EMBL-EBI wellcome trust **sanger** institute

- **Move from a gene to a location display with tabs**

- **BLAST a sequence**
- **Mine data with BioMart**
- **Query using our Perl API**

Try our tools:
- **Assembly Converter**
- **ID History Converter**
- **Variant Effect Predictor**

e! Ensembl   Login | Register | BLAST/BLAT | BioMart | Tools | Downloads | More…

Human (GRCh37) Location: 4:123,372,625-123,377,880 Gene: IL2

Location-based displays — Chromosome 4: 123,372,625–123,377,880

- Whole genome
- Chromosome summary
- Region overview
- **Region in detail**
- Comparative Genomics
  - Alignments (image) (51)
  - Alignments (text) (51)
  - Multi-species view (47)
  - Synteny (13)
- Genetic Variation
  - Resequencing (2)
  - Linkage Data
- Markers
- Other genome browsers
  - UCSC
  - NCBI
  - Vega

- **Search for a gene, location, variation, clone, probeset, or phenotype**

- **Current location is indicated**

- **Alternate haplotypes are available**

Assembly exceptio… chromosome 4
Assembly exceptio…
HSCHR4_1
Export Image

- **View whole genome alignments**

« Region overview   Region in detail *help*   Alignments (image) »

1.00 Mb   Forward strand
122.90 Mb 123.00 Mb 123.10 Mb 123.20 Mb 123.30 Mb 123.40 Mb 123.50 Mb 123.60 Mb 123.70 Mb 123.80 Mb
q27   q28.1
Chromosome bands
Contigs AC097533.2 > AC104658.6 > < AC022489.7 AC053545.5 > AC021205.6 >
Ensembl/Havana g… KIAA1109 ADAD1 IL21 BBS12 FGF2 NUDT6
AC097533.1 IL2 AC053545.3 CETN4P RP11-170N16.1 RP11-170N1 AC021205.1 SPA
ncRNA gene
ncRNA pseudogene AC097533.1
All Structural varia…
122.90 Mb 123.00 Mb 123.10 Mb 123.20 Mb 123.30 Mb 123.40 Mb 123.50 Mb 123.60 Mb 123.70 Mb 123.80 Mb
Ensembl Homo sapiens version 59.37d (GRCh37) Chromosome 4: 122,875,253 - 123,875,252
Gene Legend merged Ensembl/Havana pseudogene
RNA gene
Export Image

- **Configure this page to customise your view**

🔧 Configure this page
💾 Manage your data
📤 Export data
⭐ Bookmark this page

- **Browse genes & annotation for over 50 species in our chordate site**

Location: 4 : 123372625 - 123377880 Go > << < + [ ] − > >>

- **Zoom into a region**

5.26 Kb   Forward strand
123,373,000 123,374,000 123,375,000 123,376,000 123,377,000
q27
Chromosome bands
33 way GERP elem… Constrained elements for 33 eutherian mammals EPO_LOW_COVERAGE
33 way GERP scores 4.73
-4.26 GERP scores for 33 eutherian mammals EPO_LOW_COVERAGE
33 eutherian mam… 33 eutherian mammals EPO_LOW_COVERAGE
Contigs < AC022489.7
Ensembl/Havana g…
< IL2-001 protein coding
< IL2-002 retained intron
CCDS set < CCDS3726.1 CCDS set
Human RefSeq/EM…
Sequence variants …
Reg. Feats
123,373,000 123,374,000 123,375,000 123,376,000 123,377,000
Reverse strand 5.26 Kb

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

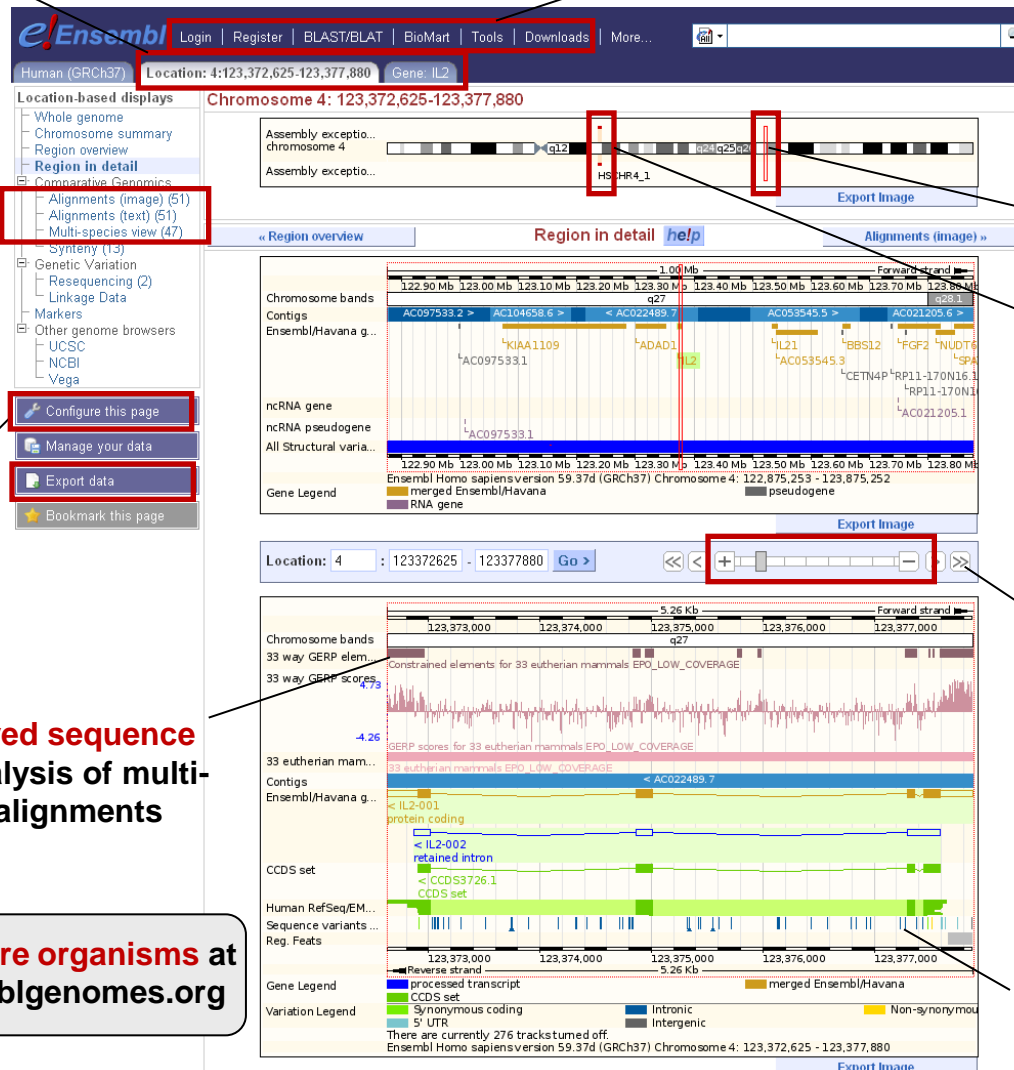**Variation: rs3087209** X
Variation Properties
bp 123377483
Status cluster, freq, hapmap
Class snp
Ambiguity code M
Mapweight 1
Alleles A/C
Source dbSNP, Illumina_Human1M-duoV3
Type NON_SYNONYMOUS_CODING

Gene Legend processed transcript merged Ensembl/Havana
CCDS set
Variation Legend Synonymous coding Intronic Non-synonymou
5' UTR Intergenic
There are currently 276 tracks turned off.
Ensembl Homo sapiens version 59.37d (GRCh37) Chromosome 4: 123,372,625 - 123,377,880
Export Image

- **Browse more organisms at www.ensemblgenomes.org**

- **Click a colour-coded sequence variant for a pop-up box of information**

www.ensembl.org

Reference: Flicek, P. *et al.* Ensembl 2011 (2011) Nucleic Acids Research 39:D800-D806
Reference: BMC Bioinformatics – Ensembl Update 2010 http://www.biomedcentral.com/series/ENSEMBL2010
Tutorials: http://www.ensembl.org/info/website/tutorials

www.ensembl.org

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

- **The transcript table lists splice variants and has sortable columns**

- **Gold transcripts are protein coding and are agreed on by Ensembl and Vega/Havana**

The Gene Tab

- **Contextual navigation for a gene**

- **Comparative and variation displays are available**

Human (GRCh37) | 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 (2)
- Regulation
- Comparative Genomics
  - Genomic alignments (51)
  - 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

Configure this page
Manage your data
Export data
Bookmark this page

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

Show/hide columns | Search:

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	-

Gene summary *he!p*

Name	IL2 (HGNC Symbol)
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.
Alternative genes	This gene corresponds to the following database identifiers:
Havana gene:	OTTHUMG00000133075 [view all locations]

- **Page-specific help is available**

- **Red transcripts are protein coding and are from Ensembl or VEGA/Havana**

- **Blue, Grey, or Pink transcripts are non-coding**

- **Human protein coding transcripts make the GENCODE set**

- **Export sequence**

Contigs
Ensembl/Havana g...

< AC022489.7
< IL2-001 protein coding
< IL2-002 retained intron

25.26 Kb
123.36 Mb | 123.37 Mb | 123.38 Mb | 123.38 Mb | 123.39 Mb | Forward strand

123.36 Mb | 123.37 Mb | 123.38 Mb | 123.38 Mb | 123.39 Mb
Reverse strand 25.26 Kb

Export Image

The Transcript Tab: Exons View

- **Protein signatures**

- **Colour key for variations**

- **Click a variation for population frequencies, phenotypes, and risk alleles**

- Comparison image
- Protein Information
  - Protein summary
  - Domains & features (13)
  - Variations (3)
- External Data
  - Personal annotation
- ID History
  - Transcript history
  - Protein history

Configure this page
Manage your data
Export data
Bookmark this page
Download view as RTF

« Supporting evidence | **Exons** *he!p* | cDNA sequence »

Key

Variations | 5' UTR | Downstream | Intronic
Non-synonymous coding | Regulatory region | Synonymous coding
Upstream

Show/hide columns | Search:

No.	Exon / Intron	Start	End	Start Phase	End Phase	Length	Sequence
	5' upstream sequence						...tgacaaagaaaatttctgagttacttttgtatcgcca... cccttaaagaaaggaggaaaaactgtttcatacagaagaggcgttaattgcatgaattagag
1	ENSE00001293064	123,377,449	123,377,880 -		0	432	CTATCACCTAAGTGTGGGCTAATGTAACAAAGAGGGATTTCACCTACATCCATTCAGTCA GTCTTTGGGGGTTTAAAGAAATTCCAAAGAGTCATCAGAAGAGGAAAAATGAAGGTAATG TTTTTCAGACAGGTAAAGTCTTTGAAAATATGTGTAAATATGTAAAACATTTTGACACCC CCATAATATTTTTCCAGAATTAACAGTATAAATTGCATCTCTTGTTCAAGAGTTCCCTAT CACTCTCTTTTAATCACTACTCACAGTAACCTCAACTCCTGGACATTTACTTCTGGATTTACAGATGATTTTG TCTTCAAAGAAAACACAGCTACAACTGGAGCATTTACTGTGGTTTTACAGATGATTTTTG AATGGAATTAAT
	Intron 1-2	123,377,359	123,377,448			90	gtaagtatattgtcttttactaaaattattacatttagtaatctagctggagatcatt tcttaatacaatgcattatactttcttag
2	ENSE00000935280	123,377,299	123,377,358 0		0	60	AATTACAAGAATCCCAAACTCACCAGGATGCTCACATTTAAGTTTTACATGCCCAAGAAG

- **UTR**

- **Coding sequence**

- **Upstream sequence**

- **Intron**

- **Download to open in MS® Word**

Ensembl

Contact us at helpdesk@ensembl.org