

Finding the genes that are close to SNPs using the SNP name, the SNP position or a region (e.g. window of 1Mb):

1) Open Ensembl database

www.ensembl.org

2) Select the specie: cow

3) Insert the SNP name: rs432423874

SNP position: 21:65164887

or SNP region: 21:64664887-65664887

4) Go

The image displays three sequential screenshots of the Ensembl BLAST/BLAT search interface, illustrating different search methods. Each screenshot shows a search bar with a species dropdown set to 'Cow' and a 'Go' button. Below the search bar, example results are provided: 'e.g. BRCA2 or rat 5:62797383-63627669 or rs699 or coronary heart disease'.

- Top Screenshot:** The search bar contains the SNP name 'rs432423874'. A green arrow points from the text 'rs432423874' in the instructions to this input field.
- Middle Screenshot:** The search bar contains the SNP position '21:65164887'. A green arrow points from the text '21:65164887' in the instructions to this input field.
- Bottom Screenshot:** The search bar contains the SNP region '21:64664887-65664887'. A green arrow points from the text '21:64664887-65664887' in the instructions to this input field.

The Ensembl logo and navigation links (BLAST/BLAT, VEP, Tools, BioMart, Downloads, Help & Docs, Blog) are visible at the top of the interface.

If you use the SNP name (rs432423874) you will obtain information about the location, alleles, etc., and the chance to explore specific information about the variant. Here you need to select **Genomic context**

Ensembl BLAST/BLAT | VEP | Tools | ...

Cow (ARS-UCD1.2)

Location: 21,65,074,210-65,075,210 Variant: rs432423874

Variant displays

- Explore this variant
- Genomic context
- Genes and regulation
- Flanking sequence
- Population genetics
- Phenotype data
- Sample genotypes
- Linkage disequilibrium
- Phylogenetic context
- Citations
- 3D Protein model

Configure this page

Custom tracks

Export data

Share this page

Bookmark this page

rs432423874 SNP

Most severe consequence

Alleles

Location

Evidence status ⓘ

HGVS names

Original source

About this variant

Explore this variant ⓘ

Genomic context

Genes and regulation

Flanking sequence

Population genetics

Phenotype data

Sample genotypes

Linkage disequilibrium

Phylogenetic context

Citations

3D Protein model

intron variant | See all predicted consequences

A/C/G

Primary assembly 21:65074710 (forward strand) | VCF: 21 65074710 rs432423874 A C,G

This variant has 18 HGVS names - Show ⓘ

Variants (including SNPs and indels) imported from dbSNP [remapped to ARS-UCD1.2] (release 150)

This variant overlaps 8 transcripts and is mentioned in 1 citation.

The gene EVL overlaps your SNP

Variant displays

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rs432423874 SNP

Most severe consequence

Alleles

Location

Evidence status ⓘ

HGVS names

Original source

About this variant

Context ⓘ

Genes (Ensembl)

EV1-201 > protein coding

EV1-202 > protein coding

EV1-203 > protein coding

EV1-204 > protein coding

EV1-205 > protein coding

EV1-206 > protein coding

EV1-207 > protein coding

EV1-208 > protein coding

Contigs

All sequence variants (dbSNP and all other sources)

SNP position

In the case of using a region surrounding the SNP then you could obtain more genes in this window

The information on this region can be **exported** in different formats (CSV, txt, GFT.. files)

Ensembl

BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog

Cow (ARS-UCD1.2) ▼

location-based displays

- Whole genome
- Chromosome summary
- Region overview
- Region in detail
- Comparative Genomics
 - Synteny
 - Alignments (image)
 - Alignments (text)
 - Region Comparison
- Genetic Variation
 - Variant table
 - Resequencing
 - Linkage Data
- Markers
- Other genome browsers
 - UCSC
 - NCBI

Configure this page

Custom tracks

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Primary_assembly 21: 64,664,887-65,664,887

primary_assembly 21

Region in detail

Contigs

Genes (Ensembl)

Gene Legend

- Ensembl protein coding
- RNA gene

Location: 21:64664887-65664887 Go Gene: Go

88 way GERP elements

Proteins from UniProtKB

cDNA alignment, EST cluster (UniGene)

Genes (Ensembl)

Cow (ARS-UCD1.2) ▼

Location: 21:64664887-65664887

Export data

Export Configuration - Feature List

Location to export: primary_assembly: ARS-UCD1.2:21:64664887-65664887:1

Output: Tab separated values *

Select location: 21 * 64664887 * 65664887 * 1 ▼

5' Flanking sequence (upstream): 0 * (Maximum of 10000)

3' Flanking sequence (downstream): 0 * (Maximum of 10000)

Next >

Fields marked * are required

Options for Tab separated values


Select/deselect all: ☐

Output:

seqname	source	feature	start	end	score	strand	frame	hid	hstart	hend	gencode	gene_id	transcript_id	exon_id
21	Ensembl	similarity	64669024	64669161	938	+	.				A0A146WEU6.1	9	49	
21	Ensembl	similarity	64669024	64669161	1265	+	.				A0A147A2B9.1	9	49	
21	Ensembl	similarity	64669024	64669161	674	+	.				A0A146WCF2.1	9	49	
21	Ensembl	similarity	64669024	64669161	945	+	.				A0A146P8U2.1	19	59	
21	Ensembl	similarity	64669036	64669161	1126	+	.				W5KPC4.1	18	59	
21	Ensembl	similarity	64669036	64669161	678	+	.				A0A2G9RWX5.1	5	45	
21	Ensembl	similarity	64669036	64669161	1458	+	.				A0A1U8DGX9.1	5	45	
21	Ensembl	similarity	64669036	64669161	1163	+	.				A0A2L0EBY7.1	11	49	
21	Ensembl	similarity	64669042	64669161	2300	+	.				G3U5G2.1	1	39	
21	Ensembl	similarity	64669042	64669161	2330	+	.				U3E8W7.1	1	39	
21	Ensembl	similarity	64669042	64669161	2343	+	.				H0WSX2.1	1	39	
21	Ensembl	similarity	64669042	64669161	2352	+	.				A0A1S2ZF30.1	1	40	
21	Ensembl	similarity	64669042	64669161	2492	+	.				A0A2U3VKW5.1	1	40	
21	Ensembl	similarity	64669042	64669161	2632	+	.				Q08DD0.1	1	40	
21	Ensembl	similarity	64669042	64669161	2583	+	.				F15AQ2.3	1	40	



Ensembl BLAST/BLAT | VEP | Tools | BioMart | Downloads | Help & Docs | Blog

 **Cow (ARS-UCD1.2)** ▼

Location: 21:64,664,887-65,664,887

Location-based displays

- Whole genome
- Chromosome summary
- Region overview
- Region in detail**
- Comparative Genomics
- Synteny
- Alignments (image)
- Alignments (text)
- Region Comparison
- Genetic Variation
- Variant table
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Other genome browsers


- UCSC
- NCBI

Configure this page

Primary_assembly 21: 64,664,887-65,664,887

primary_assembly 21

Region in detail



Genome Data Viewer

Bos taurus: ARS-UCD1.2 (GCF_002263795.1) Chr 21 (NC_037348.1): 64,664,887 - 65,664,887

Ideogram View

Unplaced/unlocalized scaffolds: 2,180

Region: EML1 XM_024982153.1
Gene Transcript

Exons: click an exon above to zoom in, mouse over to see details

NC_037348.1

Genes, NCBI Bos taurus Annotation Release 106, 2018-05-11

The ideogram displays genomic features across a coordinate range from 64,700 K to 65,300 K. Key genes shown include:

- EML1 (+12)**: Located at approximately 64,700 K.
- CYP46A1**: Located at approximately 64,750 K.
- EVL (+34)**: Located at approximately 64,850 K.
- MIR342**: Located at approximately 64,900 K.
- LOC112443168**, **XP_002696881**, **XP_003031472**, **LOC101906901**, **XP_003031543**, **DEB2**, **NP_001069719**, **LOC614244**, **MIR345 (+3)**, **LOC112443193**, **XP_024838802**, **XM_024982244**: Various other genes and transcripts located between 64,800 K and 65,000 K.
- YY1 (+4)**, **MOR25 (+8)**, **SLC25A29 (+6)**, **NP_776643**, **NP_1J74218**, **SLC25A47**, **NP_001205829**, **NP_001927582**: Genes located between 65,000 K and 65,300 K.

Search Location, gene or phenotype

Enter a location, gene name or phenotype

Search examples:

UCSC Genome Browser on Cow Oct. 2007 (Baylor 4.0/bosTau4) Assembly

move <<< << < > >> >>> zoom in 1.5x 3x 10x base zoom out 1.5x 3x 10x 100x

chr21:64,664,887-65,664,887 1,000,001 bp. enter position, gene symbol or search terms go

chr21 21

Scale chr21: 64,600,000 64,900,000 65,000,000 65,100,000 65,200,000 65,300,000 65,400,000 65,500,000 65,600,000

Gap

RefSeq Genes

Other RefSeq

Non-Cow RefSeq Genes

Human Proteins Mapped by Chained tBLASTn

Cow mRNAs from GenBank

Cow ESTs That Have Been Spliced

5 Mammals Conservation by PhastCons

5 Mammals E1

Dog

Human

Mouse

Platypus

Human Chain

Human Net

RepeatMasker

move start < 2.0 > move < 2.0 >

track search default tracks default order hide all add custom tracks track hubs configure multi-region reverse resize refresh

Chromosome Color Key:

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 X Y M Un

Use drop-down controls below and press refresh to alter tracks displayed.

Tracks with lots of items will automatically be displayed in more compact modes.

collapse all expand refresh

Mapping and Sequencing