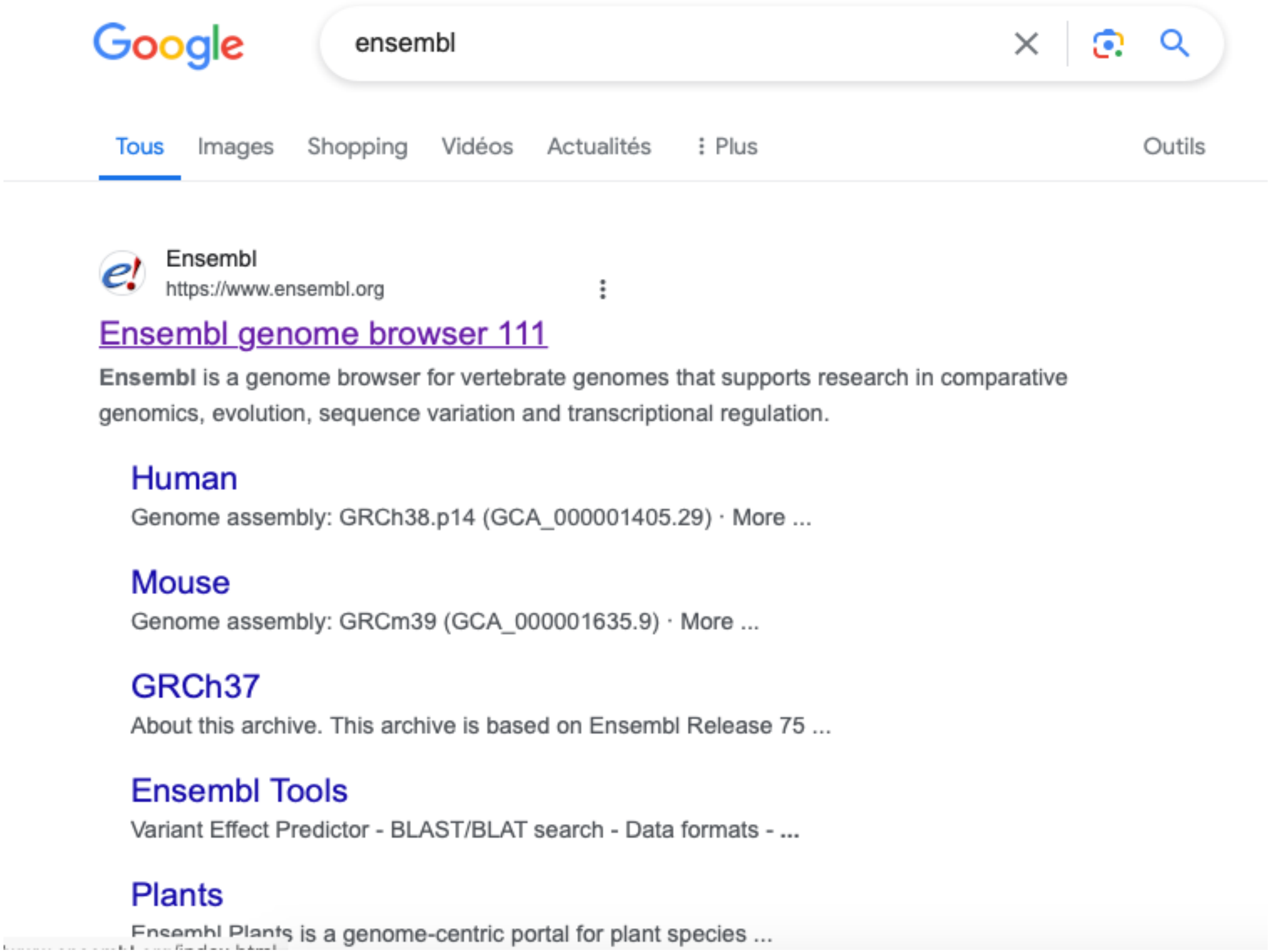


ensembl

Ensembl
https://www.ensembl.org

Ensembl genome browser 111

Ensembl is a genome browser for vertebrate genomes that supports research in comparative genomics, evolution, sequence variation and transcriptional regulation.

Human

Genome assembly: GRCh38.p14 (GCA_000001405.29) · More ...

Mouse

Genome assembly: GRCm39 (GCA_000001635.9) · More ...

GRCh37

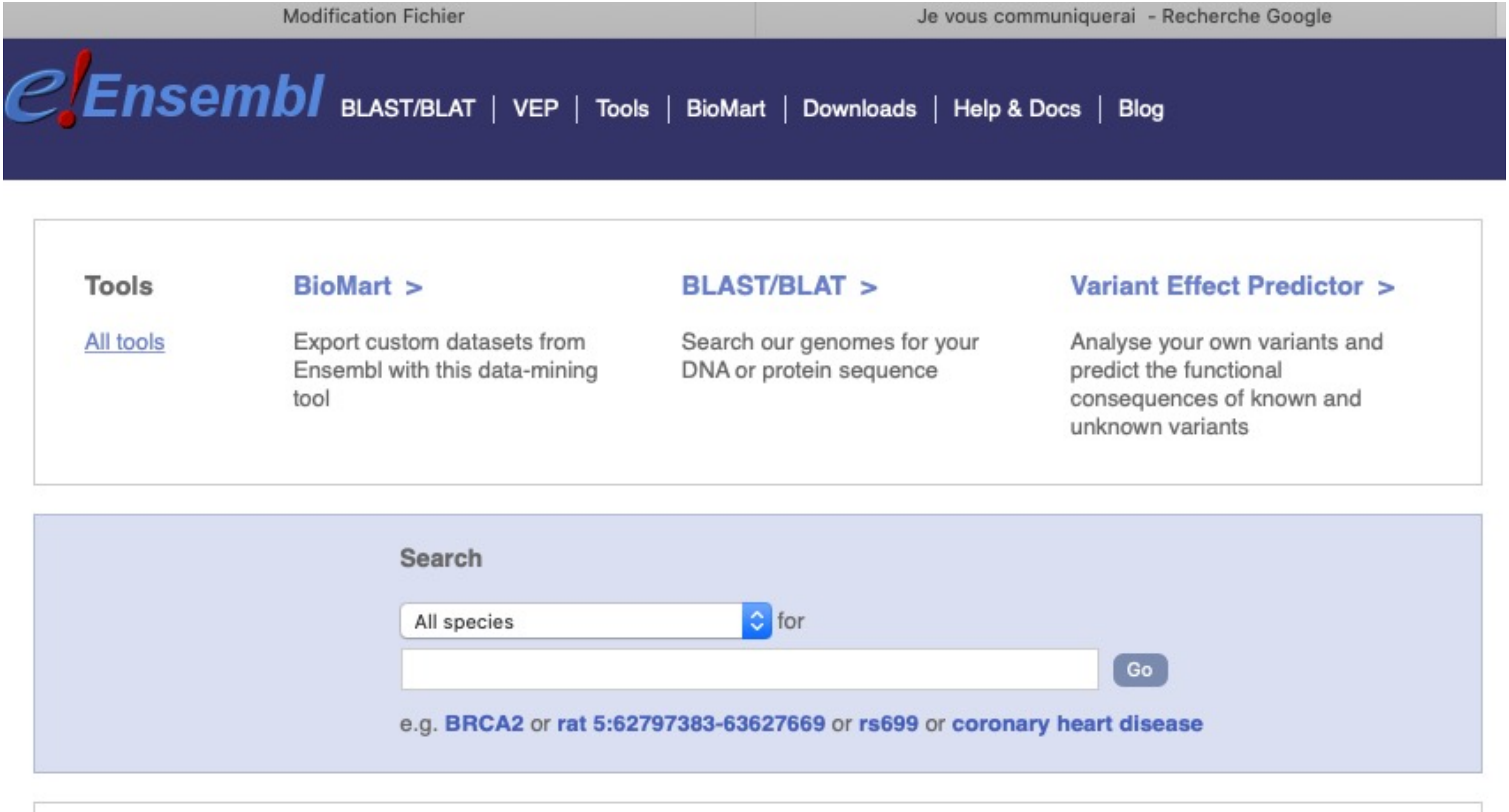
About this archive. This archive is based on Ensembl Release 75 ...

Ensembl Tools

Variant Effect Predictor - BLAST/BLAT search - Data formats - **...**

Plants

Ensembl Plants is a genome-centric portal for plant species ...



Tools

BioMart >

Export custom datasets from Ensembl with this data-mining tool

BLAST/BLAT >

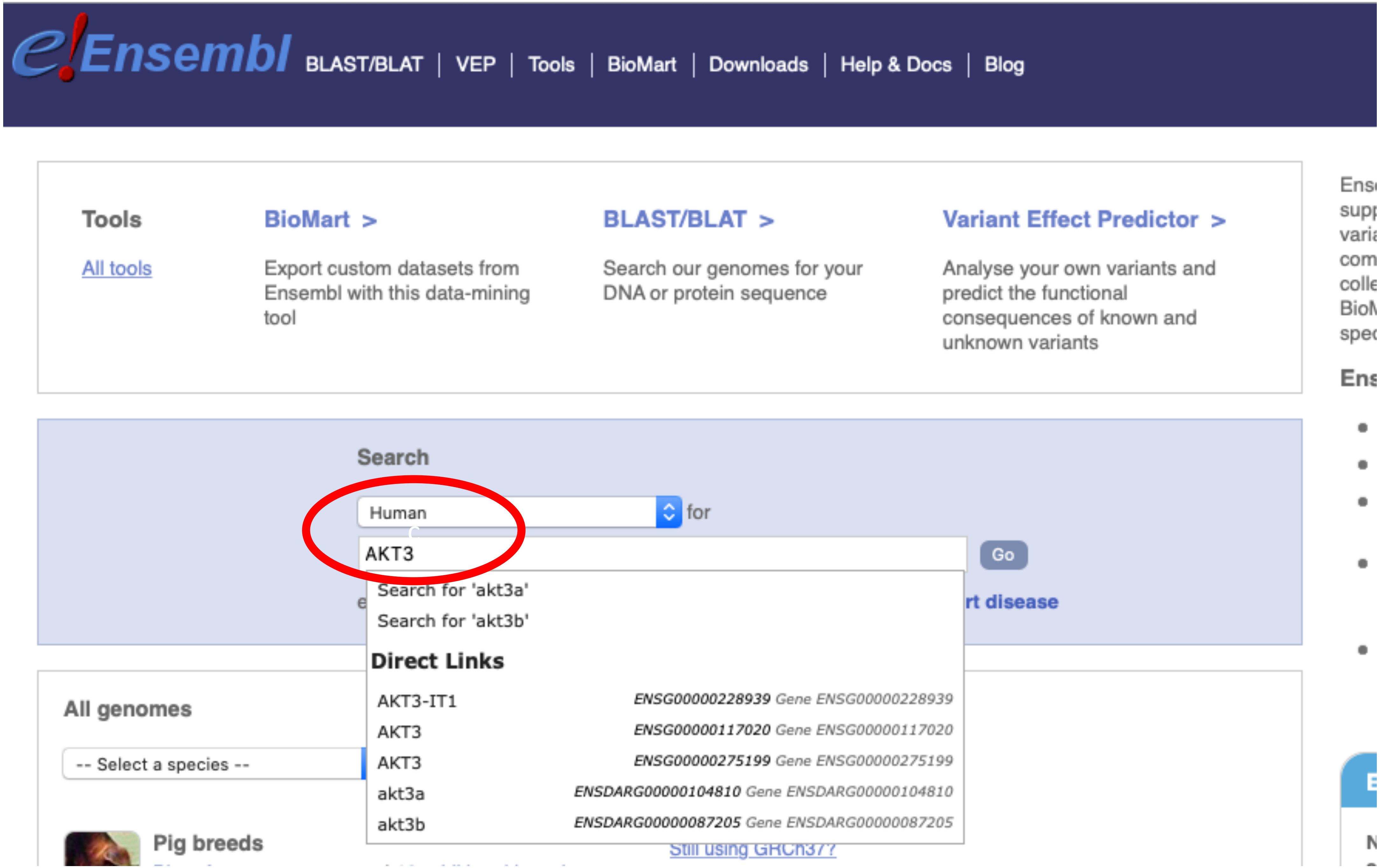
Search our genomes for your DNA or protein sequence

Variant Effect Predictor >

Analyse your own variants and predict the functional consequences of known and unknown variants

Search

e.g. **BRCA2** or **rat 5:62797383-63627669** or **rs699** or **coronary heart disease**



Tools

All tools

BioMart >

Export custom datasets from Ensembl with this data-mining tool

BLAST/BLAT >

Search our genomes for your DNA or protein sequence

Variant Effect Predictor >

Analyse your own variants and predict the functional consequences of known and unknown variants

Search

AKT3

Search for 'akt3a'

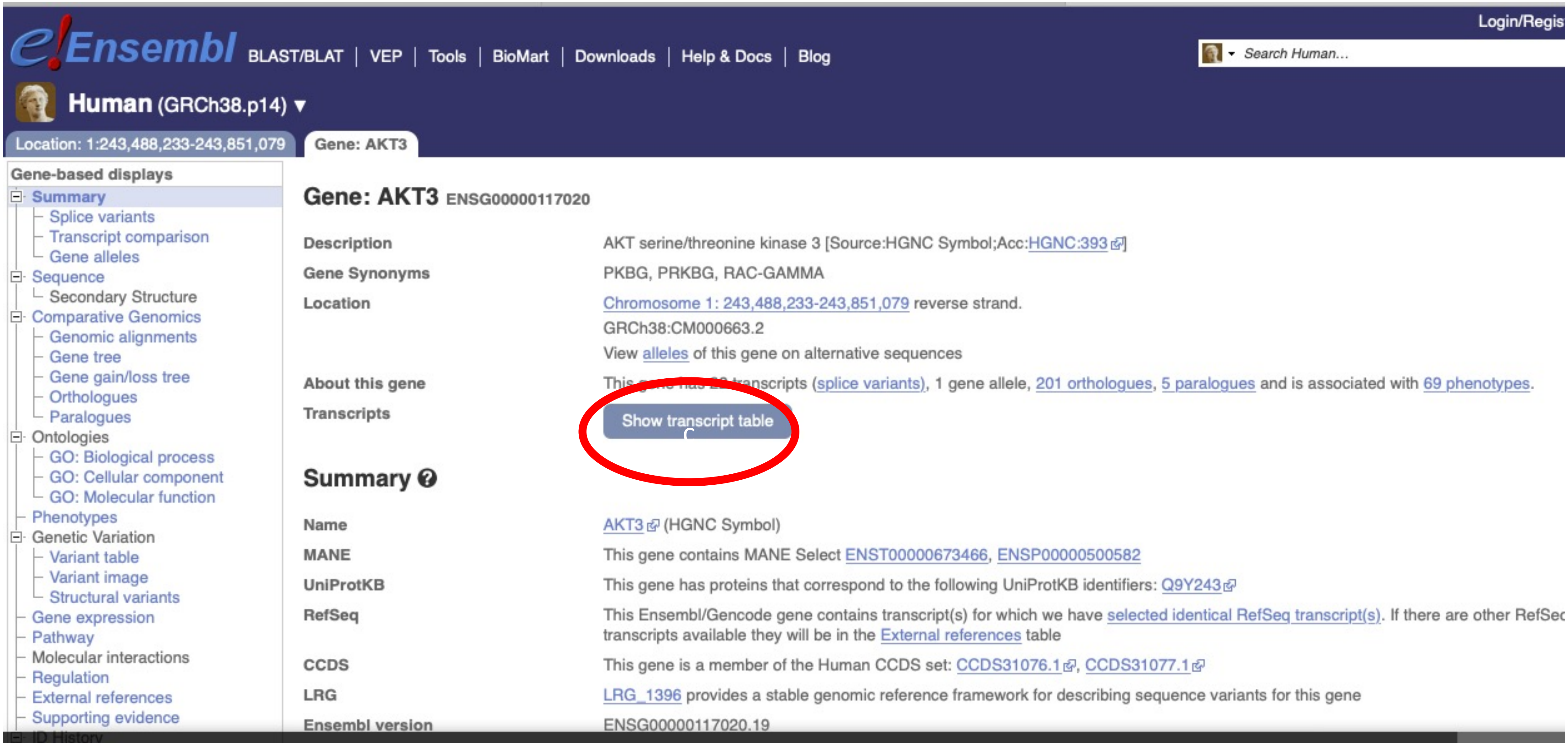
Search for 'akt3b'

Direct Links

AKT3-IT1	*ENSG00000228939 Gene ENSG00000228939*
AKT3	*ENSG00000117020 Gene ENSG00000117020*
AKT3	*ENSG00000275199 Gene ENSG00000275199*
akt3a	*ENSDARG00000104810 Gene ENSDARG00000104810*
akt3b	*ENSDARG00000087205 Gene ENSDARG00000087205*

All genomes

Pig breeds



Gene-based displays

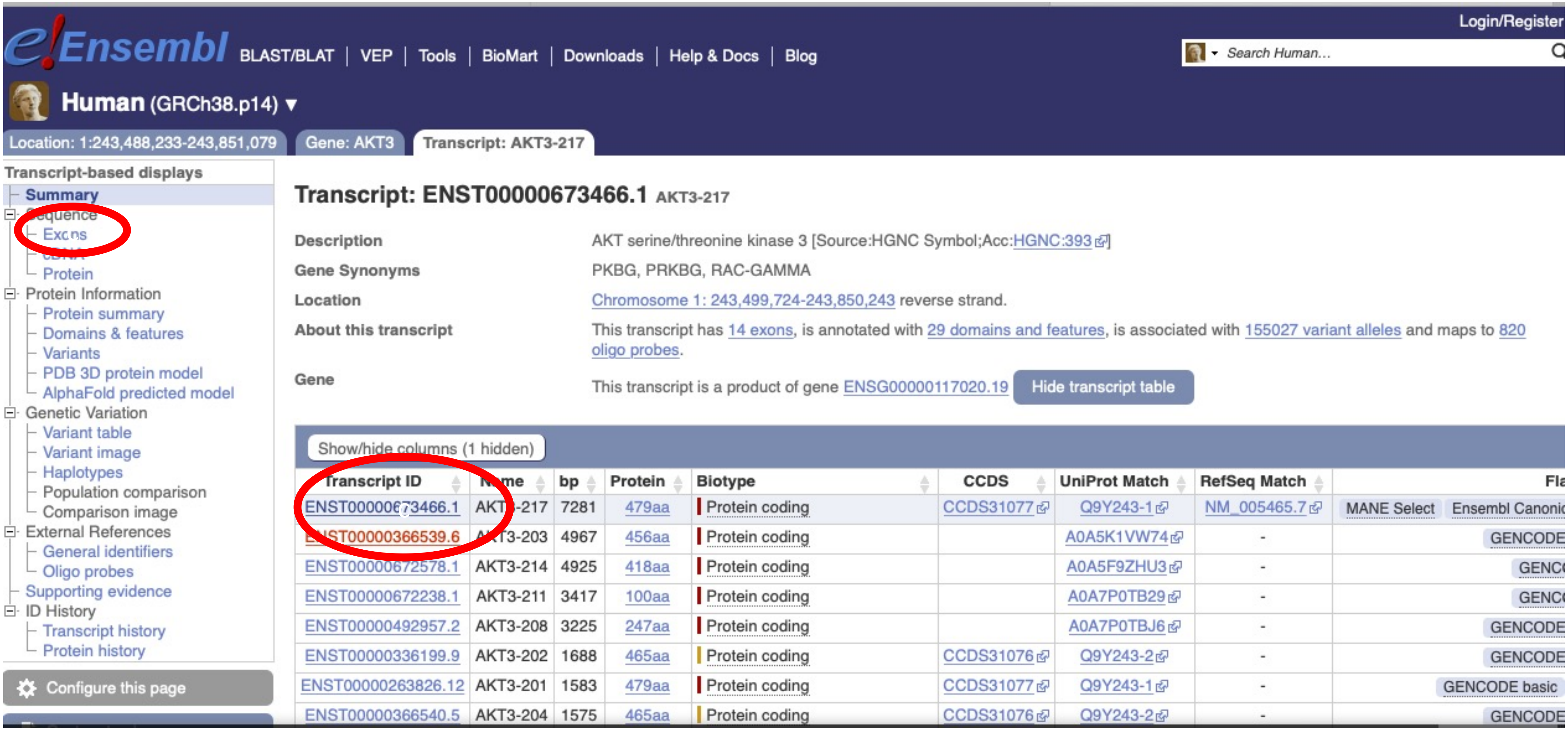
- Summary
  - Splice variants
  - Transcript comparison
  - Gene alleles
- Sequence
  - Secondary Structure
- Comparative Genomics
  - Genomic alignments
  - Gene tree
  - Gene gain/loss tree
  - Orthologues
  - Paralogues
- Ontologies
  - GO: Biological process
  - GO: Cellular component
  - GO: Molecular function
- Phenotypes
- Genetic Variation
  - Variant table
  - Variant image
  - Structural variants
- Gene expression
- Pathway
- Molecular interactions
- Regulation
- External references
- Supporting evidence
- ID History

Gene: AKT3 ENSG00000117020

Description	AKT serine/threonine kinase 3 [Source:HGNC Symbol;Acc:HGNC:393]
Gene Synonyms	PKBG, PRKBG, RAC-GAMMA
Location	Chromosome 1: 243,488,233-243,851,079 reverse strand. GRCh38:CM000663.2 View alleles of this gene on alternative sequences
About this gene	This gene has [illegible] transcripts (splice variants), 1 gene allele, 201 orthologues, 5 paralogues and is associated with 69 phenotypes.
Transcripts	Show transcript table

Summary ?

Name	AKT3 (HGNC Symbol)
MANE	This gene contains MANE Select ENST00000673466, ENSP00000500582
UniProtKB	This gene has proteins that correspond to the following UniProtKB identifiers: Q9Y243
RefSeq	This Ensembl/Gencode gene contains transcript(s) for which we have selected identical RefSeq transcript(s). If there are other RefSe transcripts available they will be in the External references table
CCDS	This gene is a member of the Human CCDS set: CCDS31076.1, CCDS31077.1
LRG	LRG_1396 provides a stable genomic reference framework for describing sequence variants for this gene
Ensembl version	ENSG00000117020.19



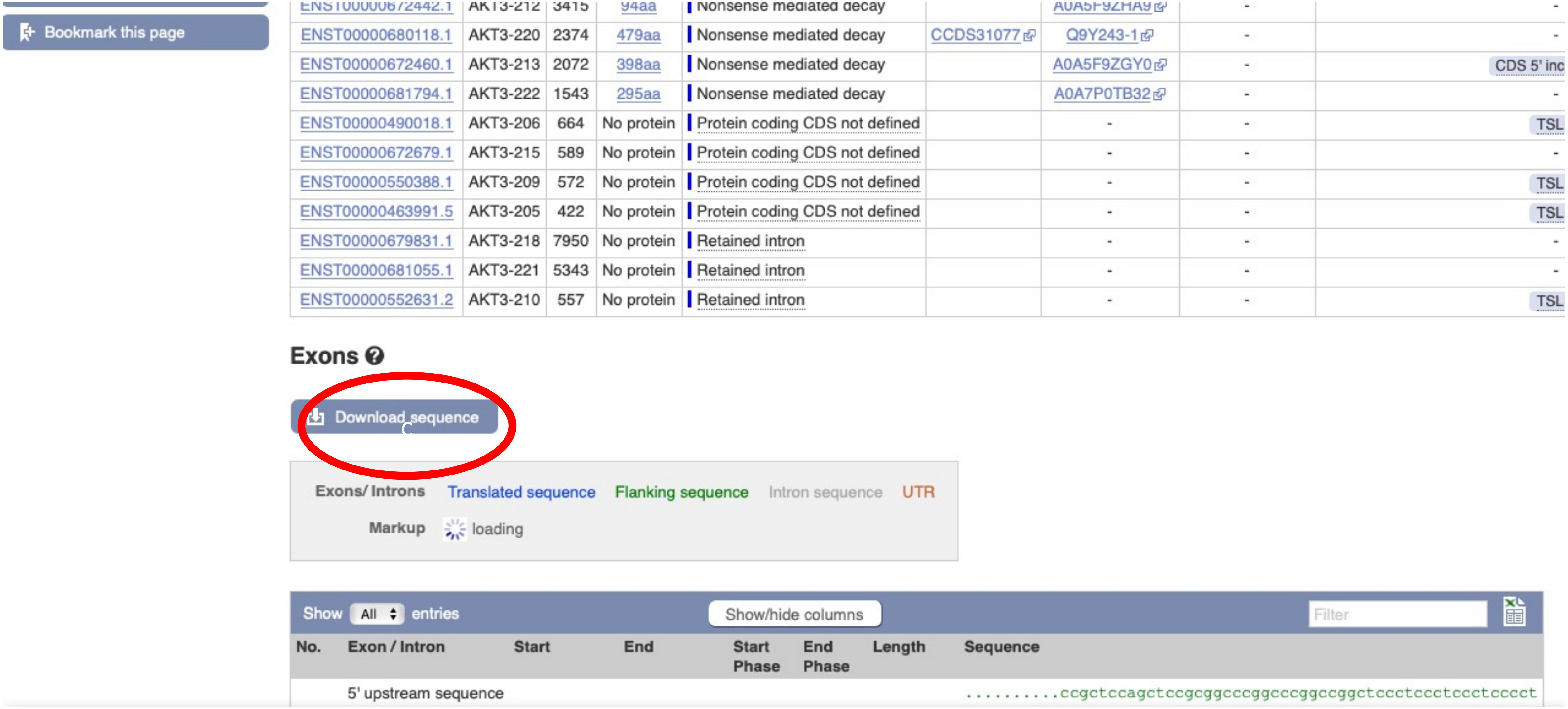
Transcript-based displays

- **Summary**
- Sequence
  - Exons
  - cDNA
  - Protein
- Protein Information
  - Protein summary
  - Domains & features
  - Variants
  - PDB 3D protein model
  - AlphaFold predicted model
- Genetic Variation
  - Variant table
  - Variant image
  - Haplotypes
  - Population comparison
  - Comparison image
- External References
  - General identifiers
  - Oligo probes
- Supporting evidence
- ID History
  - Transcript history
  - Protein history

Transcript: ENST00000673466.1 AKT3-217

Description	AKT serine/threonine kinase 3 [Source:HGNC Symbol;Acc:HGNC:393]
Gene Synonyms	PKBG, PRKBG, RAC-GAMMA
Location	Chromosome 1: 243,499,724-243,850,243 reverse strand.
About this transcript	This transcript has 14 exons, is annotated with 29 domains and features, is associated with 155027 variant alleles and maps to 820 oligo probes.
Gene	This transcript is a product of gene ENSG00000117020.19

Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	RefSeq Match	Fla
ENST00000673466.1	AKT3-217	7281	479aa	Protein coding	CCDS31077	Q9Y243-1	NM_005465.7	MANE Select Ensembl Canonic
ENST00000366539.6	AKT3-203	4967	456aa	Protein coding		A0A5K1VW74	-	GENCODE
ENST00000672578.1	AKT3-214	4925	418aa	Protein coding		A0A5F9ZHU3	-	GENC
ENST00000672238.1	AKT3-211	3417	100aa	Protein coding		A0A7P0TB29	-	GENC
ENST00000492957.2	AKT3-208	3225	247aa	Protein coding		A0A7P0TBJ6	-	GENCODE
ENST00000336199.9	AKT3-202	1688	465aa	Protein coding	CCDS31076	Q9Y243-2	-	GENCODE
ENST00000263826.12	AKT3-201	1583	479aa	Protein coding	CCDS31077	Q9Y243-1	-	GENCODE basic
ENST00000366540.5	AKT3-204	1575	465aa	Protein coding	CCDS31076	Q9Y243-2	-	GENCODE



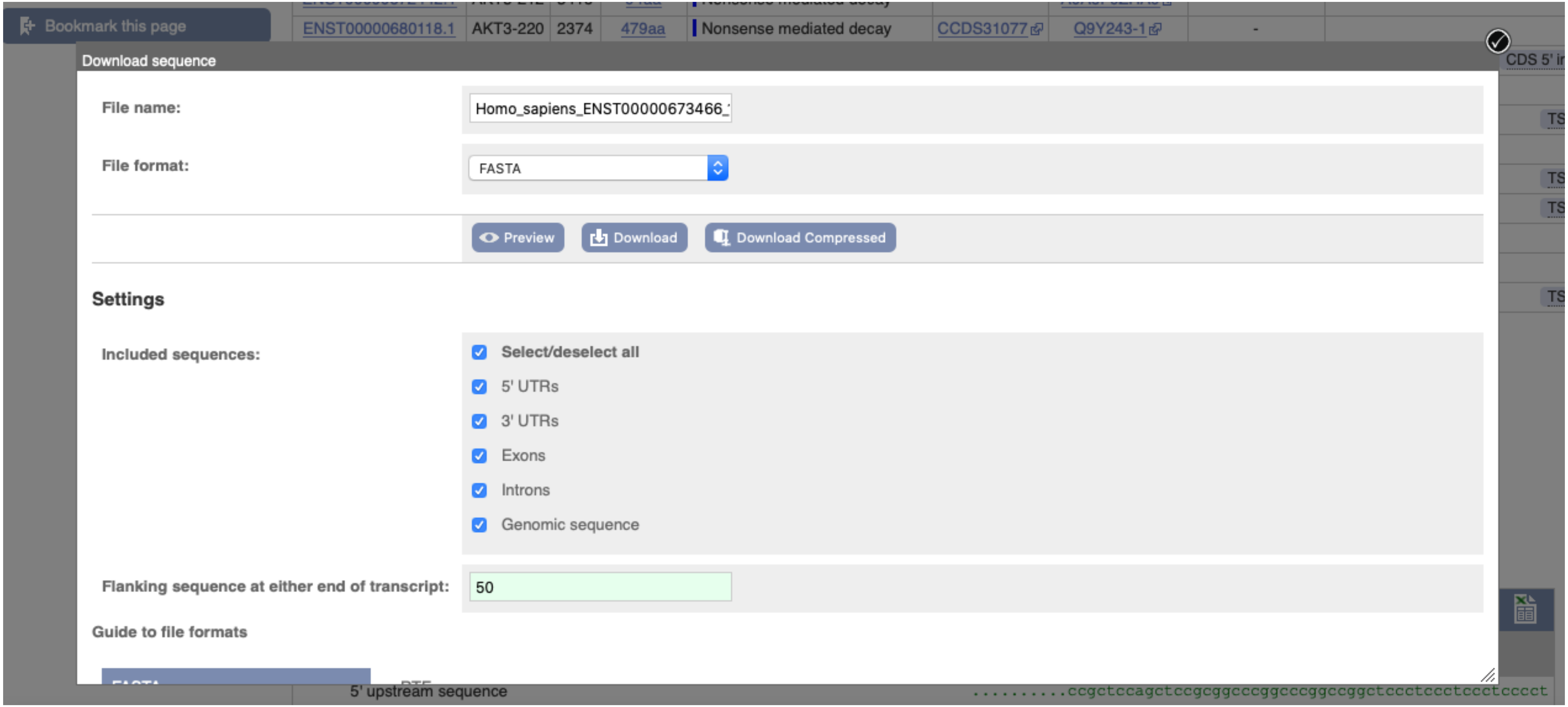
ENST00000672442.1	AKT3-212	3415	94aa	Nonsense mediated decay		A0A5F9ZHA9	-	-
ENST00000680118.1	AKT3-220	2374	479aa	Nonsense mediated decay	CCDS31077	Q9Y243-1	-	-
ENST00000672460.1	AKT3-213	2072	398aa	Nonsense mediated decay		A0A5F9ZGY0	-	CDS 5' inc
ENST00000681794.1	AKT3-222	1543	295aa	Nonsense mediated decay		A0A7P0TB32	-	-
ENST00000490018.1	AKT3-206	664	No protein	Protein coding CDS not defined		-	-	TSL
ENST00000672679.1	AKT3-215	589	No protein	Protein coding CDS not defined		-	-	-
ENST00000550388.1	AKT3-209	572	No protein	Protein coding CDS not defined		-	-	TSL
ENST00000463991.5	AKT3-205	422	No protein	Protein coding CDS not defined		-	-	TSL
ENST00000679831.1	AKT3-218	7950	No protein	Retained intron		-	-	-
ENST00000681055.1	AKT3-221	5343	No protein	Retained intron		-	-	-
ENST00000552631.2	AKT3-210	557	No protein	Retained intron		-	-	TSL

Exons

Exons/ Introns Translated sequence Flanking sequence Intron sequence UTR

Markup loading

No.	Exon / Intron	Start	End	Start Phase	End Phase	Length	Sequence
	5' upstream sequence						..........ccgctccagctccgcggcccggcccggccggctccctccctccctcccct



ENST00000680118.1 AKT3-220 2374 479aa Nonsense mediated decay CCDS31077 Q9Y243-1 -

Download sequence

File name: Homo_sapiens_ENST00000673466_

File format: FASTA

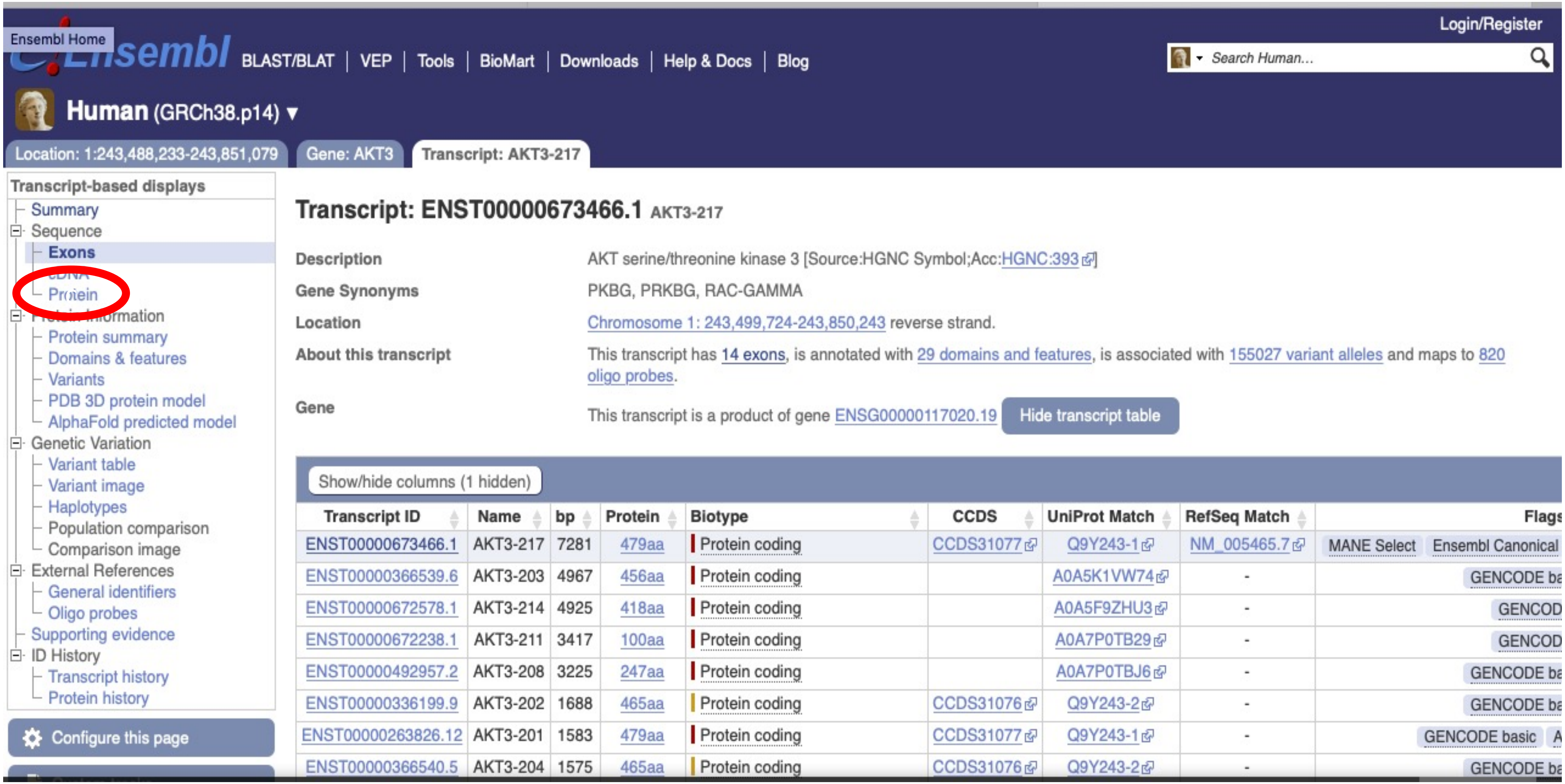
Settings

Included sequences:

- ☑ **Select/deselect all**
- ☑ 5' UTRs
- ☑ 3' UTRs
- ☑ Exons
- ☑ Introns
- ☑ Genomic sequence

Flanking sequence at either end of transcript: 50

5' upstream sequence ....ccgctccagctccgcggcccggcccggccggctccctccctccctcccct



Transcript: ENST00000673466.1 AKT3-217

Description	AKT serine/threonine kinase 3 [Source:HGNC Symbol;Acc:HGNC:393]
Gene Synonyms	PKBG, PRKBG, RAC-GAMMA
Location	Chromosome 1: 243,499,724-243,850,243 reverse strand.
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Transcript ID	Name	bp	Protein	Biotype	CCDS	UniProt Match	RefSeq Match	Flags
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ENST00000366539.6	AKT3-203	4967	456aa	Protein coding		A0A5K1VW74	-	GENCODE ba
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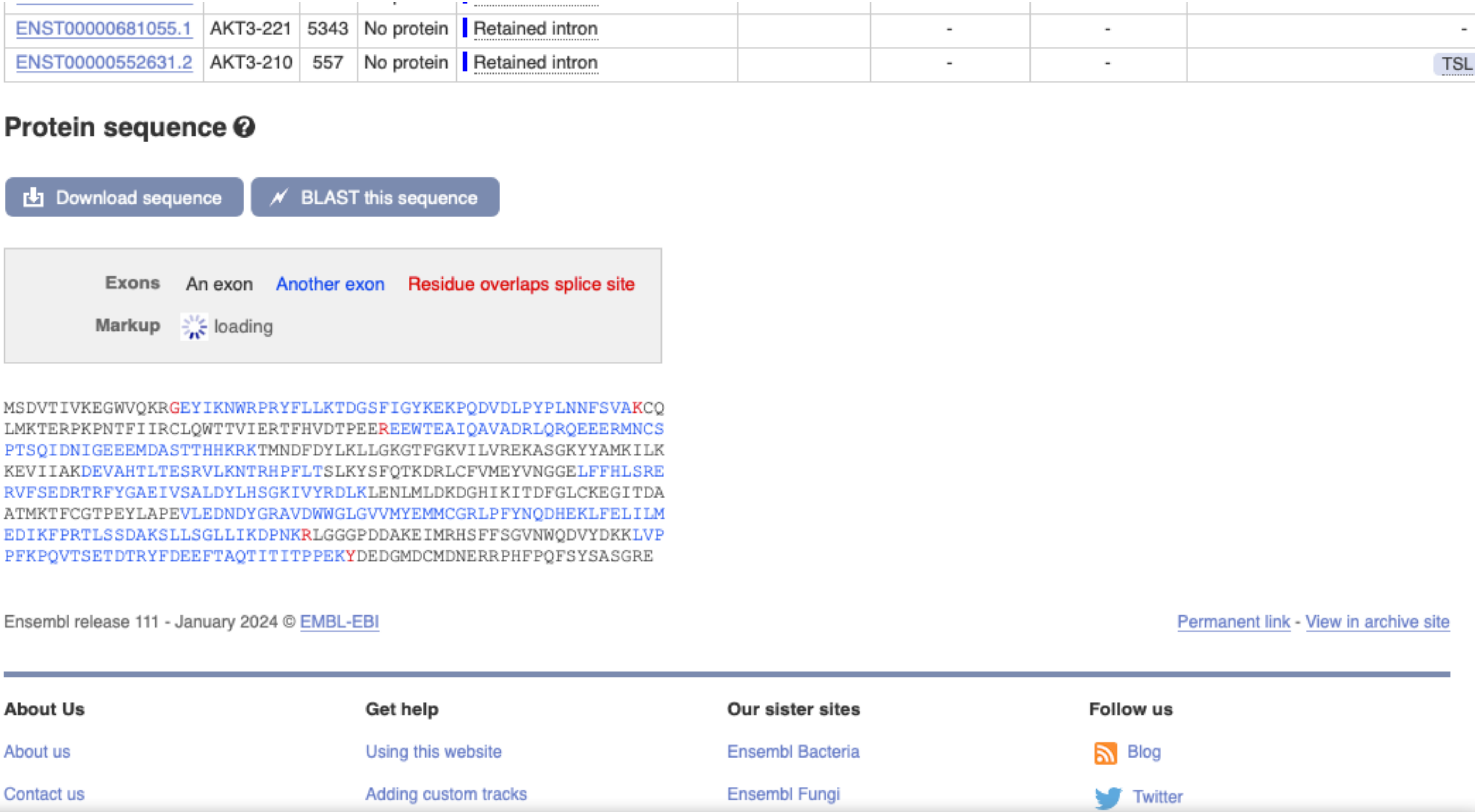
ENST00000336199.9	AKT3-202	1688	465aa	Protein coding	CCDS31076	Q9Y243-2	-	GENCODE ba
ENST00000263826.12	AKT3-201	1583	479aa	Protein coding	CCDS31077	Q9Y243-1	-	GENCODE basic A
ENST00000366540.5	AKT3-204	1575	465aa	Protein coding	CCDS31076	Q9Y243-2	-	GENCODE ba



ENST00000681055.1	AKT3-221	5343	No protein	Retained intron		-	-	-
ENST00000552631.2	AKT3-210	557	No protein	Retained intron		-	-	TSL

Protein sequence ❓

Exons	An exon	Another exon	Residue overlaps splice site
Markup	loading		

```
MSDVTIVKEGWVQKRGEYIKNWRPRYFLLKTDGSFIGYKEKPQDVDLPYPLNNFSVAKCQ
LMKTERPKPNTFIIRCLQWTTVIERTFHVDTPEEREEWTEAIQAVADRLQRQEEERMNCS
PTSQIDNIGEEEMDASTTHHKRKTMNDFDYLKLLGKGTFGKVILVREKASGKYYAMKILK
KEVIIAKDEVAHTLTESRVLKNTRHPFLTSLKYSFQTKDRLCFVMEYVNGGELFFHLSRE
RVFSEDRTRFYGAEIVSALDYLHSGKIVYRDLKLENLMLDKDGHIKITDFGLCKEGITDA
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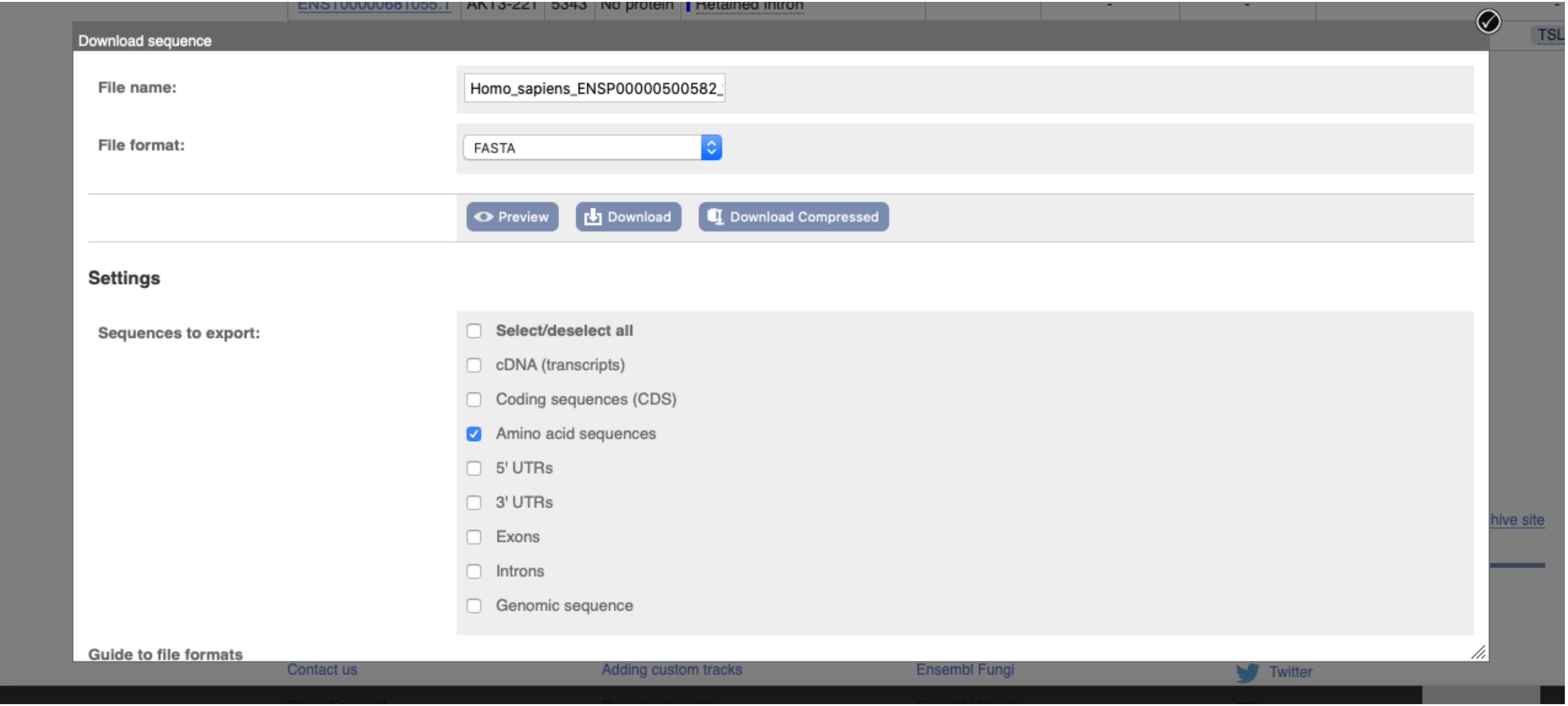

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File name: Homo_sapiens_ENSP00000500582_

File format: FASTA

Settings

Sequences to export:

- ☐ **Select/deselect all**
- ☐ cDNA (transcripts)
- ☐ Coding sequences (CDS)
- ☑ Amino acid sequences
- ☐ 5' UTRs
- ☐ 3' UTRs
- ☐ Exons
- ☐ Introns
- ☐ Genomic sequence