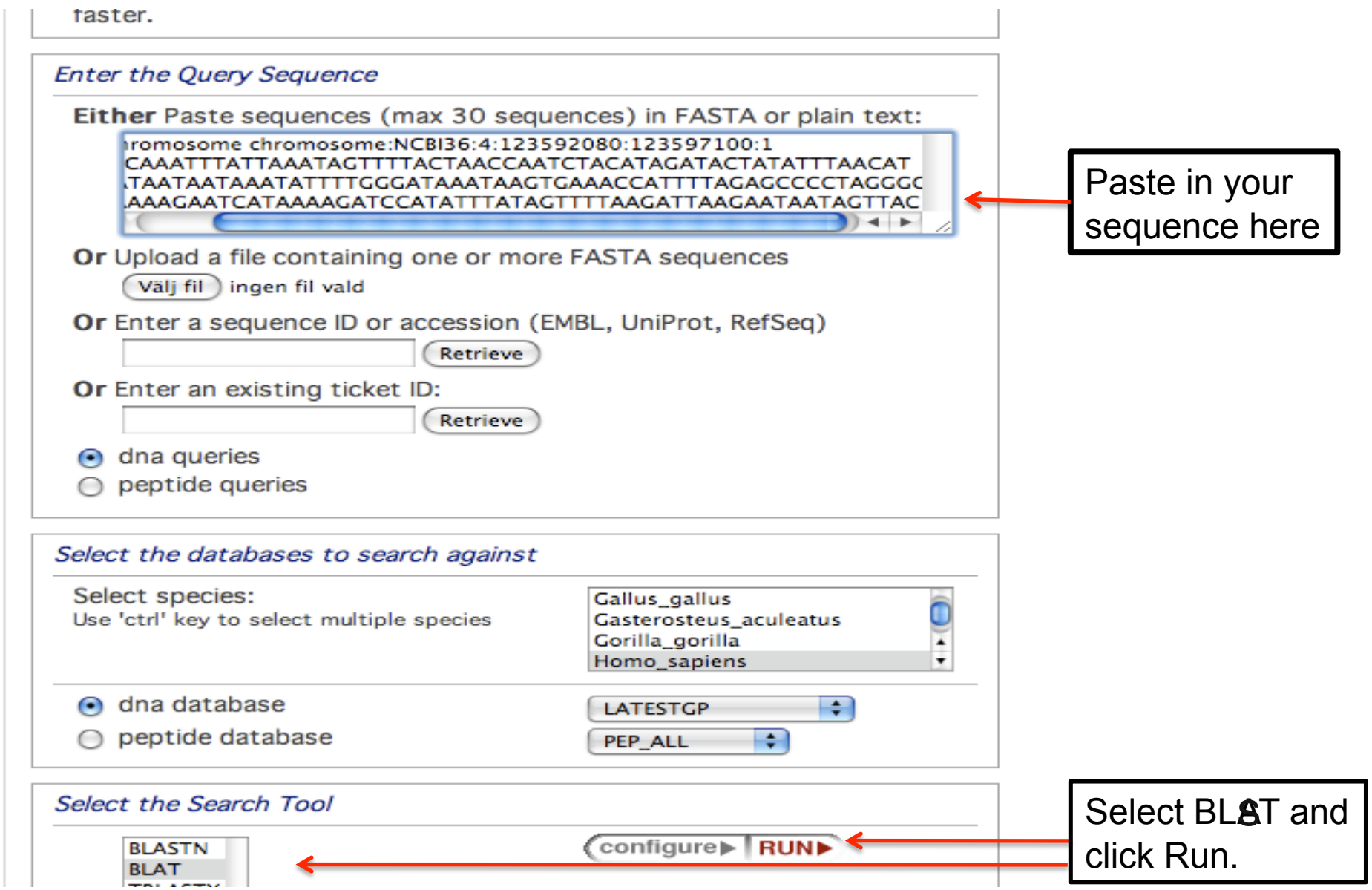
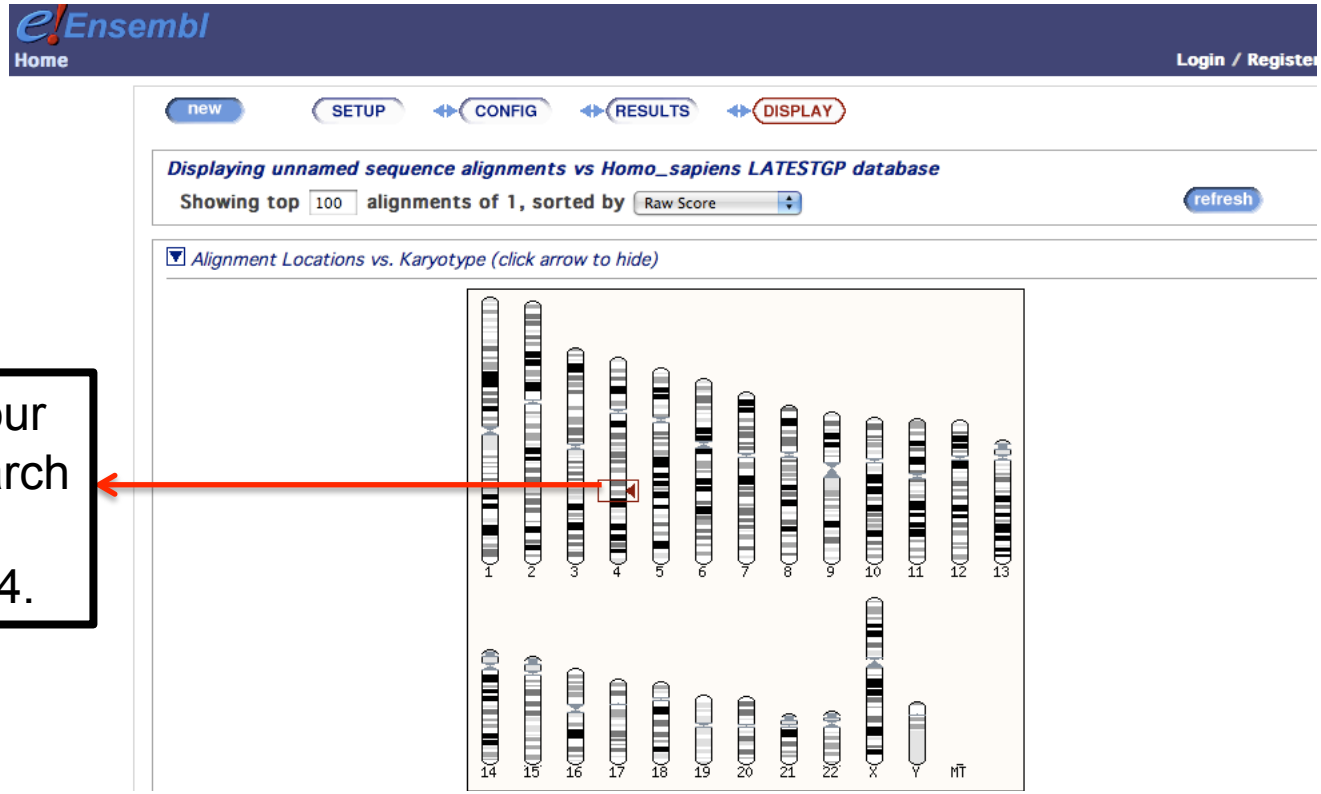
CATAATTGTTTAAATATTGTCATATCTTGGGATTTTTTTATTTTAAAAAGTGTTTGGCTT
TTGAAACACAGTTTTCAGATTTTTGCATGGTTTTGTCTTAAATTTGTATCAAGAGTTAAG
AATGAGTTTTCTGATGTTAATTATTTTAGAGTAAAACTCTTGCCATAGATAAGGAACTGA
```

Copy the header and a few lines of sequence and then follow the **BLAST/BLAT** link in the bar at the top of the page.


faster.
Enter the Query Sequence
Either Paste sequences (max 30 sequences) in FASTA or plain text:
romosome chromosome:NCBI36:4:123592080:123597100:1
CAAATTTATTAAATAGTTTTACTAACCAATCTACATAGATACTATATTTAACAT
TAATAATAAATATTTTGGGATAAATAAGTGAAACCATTTTAGAGCCCCTAGGGC
AAAGAATCATAAAAGATCCATATTTATAGTTTTAAGATTAAGAATAATAGTTAC
Or Upload a file containing one or more FASTA sequences
Välj fil
ingen fil vald
Or Enter a sequence ID or accession (EMBL, UniProt, RefSeq)
Retrieve
Or Enter an existing ticket ID:
Retrieve
dna queries
peptide queries
Paste in your sequence here
Select the databases to search against
Select species:
Use 'ctrl' key to select multiple species
Gallus_gallus
Gasterosteus_aculeatus
Gorilla_gorilla
Homo_sapiens
dna database
LATESTGP
peptide database
PEP_ALL
Select the Search Tool
BLASTN
BLAT
configure▶
RUN▶
Select BLAT and click Run.



Location of your sequence search marked at chromosome 4.

Alignment Summary (click arrow to hide)

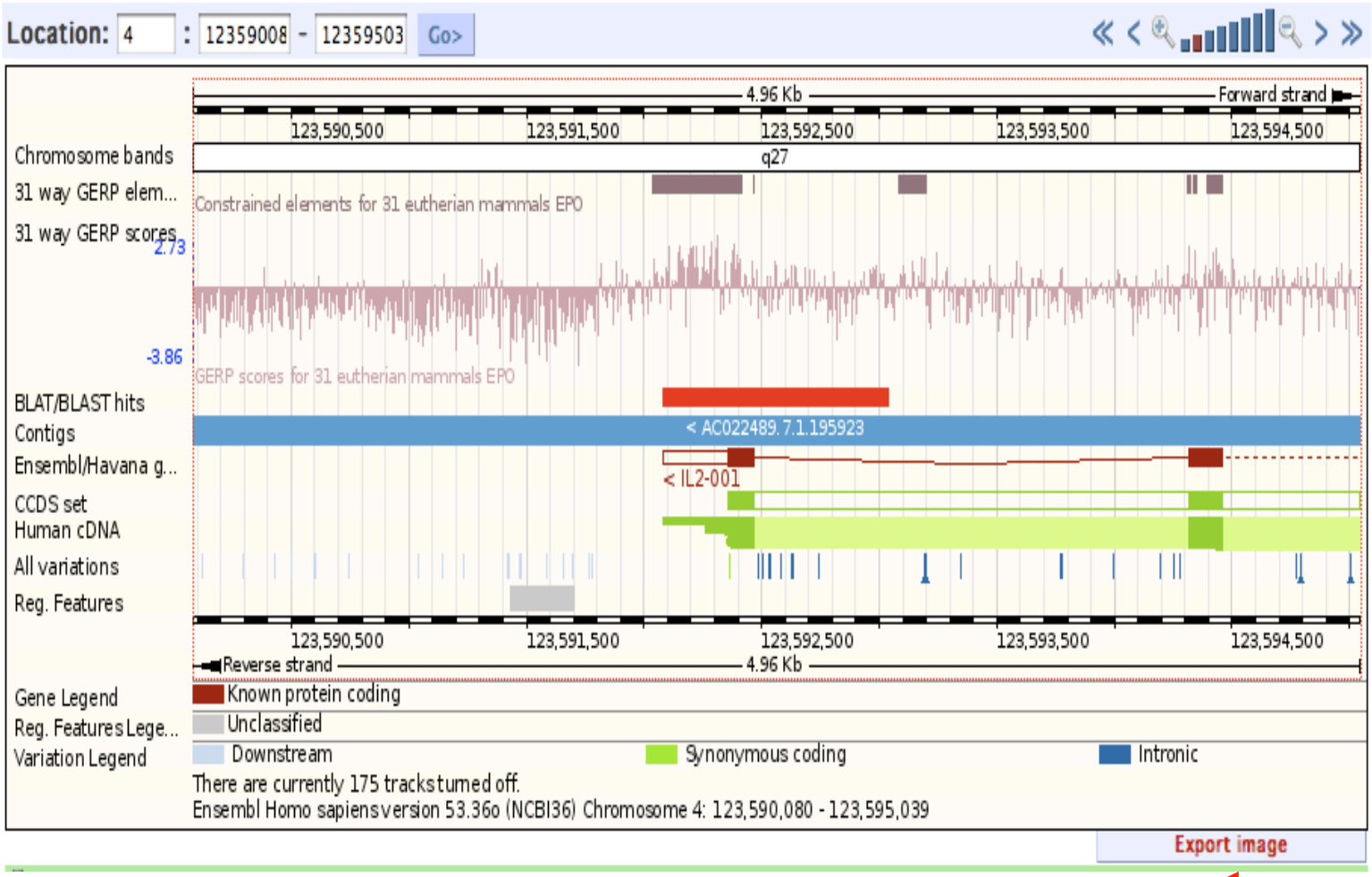
Select rows to include in table, and type of sort
(Use the 'ctrl' key to select multiples)

refresh

Query	Subject	Chromosome	Supercontig	Clone	Contig	Chromosome	Stats	Sort By
off	_off_	_off_	_off_	_off_	_off_	_off_	_off_	<Chromosome
Name	Name	Name	Name	Name	Name	Name	Score	>Chromosome
Start	Start	Start	Start	Start	Start	Start	E-val	<Score
End	End	End	End	End	End	End	P-val	>Score

Links	Query			Chromosome				Chromosome				Stats			
	Start	*End*	*Ori*	*Name*	*Start*	*End*	*Ori*	*Name*	*Start*	*End*	*Ori*	*Score*	*E-val*	*%ID*	*Length*
[A] [S] [G] [C]	28	987	+	Chr:4	123592080	123593039	+	Chr:4	123592080	123593039	+	4726	0.0e+00	100.00	960

Click at [C] to see the corresponding location view.



Note that you can export the image using the link at the buttom.