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Search: for

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NCB006 
-  **Mouse**
NCBIM37
-  **Zebrafish**
ZFISH7

All genomes

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and export sequences or tables in text, html, or Excel format

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What's New in Release 53 (4 March 2009)

- [New species - Taeniopygia guttata](#) (Zebra finch)
- [New species - Anolis carolinensis](#) (Anole lizard)

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

e/Ensembl
Home > Human

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About this species

- Description
- Genome Statistics
 - Assembly and Genebuild
 - Top 40 InterPro hits
 - Top 500 InterPro hits
- What's New
- Sample entry points
 - Karyotype
 - Location (AL032821.2)
 - Gene (BRCA2)
 - Transcript (FOXP2-203)

- Configure this page
- Add custom data to page
- Export data
- Bookmark this page

Search Ensembl Human

Search for: Go
e.g. gene BRCA2 or AL032821.2.1.143563 or muscular dystrophy

Description [Assembly and Genebuild »](#)

Assembly



This release is based on the NCBI 36 assembly of the [human genome](#) [November 2005]. The data consists of a reference assembly of the complete genome plus the Celera WGS and a number of alternative assemblies of individual haplotypic chromosomes or regions. [Full list of assemblies →](#)

The International Human Genome Sequencing Consortium have published their scientific analysis of the finished human genome.

- [Nature 431, 931 - 945 \(21 October 2004\)](#)
- [WT Sanger Institute Press Release](#)

Annotation

Since release 38 (April 2006) the gene annotation presented has been a combined Ensembl-[Havana](#), geneset which incorporates more than 18,000 full-length protein-coding transcripts annotated by the Havana team with the Ensembl automatic gene build. The human genome sequence is now considered sufficiently stable that since 2004 the major genome browsers have come together to produce a common set of identifiers where CDS annotations of transcripts can be agreed and these identifiers are also shown.

- More information about the [CCDS project](#).

The [ENCODE](#) (ENCyclopedia Of DNA Elements) project aims to find functional elements in the human genome.

- More information about the [ENCODE resources](#) at Ensembl.

Vega* Additional manual annotation of this genome can be found in [Vega](#)

Select the Ensembl gene ENSG00000109471.

 Home > Human Login / Register | BLAST/BLAT | BioMart | Docs & FAQ

Genome

Search Ensembl

- Feature type (7)
 - Gene (6)
 - Homo sapiens (6)
 - SNP (1)
 - Homo sapiens (1)
- Species (1)
 - Homo sapiens (7)
 - Gene (6)
 - SNP (1)

- Configure this page
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Ensembl text search

Your query matched 7 entries in the search database

[Ensembl protein_coding Gene: ENSG00000109471 \(HGNC \(curated\): IL2\)](#) [\[Region in detail\]](#)

Ensembl protein_coding gene ENSG00000109471 has 1 transcript: ENST00000226730, associated peptide: ENSP00000226730 and 4 exons: ENSE00000935278, ENSE00000935280, ENSE00001138256, ENSE00001293064

Interleukin-2 Precursor (IL-2)(T-cell growth factor)(TCGF)(Aldesleukin) [Source:UniProtKB/Swiss-Prot;Acc:P60568]

The gene has the following external identifiers mapped to it:

Affymx Microarray Focus: 207849_at
Affymx Microarray HCG110: 1538_s_at
Affymx Microarray HuGeneFL: S77835_s_at, X00695_s_at
Affymx Microarray Human Exon 1.0 ST v2: 2784269, 2784268, 2784272, 2784270, 2784266, 2784267
Affymx Microarray Human Gene 1.0 ST: 8102697
Affymx Microarray U133: 207849_at, g10835148_3p_at
Affymx Microarray U95: 34021_at, 1538_s_at
Agilent Probe: A_23_P30115, A_23_P30122
CCDS: CCDS3726, CCDS3726.1
EMBL: U25676, BC070338, AF031845, S82692, AB451325, AF532913, BC066257, V00564, DQ231169, DQ861285, X01586, BC066256, AB451454, CH471056, X00695, S77835, J00264, AY283686, AF359939, AF228636, BC066254, K02056, S77834, BC066255, M22005, M13879, AY523040, M33199
EntrezGene: lymphokine, IL-2, TCGF, 3558, **IL2**
GE Healthcare/Amersham Codelink WGA: GE902998
GO: GO:0008083, GO:0005615, GO:0050672, GO:0030307, GO:0050728, GO:0051024, GO:0005515, GO:0005576, GO:0005134, GO:0042104, GO:0019209, GO:0005125, GO:0006916, GO:0007267, GO:0030101, GO:0042523, GO:0048304, GO:0045944, GO:0006955, GO:0030217, GO:0046013, GO:0008284
Havana transcript having same CDS: OTTHUMT00000256715
HGNC (curated): **IL2**-001, **IL2**, 6001
HGNC Symbol: IL-2, **IL2**, 6001
Human Protein Atlas: 10310, CAB010310
Illumina V1: GI_28178860-S
Illumina V2: ILMN_9283
IPI: IPI00003099.2, IPI00003099

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

Gene: IL2 (ENSG00000109471)
Interleukin-2 Precursor (IL-2)(T-cell growth factor)(TCGF)(Aldesleukin) [Source: UniProtKB/Swiss-Prot P60568](#)

Location [Chromosome 4: 123,592,080-123,597,100](#) reverse strand.

Transcripts There is 1 transcript in this gene: [hide transcripts](#)

Name	Transcript ID	Protein ID	Description
IL2-001	ENST00000226730	ENSP00000226730	protein_coding

Gene summary [help](#) [Splice variants »](#)

Name [IL2](#) (HGNC (curated))

Synonyms IL-2 [To view all Ensembl genes linked to the name [click here](#).]

CCDS This gene is a member of the Human CCDS set: [CCDS3726](#)

Gene type Known protein coding

Prediction Method Gene containing both Ensembl genebuild transcripts and [Havana](#) manual curation, see [article](#).

Transcripts

Export image

Configuring the display

Tip: use the "Configure this page" link on the left to show additional data in this region.

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



Ensembl Home > Human Location: 4:123,592,080-123,597,100 Gene: IL2 Transcript: IL2-001 Login / Register | BLAST/BLAT | BioMart | Docs & FA

Gene: IL2

- Gene summary
- Splice variants (1)
- Supporting evidence**
- Sequence
- External references (3)
- Regulation
- Comparative Genomics
 - Genomic alignments (3)
- Gene Tree
 - Gene Tree (text)
 - Gene Tree (alignments)
- Orthologues (28)
- Paralogues (0)
- Protein families (1)

Genetic Variation

- Variation Table
- Variation Image

External Data

ID History

- Gene history

- Configure this page
- Add custom data to page
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Gene: IL2 (ENSG00000109471)

Interleukin-2 Precursor (IL-2)(T-cell growth factor)(TCGF)(Aldesleukin) [Source: UniProtKB/Swiss-Prot P60568](#)

Location [Chromosome 4: 123,592,080-123,597,100](#) reverse strand.

Transcripts There is 1 transcript in this gene: [hide transcripts](#)

Name	Transcript ID	Protein ID	Description
IL2-001	ENST00000226730	ENSP00000226730	protein_coding

[« Splice variants](#) **Supporting evidence** [help](#) [Marked-up sequence »](#)

Transcript	CDS support	UTR support	Exon support
ENST00000226730 [view evidence]	[align] CCDS3726 [align] NP_000577.2	[align] NM_000586.3	20 features

Ensembl release 53 - Mar 2009 © [WTSI](#) / [EBI](#) [About Ensembl](#) | [Contact Us](#) | [Feedback](#)

[Permanent link](#) - [View in archive site](#)

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

The screenshot shows a web application interface with a top navigation bar containing 'Configure page', 'Custom Data', 'Your account', and a circled 'SAVE and close' button. A left sidebar has 'Configure view' and 'Configure'. The main content area is titled 'Configuration for: "Marked up gene sequence"'. It contains several settings: '5' Flanking sequence (upstream):' and '3' Flanking sequence (downstream):' both set to 600; 'Number of base pairs per row:' set to 60 bps; 'Additional exons to display:' set to 'Core exons'; 'Orientation of additional exons:' set to 'Display exons in both orientations'; 'Show variations:' set to 'Yes and show links' (indicated by a red arrow and a box labeled 'Display variations'); and 'Line numbering:' set to 'Relative to this sequence' (indicated by a red arrow and a box labeled 'Turn on line numbering'). Below these settings is a section for 'DAS sources' with a list of checkboxes and links: 'ArrayExpress Warehouse', 'cbs_func', 'cbs_ptm', 'cbs_sort', 'GAD', and 'HGNC'.

Configuration for: "Marked up gene sequence"

5' Flanking sequence (upstream): 600 *

3' Flanking sequence (downstream): 600 *

Number of base pairs per row: 60 bps

Additional exons to display: Core exons

Orientation of additional exons: Display exons in both orientations

Show variations: Yes and show links

Line numbering: Relative to this sequence

Display variations

Turn on line numbering

SAVE and close

DAS sources

- ArrayExpress Warehouse**
Gene expression profile thumbnails from the ArrayExpress warehouse [[Homepage](#)]
- cbs_func**
CBS Protein function and structure predictions [[Homepage](#)]
- cbs_ptm**
CBS Post-translational modification site predictions [[Homepage](#)]
- cbs_sort**
CBS Protein sorting predictions [[Homepage](#)]
- GAD**
Genetic Association Database - association of diseases to human Entrez genes. [[Homepage](#)]
- HGNC**
The HGNC (HUGO Gene Nomenclature Committee) DAS Reference Server serves up-to-date approved gene symbols and

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
1 TTAATTAAAATAGCGTTAAACAATACCTCAAGCTCAATAAACATTTTAAAGTATTCTAAT 60 24:G/A;
51 CTTAGTATTTCTCTAGCTGACATGTAAAGAACATCTATCTTATTGTATGCAATTAGCTC 120
121 ATTGTGTGGATAAAAAGGTAAAACCATTCTAAAACAGGAAACCATACACTTCCTGTTT 180 151:G/C; 180:T/A;
181 ATCAACAAATCTAAACATTTATTCTTTTCTCTGTTTACTCTTGCTCTTGTCCACCACAA 240 205:TTTT/-;
241 TATGCTATTACATGTTCAAGTGTAGTTTTAGGACAAAAGAAAATTTCTTGAGTTACTTTTG 300 271:T/G; 286:TC/-;
301 TATCTCCACCCCTTAAAGAAAAGGAGGAAAACTGTTTCTATACAAAGGCCTTAATTGCA 360 305:C/T; 345:G/A;
361 TGAATTAGAGCTATCACCTAAGTGTGGGCTAATGTAAACAAAAGAGGGATTTACCTACATC 420
421 CATTCACTCAGTCTTTGGGGGTTTAAAGAAATCCAAAGAGTCAATCAGAAGAGGAAAAAT 480
481 GAAAGTAAATGTTTTTTCAGACTGGGTAAAGTCTTTGAAAATATGTGTAAATATGTAAAACAT 540 502:A/T;
541 TTTGACACCCCATAAATTTTTCCAGAATTAAACAGTATAAATTGCATCTCTTGTCAAG 600
601 AGTTCCCTATCACTCTCTTTTAACTCACTACTCACAGTAACTCBACTCCTGCCACAAATGTA 660
661 CAGGATGCACTCCTGTCTTGCACTTGCCTAAAGTCTTGCACTTGTCACTAACTGCACTC 720
721 TACTTCAAGTTCTACAAAGAAAACACAGCTCACTCACTGAGGCACTTTACTGCTGGATTTACA 780 768:T/G; 769:G/T;
781 GATGATTTTGAATGGAATTAATGTAAATATTTCTTTCTACTAAATTTATTACATTT 840
841 AGTAACTCTAGCTGGAGATCAATTTCTTAAATGACAAATGCATTAATCTTTCTTAAATTA 900 870:A/T;
901 GAATCCCACTCACCAGGATGCTCACTTTAAGTTTTACTATGCCCAAGGAGGTAAATAC 960
961 AATATTTCTGTTTAAATTTCTGTTTTAAATAAAATCAAAGTAAATATGAAAATTTGACAG 1020 968:TA/-; 974:C/T; 1016:C/A;
1021 ATGGGACTAATAGCAGCTCATCTGAGGTAAAGAGTAACTTTAATTTGTTTTTTTAAAAAC 1080
1081 CCAAGTTTGAATAAAGGCTCTATTAAAACAGTTTTACCTATATTTTTAAATATATATTT 1140
1141 GTGTGTTGGTGGGGGTGGGAAGAAAACATAAAAATAAATATTCTCACTTTATCGATAAAG 1200
1201 AATCTAAACAAAATGTTCAATTTAGGTTTTCAATTTAAAATGTAAAATCTAAAATATT 1260
1261 TGATTATGTCAATTTAGTATGTAATATACAAAATCTATTTCCAAAGGACCCACTTTTAA 1320 1285:A/T; 1319:A/-;
1321 AAATCTTTTCTGTTTTAGGAAAAGGTTTTCTAAGTGAGAGGCAGCATAACTAATAGCAC 1380
1381 AGAGTCTGGGGCCAGATATCTGAAAGTAAATCTCAGCTCTGCCATGTCTTAGCTTTCTAG 1440
1441 ATCTTTGGCAAAATACCCTACTCTGTTTGTGATTCAATTTCTACTAAATGAATAA 1500 1458:T/C;
1501 CTGTATATCTTAAATATGGCTTTGTGAGAAATAGTAAATGAATGTAAAGCACTCAGAACC 1560
1561 GTGTCTGGCATAAAGTAAATACCATACAAAGCATTAGCTATTATTAGTAGTATTAAAGATA 1620
1621 AAATTTTCACTGAGAAATACAAAGTAAAATTTTGGACTTTATCTTTTTACCAGAGAACT 1680 1674:T/A;
1681 TGAGATTTAATAGCTATATGACTATTTTCCAAAGATTAAAAGCTTCAATAGGTTGTTTT 1740
1741 TGGATTCAAGATAGAGCATAAAGCATAAATCATCCAAAGCTCTAGGCTACATTAGGTGTGTA 1800
1801 AGCTACCTAGTAGTGTGCCAGTTAAAGAGAAATGAACAAAATCTGGTGCCAGAAAGAGC 1860 1814:C/T;
1861 TTGTGCCAGGGTGAATCCAAAGCCAGAAAATAAATAGGATTTAAGGGGACACAGATGCAAT 1920
1921 CCCATTGACTCAAATTTCTATTAAATCAAGAGAAATCTGCTTCTAACTACCTTTCTGAAAG 1980
1981 ATGTAAAGGAGACAGCTTACAGATGTTACTCTAGTTTAAATCAGAGCCACATAATGCAACT 2040
2041 CCAACCAACATAAAGATACTAGATGCTGTTTTCTGAAAGAAAATTTCTCCACATTGTTCAAG 2100 2044:G/A; 2099:T/C;
2101 CCAAAAATTTAAACCAGAAATTTGTAGAATTTGTAGTGGTGAATGAAAAGCGCAATAGATG 2160 2116:C/T;
2161 GACATATCAGGGGATTGGTATTGTCTTGACCTACTTTCCCCTAAAGAGTGTAGAAAAG 2220
2221 ATGAGATTATGTGCATATTTAGGGGGTGGTAAATTCATGGAATCTAAGTTTGAACC 2280
2281 AAAAGTAAATGATAAACTCTATTCAATTTGTTCAATTTAACCTCATTGCACATTTACAAAAG 2340
2341 ATTTTAGAACTAAATAAAATATTTGATTTCCAAAGGATGCTATGTTAATGCTATAATGAGA 2400
2401 AAGAAATGAAATCTAATCTGGCTCTACTCTTATGCTTCTGCTTCTAACTAAAGAGTGTAGTG 2460
2461 TGCTTATTTAATAAAGTGGAGATGATACTTCACTGCCTACTTCAAAGATGACTGTGAGAA 2520
2521 GTAAATGGGCTATTTTGGAGAAAATCTTTTAAATTTGTAATATACCATAGAAATATGAA 2580 2538:G/C;
2581 ATATATATATATATAGAAATCAAGAGGCTGTCCAAAAGTCTCCAAAGTATTATAT 2640
2641 TTTTATTTCACTGGGACAAAACATTTTTAAAATGCATCTTAAATGTAGTGATTGTAGAAA 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.

Location: 4:123,592,080-123,597,100 **Gene: IL2** Transcript: IL2-001

Gene: IL2 (ENSG00000109471)
 Interleukin-2 Precursor (IL-2)(T-cell growth factor)(TCGF)(Aldesleukin) [Source: UniProtKB/Swiss-Prot P60568](#)
Location [Chromosome 4: 123,592,080-123,597,100 reverse strand.](#)
Transcripts There is 1 transcript in this gene: [hide transcripts](#)

Name	Transcript ID	Protein ID	Description
IL2-001	ENST00000226730	ENSP00000226730	protein_coding

◀ Genomic alignments **Gene Tree** [help](#) [Orthologues](#) ▶

LEGEND

- x1 branch length
- - - x10 branch length
- ⋯ x100 branch length
- Gene ID current gene
- Gene ID within-sp. paralog
- speciation node
- duplication node
- ambiguous node
- ◀ collapsed sub-tree
- ◀ collapsed (current gene)
- ◀ collapsed (paralog)
- AA alignment match/mismatch
- AA consensus > 66% (mis)mat
- AA consensus > 33% (mis)mat
- AA alignment gap

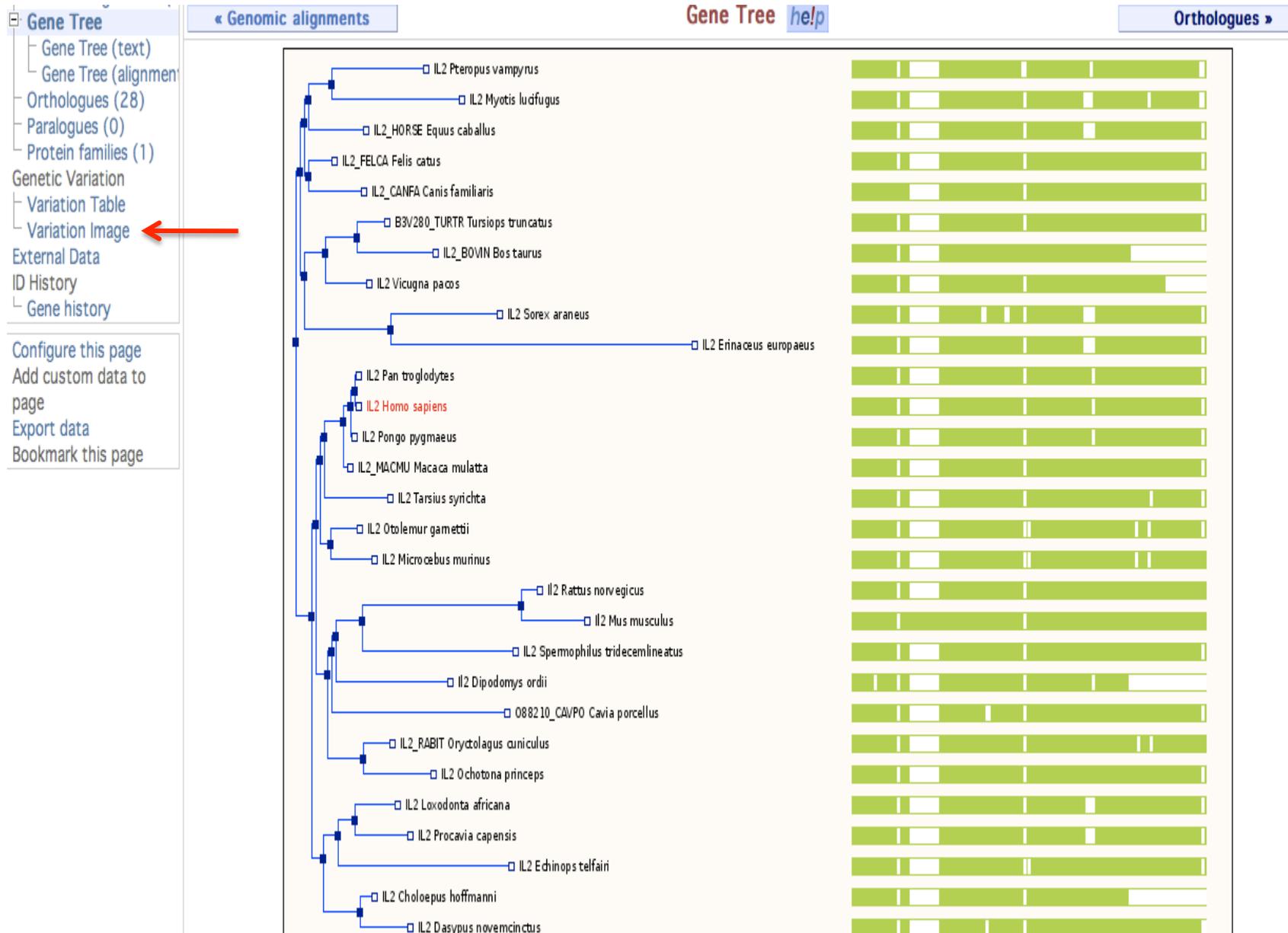
[Export image](#)

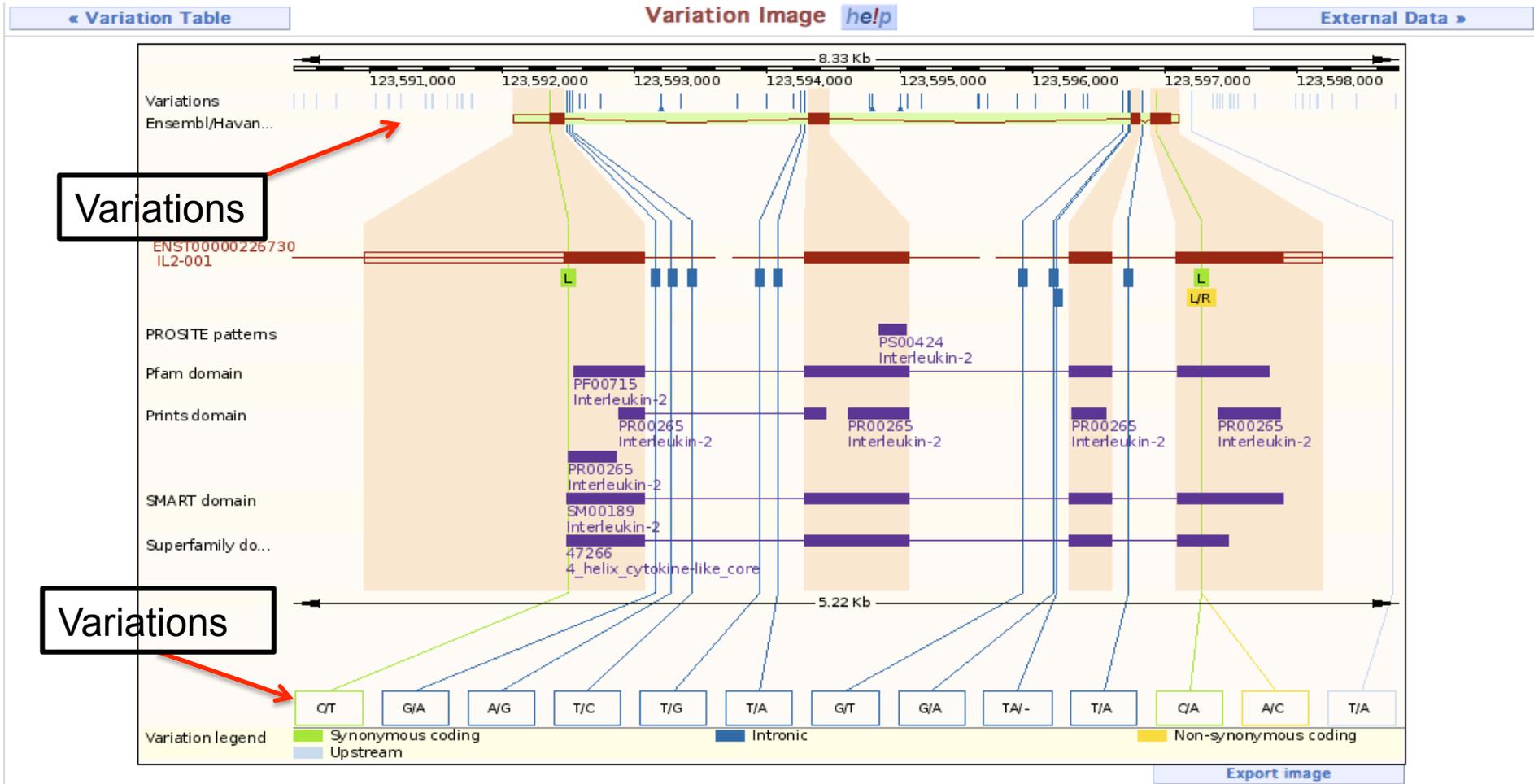
View options:

- [View current gene only](#)
- [View paralogs of current gene](#)
- [View all duplication nodes](#)
- [View fully expanded tree](#)

To view a fully expanded tree click here!

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





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

Variation: rs3087209

Export **Variation Properties**

displayed above.

bp: 123596933
 status: cluster, freq, hapmap
 class: snp
 ambiguity M
 code:
 mapweight: 1
 alleles: A/C
 source: HGVBbase, dbSNP
 type: NON_SYNONYMOUS_CODING



Variation: rs3087209

- Summary
- Gene/Transcript (1)
- Population genetics (10)
- Individual genotypes (27)
- Context
- Phenotype Data (0)

- Configure this page
- Add custom data to page
- Export data
- Bookmark this page

Variation: rs3087209

Variation type SNP (source [dbSNP](#))
Synonyms None currently in the database
Alleles A/C (Type: **Unknown**)
Ancestral allele: A
Location This feature maps to 1 genomic location(s). [hide locations](#)

4:123596933 (forward strand) [Jump to region in detail](#)

Variation summary

Validation status Proven by cluster, frequency (Feature tested and validated by a non-computational method).
 HapMap SNP

Linkage disequilibrium data **Links to Linkage disequilibrium data per population:**
[CSHL-HAPMAP:HapMap-HCB](#) (Tag SNP) [CSH](#)

Flanking Sequence

```

ATT AAAACAGAAATTGAACAT AAAATATTGTACTT ACCTTCTTGGGCATGT AAAACTTAA
ATGTGAGCATCCTGGTGACTTTGGGATTCTTGT AATTCTAAGAAAGTAT AATGCATTGTW
ATTAAGAAATGATCTCCAGCTAGATTACTAAATGT AAT AATTTT AGT AAGAAAGGAAATA
TACTTACATT AATTCCATTCAAATCATCTGT AATCCAGM[A/C]G AATGCTCCAGT
TGTAGCTGTGTTTTCTTTGTAGAACTTGAAGTAGGTGC ACTGTTTGTGACAAAGTGC AAGA
CTTAGTGCAATGC AAGACAGGAGTTGCATCCTGTACATTGTGGCAGGAGTTGAGGTTACT
GTGAGTAGTGATT AAGGAGAGTGATAGGGAACTCTTGAAACAAGAGATGC AATTTTACTG
TTAATTTCTGGAAAAATATTATGGGGGTGTC AAAATGTTTTACATATTACACATATTTTCA
AAGACTTTACCTGTCTGAAAAAACATTACCTTCATTTTCTCTTCTG&T GACTCTTTGG
AATTTCT
    
```

(Variant highlighted)

Variation of interest

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.

e/Ensembl Home > Human Login / Register | BLAST/BLAT | BioMart | Docs & FAQs

Location: 4:123,592,080-123,597,100 Gene: IL2 Transcript: IL2-001 Variation: rs3087209

Transcript-based displays

- [-] Transcript summary
- [-] Supporting evidence (23)
- [-] Sequence
 - Exons (4)
 - [-] cDNA
 - [-] Protein
- [-] External References
 - [-] General identifiers (95)
 - [-] Oligo probes (18)
 - [-] Gene ontology (22)
- [-] Genetic Variation
 - [-] Population comparison
 - [-] Comparison image
- [-] Protein Information
 - [-] Protein summary
 - [-] Domains & features (1)
 - [-] Variations (2)
- [-] External Data
- [-] ID History
 - [-] Transcript history
 - [-] Protein history

- Configure this page
- Add custom data to page
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- Bookmark this page

Transcript: IL2-001 (ENST00000226730)

Interleukin-2 Precursor (IL-2)(T-cell growth factor)(TCGF)(Aldesleukin) [Source:UniProtKB/Swiss-Prot;Acc:P60568]

Location [Chromosome 4: 123,592,080-123,597,100](#) reverse strand.

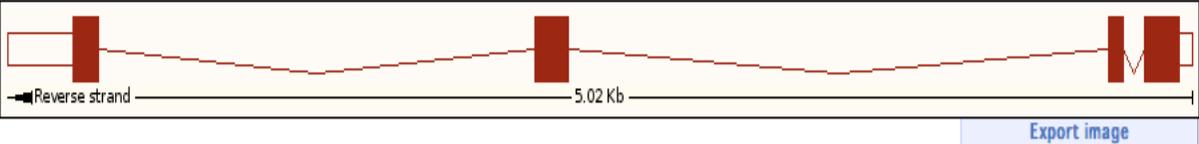
Gene This transcript is a product of gene [ENSG00000109471](#) - There is 1 transcript in this gene: [hide transcripts](#)

Name	Transcript ID	Protein ID	Description
IL2-001	ENST00000226730	ENSP00000226730	protein_coding

Transcript and Gene level displays

In Ensembl a gene is made up of one or more transcripts. Views in Ensembl are separated into Gene based views and Transcript based views according to which level the information is more appropriately associated. This view is a transcript level view. To flip between the two sets of views you can click on the Gene and Transcript tabs in the menu bar at the top of the page.

Transcript summary [help](#)
[Supporting evidence >](#)



Statistics Exons: 4 Transcript length: 794 bps Translation length: 153 residues

CCDS This transcript is a member of the Human CCDS set: [CCDS3726](#)

Type Known protein coding

Prediction Method Transcript where the Ensembl genebuild transcript and the [Vega](#) manual annotation have the same sequence, for every base pair. See [article](#).

Alternative transcripts This Ensembl/Havana merge transcript entry corresponds to the following database identifiers:
Havana transcript having same CDS: [OTTHUMT00000256715](#) [\[view all locations\]](#)

[« Supporting evidence](#) Exons [help](#) [cDNA sequence »](#)

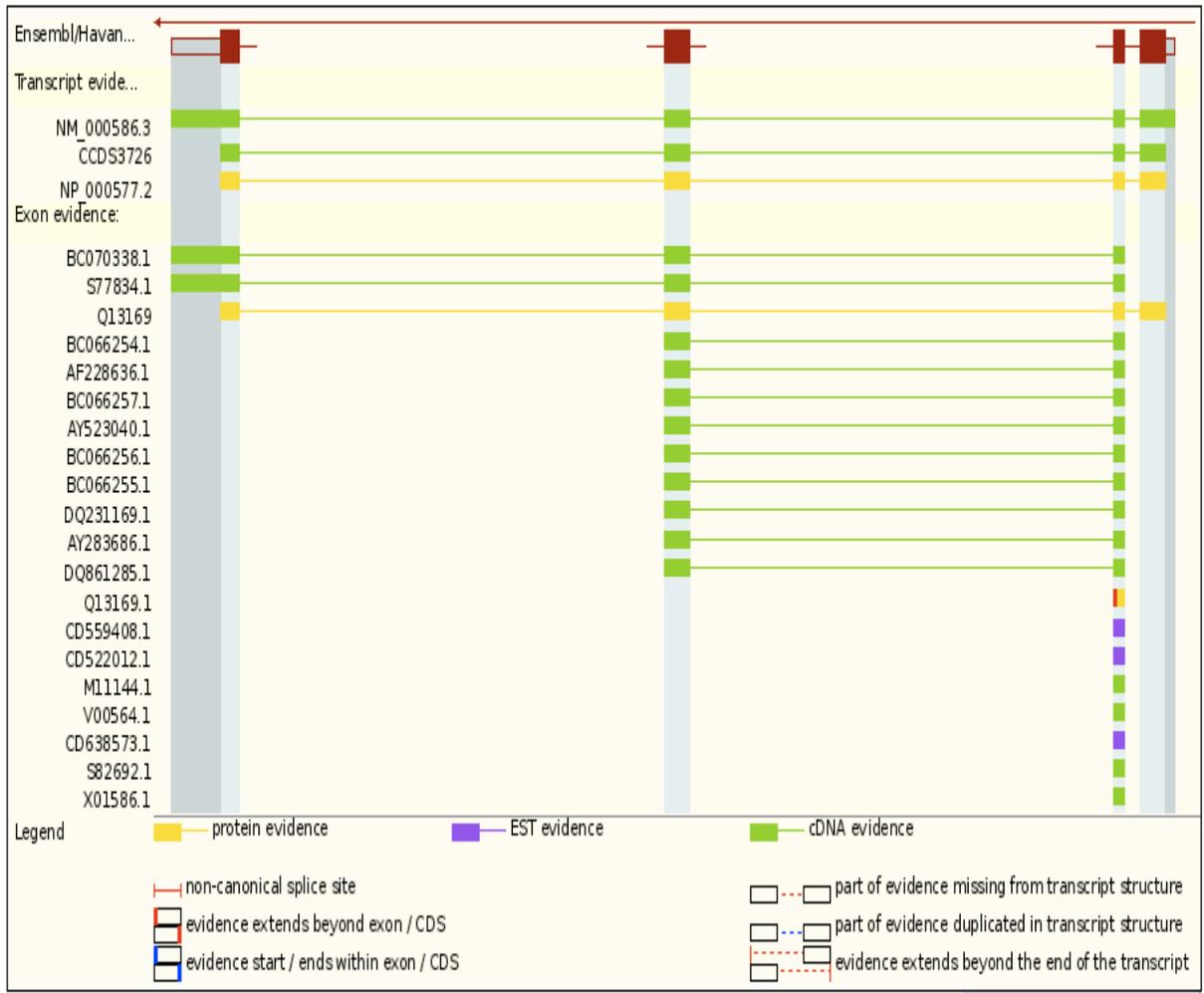
No.	Exon / Intron	Start	End	Start Phase	End Phase	Length	Sequence
	5' upstream sequence					ccataaatatctttccagaatbaaacagtataaaattgcatctctgtgtcaag
1	ENSE00001293064	123,596,899	123,597,100	-	0	202	AGTTCCTCATCACTCTCTTTAATCACTACTCACAGTAACCTCAACTCCTGCCACAATGTA CAGGATGCAACTCCTGTCTTGCATTGCACCTAAGTCTTGCACACTTGCACAAACAGTGCACC TACTTCAAGTTCTACAAAGAAAACACAGCTACAACTGGAGCATTACTGCTGGATTACA GATGATTTTGAATGGATTAAAT
	Intron 1-2	123,596,809	123,596,898			90	gtaagtabatcttctcttactaa.....ataacaatgcattatactctcttag
2	ENSE00000935280	123,596,749	123,596,808	0	0	60	AATTACAAGAAATCCAAAACCTCACCAGGATGCTCACATTTAAGTTTTACATGCCAAAGAAAG
	Intron 2-3	123,594,459	123,596,748			2,290	gtaagtabacaatctttatgttcaat.....gagctgatgataattattcttag
3	ENSE00000935278	123,594,315	123,594,458	0	0	144	GCCACAGAAGTGAACATCTTCAGTGTCTAGAAGAAGAACTCAAACCTCTGGAGGAAGTG CTAAATTTAGCTCAAAGCAAAAACCTTCACTTAAAGACCCAGGGACTTAACTCAGCAATATC AACGTAAATAGTTCTGGAACTAAAG
	Intron 3-4	123,592,468	123,594,314			1,847	gtaaggcattactcttattgtctctc.....aaaaattaacattctctttatag
4	ENSE00001138256	123,592,080	123,592,467	0	-	388	GGATCTGAAACAACATTCATGTGTGAATATGCTGATGAGACAGCAACCTTGTAGAAATTT CTGAACAGATGGATTACCTTTTGTCAAAGCMTCTCAACACTGACTTGTAAATTAAGT GCTTCCCACTTAAACATATCAGGCCTTCTATTTATTTAAATATTTAAATTTTATATTTA TTGTTGAATGTATGGTTTGTACCTATTGTAACTATTATTCTTAACTTAAAACCTATAAA TATGGATCTTTTATGATTCCTTTTGTAAAGCCTAGGGGCTCTAAAATGGTTTCACTTATT TATCCAAAATATTTATTTATTTGTTGAATGTTAAATATAGTATCTATGTAGATTGGTTA GTAAAACATTTAAATTTGATAAAT
	3' downstream sequence						ataaacaaagcctggatatttggatattttgaaacagcacagagtaagcat.....

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**.

« Transcript summary

Supporting evidence [help](#)

Exons »



Red boxes:
Exons in the
Ensembl transcript

Alignment of cDNA
and proteins to the
Ensembl exons.

Export image

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



The screenshot displays the Ensembl genome browser interface for the gene **IL2** on **Chromosome 4**. The main display area shows a genomic region from 123,592,083 to 123,597,098. The interface includes a navigation sidebar on the left with options like "Whole genome", "Chromosome summary", "Region overview", "Region in detail", "Comparative Genomics", "Genetic Variation", "Resequencing (6)", "Linkage Data", and "Markers". The main display area shows a genomic region with tracks for "Chromosome bands", "Contigs", "Ensembl/Havana g...", "ncRNA gene", "CCDS set", and "Human cDNA". The gene **IL2** is highlighted in green. The interface also includes a "Location" input field with the coordinates "4 : 12359208 - 12359709" and a "Go" button. A "Gene Legend" at the bottom indicates "Known protein coding" and notes that 178 tracks are currently turned off. A red arrow points to the "Configure this page" link in the sidebar.

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.



Main panel

Active tracks
(1/4) Sequence
(0/1) Markers
(3/10) Genes
(0/2) Prediction Transcrip
(0/7) Protein alignments
(0/5) Protein features
(2/4) cDNA/mRNA alignm
(0/4) EST alignments
(0/2) RNA alignments
(0/2) Other DNA alignme
(0/20) Oligo features
(0/3) Ditag features
(0/1) External data
(0/4) Simple features
(0/11) Misc. regions
(0/12) Repeats
(1/18) Variation featu
(1/23) Functional genom
(2/8) Multiple alignments
(0/33) BLASTZ alignmen
(0/11) Translated blat ali
(5/5) Additional decorati
(5/5) Information

Search display:

Variation features

- All variations [Show info](#)
- Genotyped variations [Show info](#)
- Affy GeneChip 100K Array variations [Show info](#)
- Affy GeneChip 500K Array variations [Show info](#)
- Affy GenomeWideSNP_6.0 variations [Show info](#)
- EGA variations [Show info](#)
- ENSEMBL:Venter variations [Show info](#)
- ENSEMBL:Watson variations [Show info](#)
- ENSEMBL:celera variations [Show info](#)
- HGVBbase variations [Show info](#)
- NHGRI_GWAS_catalog variations [Show info](#)
- TSC variations [Show info](#)
- dbSNP variations [Show info](#)
- ▲ DAS** ASTD human SNPs [Show info](#)
- ▲ DAS** CONDOR human [Show info](#)
- ▲ DAS** DECIPHER [Show info](#)
- ▲ DAS** DGV loci [Show info](#)
- ▲ DAS** WGTP regions [Show info](#)

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



Main panel

Active tracks
(1/4) Sequence
(0/1) Markers
(3/10) Genes
(0/2) Prediction Transcrip
(0/7) Protein alignments
(0/5) Protein features
(2/4) cDNA/mRNA alignm
(0/4) EST alignments
(0/2) RNA alignments
(0/2) Other DNA alignme
(0/20) Oligo features
(0/3) Ditag features
(0/1) External data
(0/4) Simple features
(0/11) Misc. regions
(0/12) Repeats
(1/18) Variation features
(1/23) Functional genom
(2/8) Multiple alignme
(0/33) BLASTZ alignmen
(0/11) Translated blat ali
(5/5) Additional decorati
(5/5) Information

Search display:

Multiple alignments

- 31 eutherian mammals EPO [Show info](#)
- Conservation score for 31 eutherian mammals EPO [Show info](#)
- Constrained elements for 31 eutherian mammals EPO [Show info](#)
- 12 amniota vertebrates Pecan [Show info](#)
- Conservation score for 12 amniota vertebrates Pecan [Show info](#)
- Constrained elements for 12 amniota vertebrates Pecan [Show info](#)
- 9 eutherian mammals EPO [Show info](#)
- 4 catarrhini primates EPO [Show info](#)

To update this configuration, select your tracks and other options in the box above and close this popup window. Your view will then be updated automatically.
[Reset configuration for Main panel to default settings.](#)

Notes:

- To change whether a track is drawn OR how it is drawn, click on the icon by the track name and then select the way the track is to be rendered.
- On the left hand side of the page the number of tracks in a menu, and the number of tracks currently turned on from that menu are shown by the two numbers in parentheses (tracks on/total tracks).
- Certain tracks displayed come from user-supplied or external data sources, these are clearly marked as **▲ DAS** (Distributed Annotation Sources), **▲ URL** (UCSC style web resources) or **▲ User** data uploaded by yourself or another user. Please note that the content of these tracks is not the responsibility of the Ensembl project. In the case of URL based or DAS tracks may either slow down your ensembl browsing experience OR may be unavailable as these are served and stored from other servers elsewhere on the Internet.

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

- 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

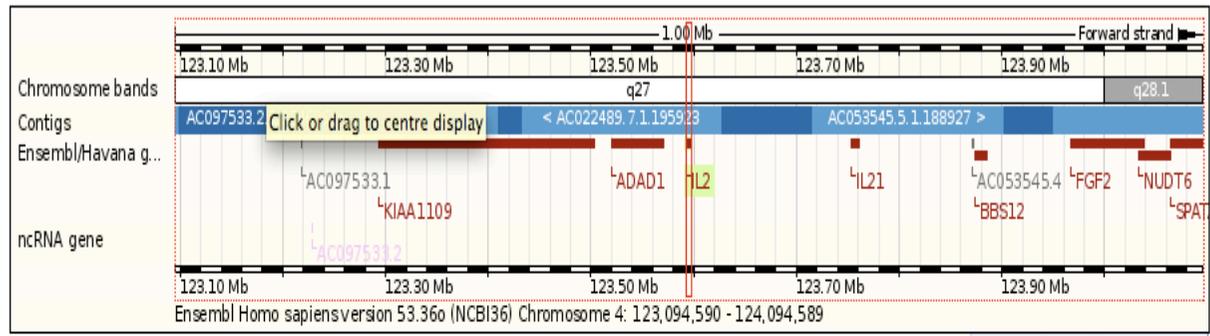


Export image

« Region overview

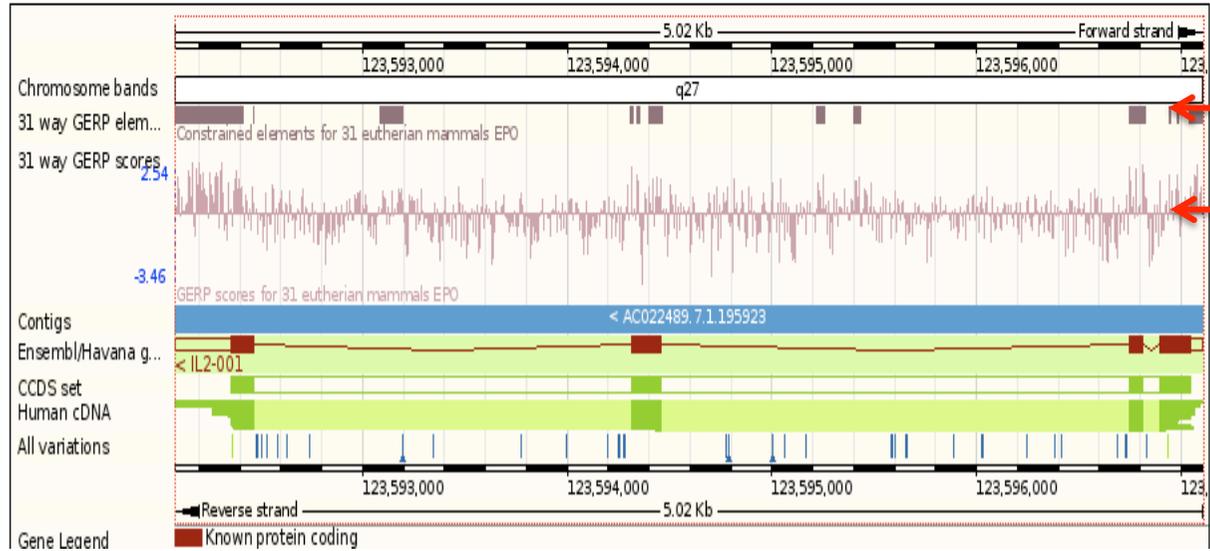
Region in detail [help](#)

Genomic alignments »



Export image

Location: 4 : 12359208 - 12359710 Go>



Conserved elements

Conserved basepairs.

Export Configuration - Feature List

Location to export: chromosome:NCBI36:4:123592080:123597100:1

Output: FASTA sequence

Strand: Forward strand

5' Flanking sequence (upstream): 0 *

3' Flanking sequence (downstream): 0 *

Next >

Select the FASTA sequence format

Click Next

Options for FASTA sequence

Genomic: Unmasked

Options for CSV (Comma separated values)

- Similarity features
- Repeat features
- Prediction features (genscan)
- Variation features
- Gene Information

Export Configuration - Output Format

- [HTML](#)
- [Text](#)
- [Compressed text \(.gz\)](#)

Choose Text

< Back

```
>4 dna:chromosome chromosome:NCBI36:4:123592080:123597100:1
ATTTATCAAATTTATTAAATAGTTTTACTAACCAATCTACATAGATACTATATTTAACAT
TCAACATAATAATAAATATTTTTGGGATAAATAAGTGAAACCATTTTAGAGCCCCTAGGGC
TTACAAAAAGAATCATAAAGATCCATATTTATAGTTTTAAGATTAAGAATAATAGTTAC
AATAGGTAGCAAACCATACATTCAACAATAAATAAATAAATTTAAATATTTAAATAAATAG
AAGGCCTGATATGTTTTAAGTGGGAAGCACTTAATTATCAAGTCAGTGTTGAGATGATGC
TTTGACAAAAGGTAATCCATCTGTTTCAGAAATCTACAATGGTTGCTGTCTCATCAGCAT
ATTCACACATGAATGTTGTTTCAGATCCCTATAAAAAGAAAAATGTTAATTTTTTAAAGTA
CAGAGTAGTTTACCTTATATACAGTTATTCCCAATTGAAGTCTTATAGGCCTGTTGCCTT
TATTTTCAAGCTTACCAAACATATTAATTATTCACATTTTCTTGAAATGATCAAAATGAA
TGCCAAAATTACATATTTTGTTATGATACCAAATGATAGTAACACAGAAGCTGAGATTTT
CCTCATTGTGTTAATTCAGTCAATGAACACAAAAATTTTTTCCCTAAATTGGGTGCAAATA
AAGATTTAAATAAAAAATAGATCTAGACAAATATTAATGCTGGATGTGAAATAAACTTGA
TCGCTTTTCCCTCTGAATGTACACCTATATTTGTGTAAGTTAAATGTATGAATTGATATGC
ACATTATACTTTCTTCTTTTCTAAATCTTGATTAGAGTCTCCTATTTTTCTACTTAAGTG
AATCTCCTTATATTTTCCCAAAGCAGAACAGAACTACACTAGAGTAAGCTAGGACATGC
TTCTGTTTGGGATAAATTTGTGTGAAGAACATCTTCATAAATACTTACACCTATCCCTAC
CCCATCATAGTATCAATGCAGGTGAATTTGCCAACTTTTAAAAGTTTAAACATTAGAAAT
TTTGTCTGTGGACTGGCTTTTTAGAAATTAGGCTTCTCTGCTGAAAGGAGCTATTTAAA
CGCTTCCCTCTAGTTGATAAGCTAAGGAGGAAATATTTTGATATATAGTGAGATTTAAAAG
AGAGCTTTTCAAATTTGAAGTGATTCCTACCCTGGGAACAAAAGCAGGTGAGATAGAGTG
TTCCCTTTAAATAAGTATTCTCTTTTAAAAAACTGTTGCAGTGTTCTGTATCCTCTTAAG
CATAATTGTTTAAATATTGTCATATCTTGGGATTTTTTTATTTTAAAAGTGTGTTGGCTT
TTGAAACACAGTTTTTCAGATTTTTGCATGGTTTTGTCTTAAATTTGTATCAAGAGTTAAG
AATGAGTTTTCTGATGTTAATTATTTTAGAGTAAAACCTTGCCATAGATAAGGAACTGA
```

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  
CAAATTTATTAATAGTTTTACTAACCAATCTACATAGATACTATATTTAACAT  
TAATAATAAATATTTTGGGATAAATAAGTGAAACCATTTTAGAGCCCCTAGGGC  
AAAGAATCATAAAAGATCCATATTTATAGTTTTAAGATTAAGAATAATAGTTAC
```

Paste in your
sequence here

Or Upload a file containing one or more FASTA sequences

ingen fil vald

Or Enter a sequence ID or accession (EMBL, UniProt, RefSeq)

Or Enter an existing ticket ID:

- dna queries
 peptide queries

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
 peptide database

LATESTGP

PEP_ALL

Select the Search Tool

BLASTN
BLAT

Select BLAST and
click Run.

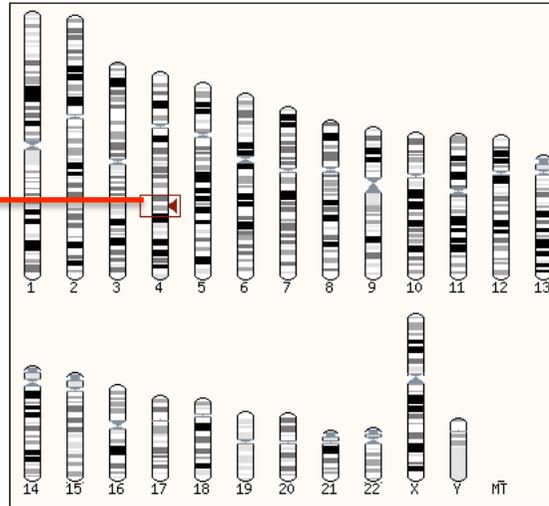
new SETUP CONFIG RESULTS **DISPLAY**

Displaying unnamed sequence alignments vs Homo_sapiens LATESTGP database

Showing top 100 alignments of 1, sorted by Raw Score

refresh

Alignment Locations vs. Karyotype (click arrow to hide)



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)

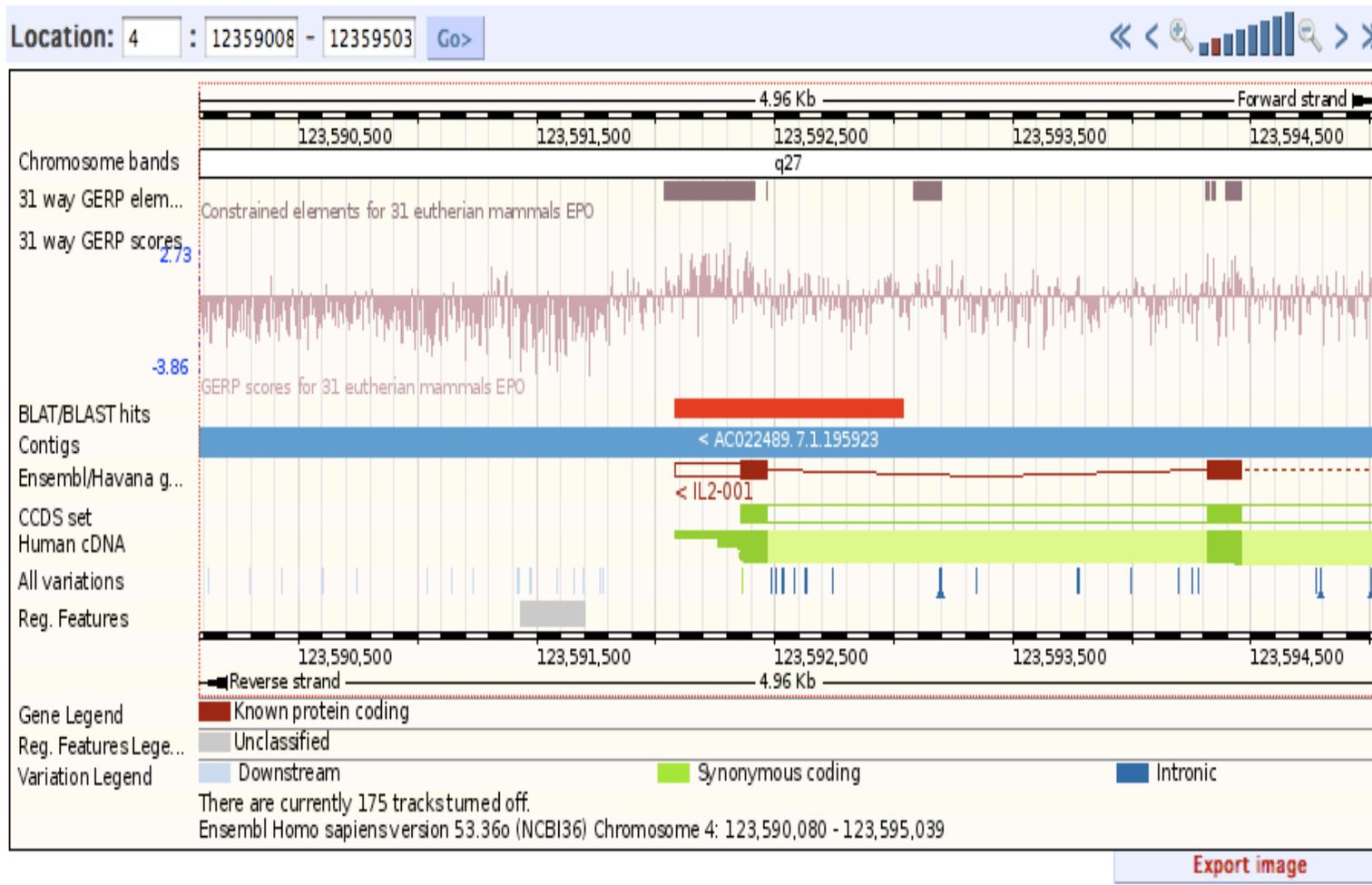
refresh

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

Links	Query	Chromosome	Stats
	Start End Ori	Name Start End Ori	Ori Score E-val %ID Length
[A] [S] [IG] [C]	28 987 +	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 bottom.