

- Browse genes & annotation for **over 50 species**
- Move from a **location** to a **gene** display with tabs
- Alternate **haplotypes** are available
- **Current location** is indicated
- **Search** for a gene, location, variation, clone, or probeset. Try our disease search

- **Navigate** to other pages using links at the left

- **View whole genome alignments**

- **Add or remove data tracks** with **Configure this page**

- **Export** a sequence

- **Conserved sequence** from analysis of multi-species alignments

- **Colour-coded polymorphisms**

- **Pop-up menus** of **variation** information

The screenshot displays the Ensembl genome browser interface for a specific genomic region on Chromosome 4 (123,372,625-123,377,880). The interface includes a top navigation bar with links for 'Home', 'Login / Register', 'BLAST/BLAT', 'Docs & FAQs', and 'Mirrors'. A left-hand navigation menu offers options like 'Whole genome', 'Chromosome summary', 'Region overview', and 'Region in detail'. The main content area shows multiple tracks: 'Chromosome bands', 'Contigs', 'Ensembl/Havana genes', 'ncRNA pseudogene', 'Gene Legend', '33 way GERP elements', 'CCDS set', 'Sequence variants', and 'Variation Legend'. A zoomed-in view of a specific region (5.26 Kb) is shown, highlighting a gene structure with exons and introns. A pop-up window titled 'Variation: rs3087209' provides detailed information about a specific SNP, including its position, status, class, and source.

- **BLAST/BLAT** a sequence
- Mine data with **BioMart**
- **Free registration/login**
- Read our **FAQs**

- **Gold genes** are reviewed. Click on one to learn more

- **Zoom** into a region in more detail

Variation: rs3087209	
Variation Properties	
bp	123377483
Status	cluster, freq, hapmap
Class	snp
Ambiguity	M
code	
Mapweight	1
Alleles	A/C
Source	dbSNP, Illumina_Human1M-duoV3
Type	NON_SYNONYMOUS_CODING

- Tabs allow navigation through location, **gene**, transcript, variation, and gene regulation information

The Gene Tab

- Click on a **variation** to open the variation tab, for population genetics and associated phenotypes

- **Hover** over transcript types for definitions

- The **transcript table** lists all splice variants for this gene

- Left hand links show information about one **gene**

- **Comparative and variation** displays are available

- Most Ensembl pages can be customised using **Configure this page**

Location: 4:123,372,625-123,377,880 **Gene: IL2** Transcript: IL2-001 Variation: rs3087209

Gene-based displays

- Gene summary
- Splice variants (2)
- Supporting evidence
- Sequence
- External references (3)
- Regulation
- Comparative Genomics
 - Genomic alignments (52)
 - Gene Tree (image)**
 - Gene Tree (text)
 - Gene Tree (alignment)
 - Orthologues (31)
 - Paralogues
 - Protein Families (1)
- Genetic Variation
 - Variation Table
 - Variation Image
- External Data
 - Personal annotation
 - ID History
 - Gene history

Gene: IL2 (ENSG00000109471)
interleukin 2 [Source:HGNC Symbol;Acc:6001]

Location: [Chromosome 4: 123,372,625-123,377,880](#) reverse strand.

Transcripts: There are 2 transcripts in this gene: [hide transcripts](#)

Name	Transcript ID	Length (bp)	Protein ID	Length (aa)	Biotype	CCDS
IL2-001	ENST00000226730	1029	ENSP00000226730	153	Protein coding	CCDS3726
IL2-002	ENST00000477645	586	No protein product	-	Retained intron	-

« Genomic alignments | **Gene Tree (image)** [help](#) | [Orthologues](#) »

Laurasiatheria: 11 homologs

- IL2 Pan troglodytes
- IL2 Homo sapiens
- IL2 Gorilla gorilla
- IL2 Pongo pygmaeus
- IL2 MACMU Macaca mulatta
- IL2 Tarsius syrichta

Strepsirrhini: 2 homologs

Eutheria: 5 homologs

Glires: 7 homologs

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% (mismatch)
- AA consensus > 33% (mismatch)
- AA alignment gap

Export Image

- Page-specific **help** is available

- **Navigate** using buttons

- **Protein alignments**, black ticks show intron-exon junctions

- **Known** transcripts have a matching sequence in another resource

The Transcript Tab

- Links to **sequence** displays

- **IDs** in other resources

- **Gene ontology** terms

Location: 4:123,372,625-123,377,880 **Transcript: IL2-001** Variation: rs3087209

Transcript-based displays

- Transcript summary
- Supporting evidence (20)
- Sequence
- Exons (4)
- cDNA
- Protein
- Protein domains
- Protein families
- Population comparison
- Comparison image
- Protein information
- Protein summary
- Domains & features (49)
- Variations (2)
- External Data
 - Personal annotation
 - ID History
 - Transcript history
 - Protein history

Transcript: IL2-001 (ENST00000226730)
interleukin 2 [Source:HGNC Symbol;Acc:6001]

Location: [Chromosome 4: 123,372,625-123,377,880](#) reverse strand.

Gene: This transcript is a product of gene [ENSG00000109471](#) - There are 2 transcripts in this gene: [hide transcripts](#)

Name	Transcript ID	Length (bp)	Protein ID	Length (aa)	Biotype	CCDS
IL2-001	ENST00000226730	1029	ENSP00000226730	153	protein coding	CCDS3726
IL2-002	ENST00000477645	586	No protein product	N/A	retained intron	N/A

Supporting evidence

Exons [help](#) | [cDNA sequence](#)

No.	Exon / Intron	Start	End	Start Phase	End Phase	Length/Sequence
1	5' upstream sequence				anagaggaaanaactgttcttcacagaggaggttaactgcatgaattagag
1	Exon 1	123,377,449	123,377,880	-	0	432 CTATCACCTAAAGTGTGGCTAATAAACAAGAGGATTCACCTACATCCATCACTCA
2	Intron 1_2	123,377,359	123,377,448	0	0	50 gtaagtataatttcctttcttaaa.....ataacaatgcatatactttttagag
2	Exon 2	123,377,299	123,377,358	0	0	60 AATTACAGAATCCCAACTACACAGGATGCTCACTATTAACTTACATCCCAAGAG
3	Intron 2_3	123,375,009	123,377,298	0	0	2,280 gtaagtacaattcttaactgccaat.....gagtgatgataaacttattcttag
3	Exon 3	123,374,865	123,375,008	0	0	144 GCCACAGAACTGAAACATCTTCAAGTGTCTAGAAAGAACTCAAACTCTGGAAGAGT
4	Intron 3_4	123,373,016	123,374,864	0	0	1,847 gtaaggatcaattattttagtctc.....aaataaacattttcttttagag
4	Exon 4	123,373,626	123,373,626	0	0	363 gllttttttaaataataataataataataataataataataataataataataataata

- **Novel** transcripts are based on homology evidence

- **Merged** transcripts are reviewed (curated)