

How to access genomic information using Ensembl (worked example)

The screenshot shows the Ensembl Genome Browser interface. At the top, there is a search bar with a dropdown menu set to 'Anything' and a 'Lookup' button. Below this is the 'Species - Ensembl v19' section, which lists various species with buttons for each. The 'Human' button is highlighted with an arrow. To the left of the species list is the 'About Ensembl' section, which provides information about the project and its funding. At the bottom right, there is a section titled 'Have you tried?' with a link to the 'Ensembl Chimp Preview Browser'.

Multi-species text searching

STEP 1
Choose human

‘About Ensembl’ plus general help and documentation – multi-species

Human Genome Browser

Ensembl Entry Points

Search for with Lookup

Display Chr From To Lookup

Retrieve a sequence Export Advanced data retrieval tool EnsMart

Search your sequence BLAST/SSAHA

Browse a Chromosome

Annotation

Ensembl human genes (ENS*) are generated automatically by the Ensembl gene builder. For a number of human chromosomes, manual annotations are also available from [Vega](#). These curated data are imported into and linked from Ensembl.

Documentation & Help

About Ensembl Home

For context-sensitive help on any web page click Help

Questions or suggestions? Try Help Desk

Documentation (includes tutorial on direct data access & instructions for installing Ensembl on your own site) Documentation

Current Release 19.34a.1

This release is based on the NCBI 34 assembly of the human genome.

View the [status history](#) of the human assemblies.
Last Update: 10-12-2003

Ensembl gene predictions: 23531
GenScan gene predictions: 65010
Ensembl gene exons: 225897
Ensembl gene transcripts: 31809
Contigs: 26814
Clones: 28814
Base Pairs: 3201762515
Golden Path Length: 2841366484

What's New

Ensembl Links and Site Map

Download
 Export
 EnsMart Home
 BLAST/SSAHA

Other Species

Mosquito
 C. briggsae
 C. elegans
Zebrafish
 Fruitfly
 Fugu
Mouse
 Rat

Search function

STEP 2
Pick chromosome 20

Help!

Quick access to the different "Views"

Find Lookup [e.g. 12, X] Help

Known Genes Z OC

Genes Repeats

Chromosome 20

Length: 63691868 bps
 Novel Ensembl genes: 63
 Known Ensembl genes: 613
 Snps: 219266

Change Chromosome

Chromosome: Go

Jump to Contigview

Click anywhere on the chromosome ideogram or one of the feature distribution plots to jump to a contig-level view of features at that point. Alternatively, you can jump to contigview between any two markers on the chromosome:

Between: Go

and: Go

[Display contig-level view between any two features.](#)

Synteny

View Human Chr 20 vs Go

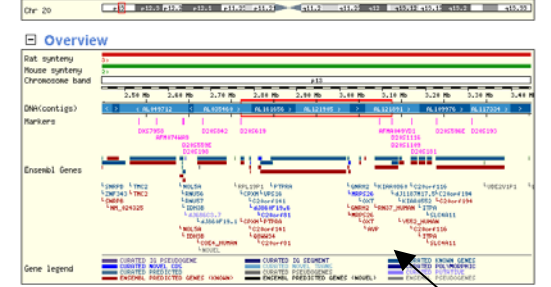
OMIM Diseases

[Browse OMIM Diseases](#) on this chromosome.

Click to display a region

STEP 3
Display the region between markers D20S619 and D20S1116

Display a region between any two features



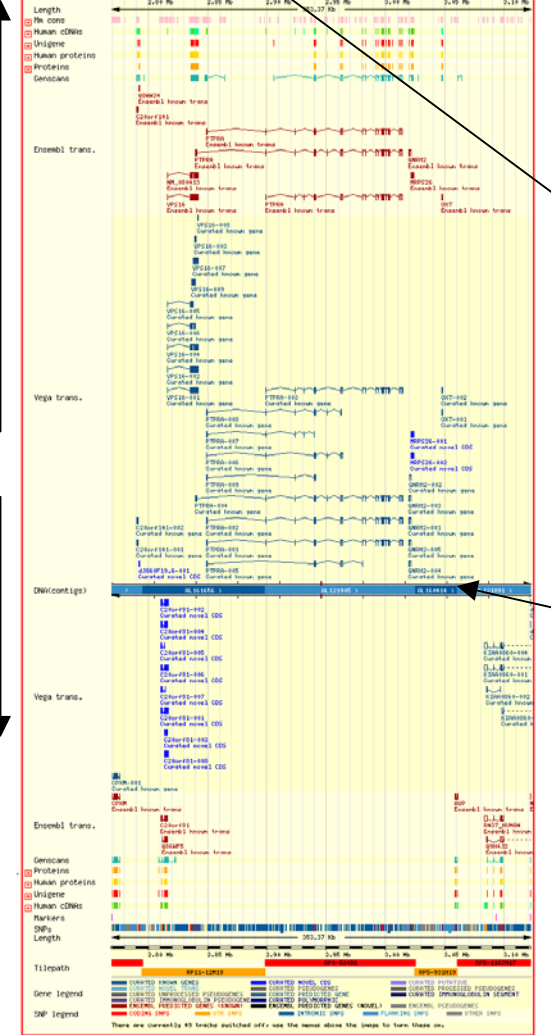
Entire chromosome

'Overview' displays chromosomal region

Detailed View

Jump to Chromosome: 20 bp [2769053 to 3122426] Refresh

Features DAS Sources Repeat Deconstructions Jump to Image size Help



'Detailed view' use menus on gold bar to customise view

STEP 4
Click on location in overview panel to center on AVP gene

and then zoom in using the "plus" button

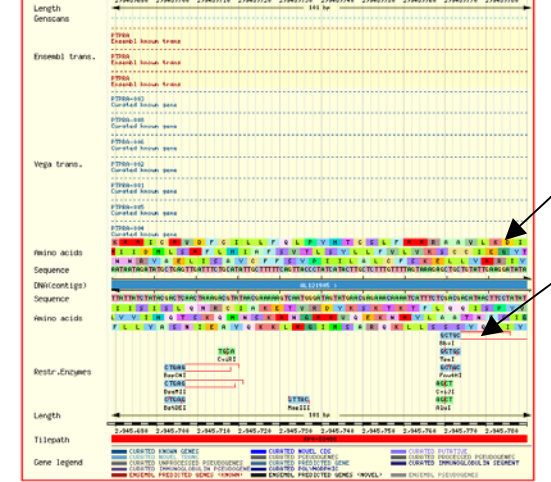
DNA (contigs) sequence assembly

Fwd strand features

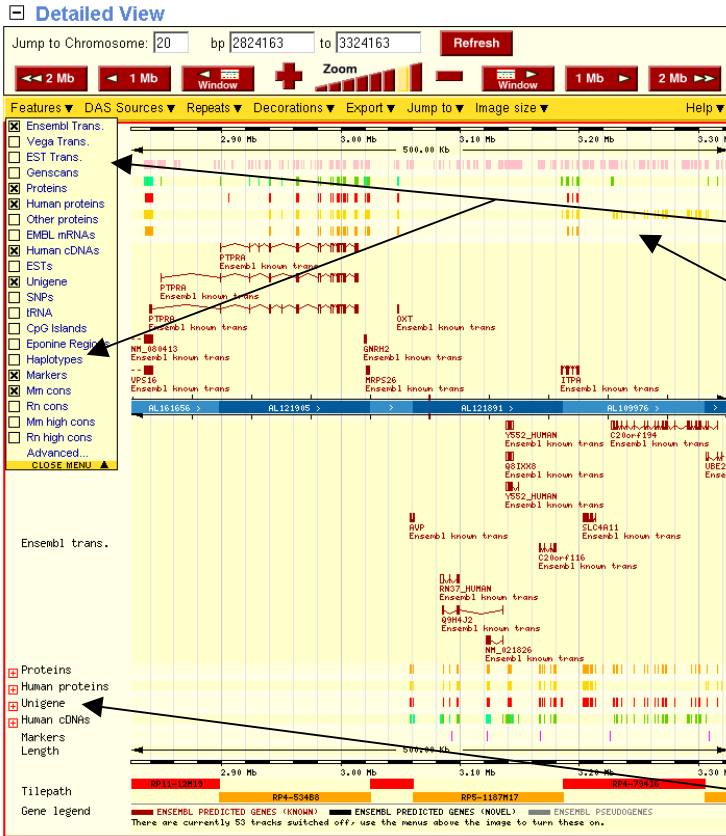
Reverse strand

Basepair View

Length Genoscan Ensembl trans. Vega trans. Amino acids Sequence DN1(contigs) Restr. Enzymes Length Tlirpath Gene legend



'Basepair View' shows six frame translations and restriction enzyme profile



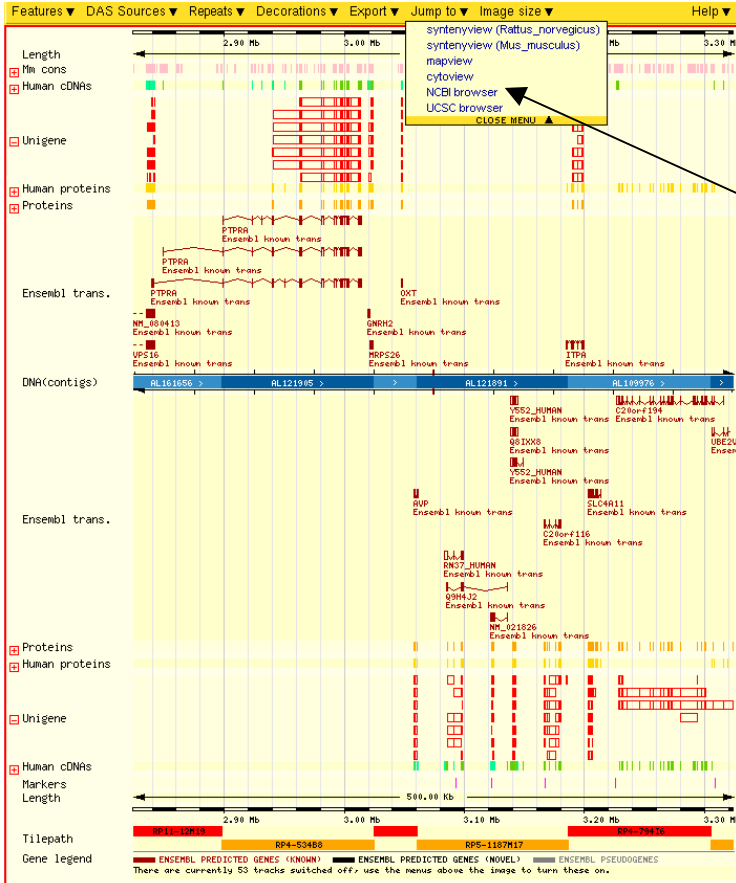
STEP 5

Customise the display – show SNPs, hide Genscans, CpG islands, Vega transcripts and EST transcripts

Evidence tracks

STEP 6

‘Expand’ or ‘compact’ the Unigene evidence track



STEP 7

Jump to CytoView

STEP 8
Zoom out to view larger region

Find Sequence [e.g. AP000462, RH9632, cancer]

Chromosome 20

Chr 20

Detailed View

Jump to Chromosome: 20 bp 2824163 to 3324163 Band:

Features ▾ DAS Sources ▾ Repeats ▾ Decorations ▾ Export ▾ Jump to ▾ Image size ▾ Help ▾

Mouse synteny
Rat synteny
Length
Chromosome band
DNA(contigs)
NT Contigs
Tilepath
Markers
Ensembl Genes
Repeats
Length
Gene Legend

As HTML CSV

Dump clones and genes

STEP 9
Use browser BACK button to return to ContigView and then click on a marker

Find Marker [e.g. RH9632, D1S2806]

Chromosome Map Marker Z67154

Assembly location: Z67154 is currently mapped to the following Ensembl location(s):

Chromosomal position	Flat file of region
20 (3045784 bp - 3046054 bp)	Export data

Marker Details:

Name	Database
24435	urists

Additional synonyms: Z67154, RH49584, STSG20223, RH5082, RH57273, W857, A049YD1, AFMA049YD1

Marker Z67154 primers:

Left Primer	Right Primer	Expected Product Size
CACCAAGCACTGACAATC	CCTGGCCCTGTTAAT	269

Marker Z67154 map locations:

Map Name	Synonym	Chromosome	Position	LOD score
wirh	AFMA049YD1	20	28.2	1.45
wiyac	AFMA049YD1	20	18	

Date: 2003-07-11 14:26:27 [Help Desk / Suggestions](#)

Map information

STEP 10
Use browser BACK button to return to ContigView, then click on a SNP

Ensembl SNP Report

SNP	2740190
Source	dbSNP
Synonyms	dbSNP: 2740190 HGbase: SNP001452001
Score	1
Validation Status	suspected (SNP arising directly from SNP detection assays)
Alleles	CIT (ambiguity code: Y)
Sequence Region	AATGTTGGAGAGAGATGCAGAGACAYTGACAGTGACGGAGAGAAGAGTGAG (SNP highlighted)
SNP neighbourhood	

Details of this SNP

Genomic neighbourhood, showing genes and SNP types

SNP location(s)

This SNP is currently mapped to the following genomic locations:

Chromosome	Start	End	Strand	Show in context
20	3057829	3057829	-1	ContigView

STEP 11

Use browser **BACK** button to return to ContigView, then click on the AVP Ensembl transcript (red)

Ensembl Gene Report

Gene	AVP (HUGO ID)																
Ensembl Gene ID	ENSG00000101200																
Genomic Location	View gene in genomic location: 3056302 - 3061050 bp (3.1 Mb) on chromosome 20 This gene is located in sequence: AL160414.19.1.35836																
Description	VASOPRESSIN-NEUROPHYSIN 2-COPEPTIN PRECURSOR (AVP-NPI) [CONTAINS: ARG-VASOPRESSIN, NEUROPHYSIN 2 (NEUROPHYSIN-II), COPEPTIN] [Source: SWISSPROT (P01188)]																
Prediction Method	Genes were annotated by the Ensembl automatic analysis pipeline using either a GeneWise model from a human/vertebrate protein, a set of aligned human cDNAs followed by GenomeWise for ORF prediction or from GenScan scores supported by protein, cDNA and EST evidence. GeneWise models are further combined with available aligned cDNAs to annotate UTRs.																
Prediction Transcript	1: AVP (ENST00000217172) [Transcript information] [Exon information] [Protein information] 																
Orthologue Prediction	The following gene(s) have been identified as putative orthologues by reciprocal BLAST analysis: <table border="1"> <thead> <tr> <th>Species</th> <th>Type</th> <th>dN/dS</th> <th>Gene Identifier</th> </tr> </thead> <tbody> <tr> <td><i>Mus musculus</i></td> <td>BRH</td> <td>0.06756</td> <td>ENSMUSG00000007727 (Arg) VASOPRESSIN-NEUROPHYSIN 2-COPEPTIN PRECURSOR (AVP-NPI) [CONTAINS: ARG-VASOPRESSIN, NEUROPHYSIN 2 (NEUROPHYSIN-II), COPEPTIN] [Source: SWISSPROT (P01188)]</td> </tr> <tr> <td><i>Rattus norvegicus</i></td> <td>BRH</td> <td>-</td> <td>ENSRNOG00000002129 (NEU2_RAT) VASOPRESSIN-NEUROPHYSIN 2-COPEPTIN PRECURSOR (AVP-NPI) [CONTAINS: ARG-VASOPRESSIN, NEUROPHYSIN 2 (NEUROPHYSIN-II), COPEPTIN] [Source: SWISSPROT (P01188)]</td> </tr> <tr> <td><i>Fugu rubripes</i></td> <td>RHS</td> <td>-</td> <td>SNFRUG00000152908 (NM_009732) No description</td> </tr> </tbody> </table> BRH = Best Reciprocal Hit ("BEST") RHS = Reciprocal Hit based on Synthesis around BRH ("FISH")	Species	Type	dN/dS	Gene Identifier	<i>Mus musculus</i>	BRH	0.06756	ENSMUSG00000007727 (Arg) VASOPRESSIN-NEUROPHYSIN 2-COPEPTIN PRECURSOR (AVP-NPI) [CONTAINS: ARG-VASOPRESSIN, NEUROPHYSIN 2 (NEUROPHYSIN-II), COPEPTIN] [Source: SWISSPROT (P01188)]	<i>Rattus norvegicus</i>	BRH	-	ENSRNOG00000002129 (NEU2_RAT) VASOPRESSIN-NEUROPHYSIN 2-COPEPTIN PRECURSOR (AVP-NPI) [CONTAINS: ARG-VASOPRESSIN, NEUROPHYSIN 2 (NEUROPHYSIN-II), COPEPTIN] [Source: SWISSPROT (P01188)]	<i>Fugu rubripes</i>	RHS	-	SNFRUG00000152908 (NM_009732) No description
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<i>Fugu rubripes</i>	RHS	-	SNFRUG00000152908 (NM_009732) No description														
Disease Matches	This Ensembl entry corresponds to the following OMIM disease identifiers: Diabetes insipidus, neurohypophysial, 125700 (3) [OMIM:125700-3] [OMIM:125700-3] [OMIM:125700-3]																

View genomic location

STEP 12
Look at the GeneView page, then click 'View transcript info' to go to TransView

Homologies with other species

GeneDAS	SwissProt
reference	NEU2_HUMAN DIMeglio L.A., Gagliardi P.C., Browning J.E., Quigley C.A., Repaske D.R., "A missense mutation encoding cyst67 -> gly in neurophysin a is associated with early onset autosomal dominant neurohypophysialdiabetes insipidus.", Mol. Genet. Metab. 72:39-44(2001).
reference	NEU2_HUMAN Fuji H., Iida S., Moriwaki K., "Familial neurohypophysial diabetes insipidus associated with a novel mutation in the vasopressin-neurophysin II gene.", Int. J. Mol. Med. 5:229-234(2000).
reference	NEU2_HUMAN Gagliardi P.C., Bernasconi S., Repaske D.R., "Autosomal dominant neurohypophysial diabetes insipidus associated with a missense mutation encoding Gly23 -> Val in neurophysin II.", J. Clin. Endocrinol. Metab. 82:3643-3646(1997).
reference	NEU2_HUMAN Grant F.D., Ahmadi A., Hosley C.M., Majzoub J.A., "Two novel mutations of the vasopressin gene associated with familialdiabetes insipidus and identification of an asymptomatic carrier infant.", J. Clin. Endocrinol. Metab. 83:3959-3964(1996).
reference	NEU2_HUMAN Ito M., Oiso Y., Murase T., Kanda K., Saika H., Chizei T., Racchi M., Lively M.O., "Possible involvement of inefficient cleavage of prevasopressin by signal peptidase as a cause for familial central diabetes insipidus.", J. Clin. Invest. 91:2565-2571(1993).
reference	NEU2_HUMAN Light A., du Vigneaud V., "On the nature of oxytocin and vasopressin from human pituitary.", Proc. Soc. Exp. Biol. Med. 96:692-696(1958).
reference	NEU2_HUMAN McLeod J.F., Kovacs L., Gaskill M.B., Rittig S., Bradley G.S., Robertson G.L., "Familial neurohypophysial diabetes insipidus associated with signal peptide mutation.", J. Clin. Endocrinol. Metab. 77:699A-699G(1993).

References from SwissProt

Export data - retrieve sequence and annotation

Export Data	Export gene data in EMBL, GenBank or FASTA
SNP information	View information about variations on this gene.

GeneSNPview

Transcript/Translation Summary

AVP	Stable ID: ENST00000217172 Exons: 3 Transcript length: 1247 bp Translation length: 164 residues [Transcript information] [Exon information] [Protein information]
Similarity Matches	This Ensembl entry corresponds to the following database identifiers: AFFY HG U133 all: 207848_at AFFY HG U133A: 207848_at AFFY HG U85 all: 34020_at AFFY HG U85A: 34020_at AFFY HG U85A2: 34020_at EMBL: AL160414 [link] M11186 [link] M05647 [link] X03172 [link] 352892 [link] 352891 [link] Search GeneCards for AVP HUGO: 551 [link] LocusLink: 125700 192340 MIM: AA461201.1 [link] AA468772.1 [link] CA426936.1 [link] CA444681.1 [link] Protein ID: CA444682.1 [link] CAC10205.1 [link] RefSeq: NM_000490 (Target Nid: 100, Query Nid: 100) [link] SWISSPROT: NEU2_HUMAN (Target Nid: 100, Query Nid: 100) [link] [Search GO]
GO	The following GO terms have been mapped to this entry via Swissprot/SpTrEMBL: GO:0005186 [neurohypophysial hormone activity] GO:0005576 [extracellular] GO:0005625 [soluble fraction] GO:0006061 [energy pathway] GO:0006933 [water transport] GO:0007165 [signal transduction] GO:0007267 [cell-cell signaling] GO:0008217 [regulation of blood pressure]
InterPro	IPR000991 Neurohypophysial hormone - [View other Ensembl genes with this domain]
Protein Family	ENSG00000000945: NEUROPHYSIN 1 PRECURSOR [CONTAINS: NEUROPHYSIN 1] This cluster contains 2 Ensembl gene member(s)
Transcript Structure	
Protein Features	

Links to other databases

GO annotation

Find related proteins

Protein structure

Ensembl Protein Report

Peptide	AVP (HUGO ID)
Ensembl Translation ID	ENSP00000217172
Ensembl Translation	This peptide is a product of gene ENSG00000101200 [Transcript Information] [Exon Information]
Description	VASOPRESSIN-NEUROPHYSIN 2-COPEPTIN PRECURSOR (AVP-NPI) [CONTAINS: ARG-VASOPRESSIN; NEUROPHYSIN 2 (NEUROPHYSIN-II); COPEPTIN]. [source: SWISSPROT (P01185)]
Prediction Method	Genes were annotated by the Ensembl automatic analysis pipeline using either a GeneWise model from a human/vertebrate protein, a set of aligned human cDNAs followed by GenomeWise for ORF prediction or from Genscan exons supported by protein, cDNA and EST evidence. GeneWise models are further combined with available aligned cDNAs to annotate UTRs.
InterPro	IPR000961 Neurohypophysial hormone - [View other Ensembl genes with this domain]
Protein Family	ENSF0000000945 : NEUROPHYSIN 1 PRECURSOR [CONTAINS: ; NEUROPHYSIN 1] This cluster contains 2 Ensembl gene member(s)
Protein Features	
Export Data	Export peptide data in EMBL, GenBank or FASTA

Links back to TransView or ExonView

STEP 16
Examine ProteinView page, then click to go to FamilyView

Peptide cDNA Sequence

No markup No numbers

MPDTMLPACFLGLLAFSSACTYFQNCPRGGKRAMDLELRQLPCGPGGKGRGCFGSPICG
DELCGFVGTAEALRCQENYLPSPCQSGGKACGSGRCAAFQVCNDRECVTEFECRECG
HRRARASDERSMATQLDGPAGALLRLVOLAGAPFPFEPFAQPDAY

Protein sequence

Peptide Stats

Isoelectric point = 4.9366
Charge = -2.5
Molecular weight = 17324.67
Number of residues = 164
Ave. residue weight = 105.638

Domains in protein

Domain type	Accession number	Description	Start	End
prints	PR00831	Neurhyp_horm	21	35
prints	PR00831	Neurhyp_horm	39	55
prints	PR00831	Neurhyp_horm	55	74
prints	PR00831	Neurhyp_horm	74	93
prints	PR00831	Neurhyp_horm	96	116
Pfam	PF00220	Neurhyp_horm	20	28
Pfam	PF00184	Neurhyp_horm	39	116
prosite	PS00264	Neurhyp_horm	20	28

SNPs

Domain type	Start	End
Signal peptide	1	19

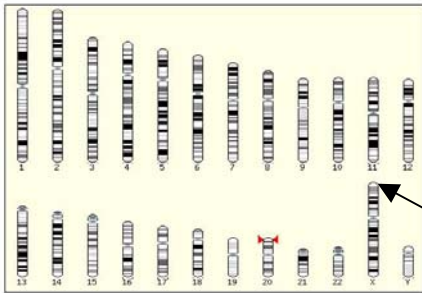
Residue	SNP ID	SNP type	Alleles	Ambiguity code	Alternate residues
34	3729864	Synonymous	G/A	R	-
82	5195	Non-synonymous	G/A	R	P, L
119	1051744	Non-synonymous	C/A	M	G, V

Ensembl Protein Family ENSF00000000888 members

Consensus Annotation: NEUROPHYSIN 1 PRECURSOR [CONTAINS: ; NEUROPHYSIN 1].

The annotation confidence score of this family is 40.

Protein families generated by TRIBEMCL. Enright A.J., Van Dongen S. and Ouzounis C.A. (2002) "An efficient algorithm for large-scale detection of protein families" *Nucl. Acids Res.* **30**, 1076-1084.



Chromosomal location and links to other human family members

The following Ensembl genes contain peptides in family ENSF00000000888

Click to view multiple alignments of the 11 Ensembl members of this family. [JaView](#)

Click to view multiple alignments of all 71 members of this family. [JaView](#)

Chr.	Ensembl Gene	Description
20	ENSG00000101200	VASOPRESSIN-NEUROPHYSIN 2-COPEPTIN PRECURSOR (AVP-NP2) [CONTAINS: ARG-VASOPRESSIN; NEUROPHYSIN 2; NEUROPHYSIN-2; COPEPTIN]. [Source: SWISSPROT (Accession: OXYTOCIN-NEUROPHYSIN 1 PRECURSOR (OT-NP1) [CONTAINS: OXYTOCIN (OXYTOCIN), NEUROPHYSIN 1] [Source: SWISSPROT (Accession: P01178)]
20	ENSG00000101405	

Other peptides in this family

SWISSPROT

CONO_LYMST	NEUI_MOUSE	NEUI_STRCA	NEU2_HUMAN	NEU2_STRCA	NEUM_BUEJA
CXPB_CONRA	NEUI_ONCKE	NEUI_ANSAN	NEU2_LOXAF	NEUI_CATCO	NEUI_BUEJA
NEUI_ANSAN	NEUI_ONCMA	NEUI_BALPH	NEUI_MOUSE	NEUI_ONCKE	NEUI_CHICK
NEUI_BOVIN	NEUI_PAPHA	NEUI_BOVIN	NEUI_ONCKE	NEUI_ONCMA	NEUI_FUGRU
NEUI_CATCO	NEUI_PIG	NEUI_CATCO	NEUI_PIG	NEUI_CATCO	NEUI_RANES
NEUI_HORSE	NEUI_RAT	NEUI_CAVRO	NEUI_RAT	NEUI_ONCKE	
NEUI_HUMAN	NEUI_SHEEP	NEUI_HORSE	NEUI_SHEEP	NEUI_FUGRU	

STEP 17
See multiple alignment

Family members in other Ensembl species

SPTREMBL

O14935	Q8AV79	Q8U484	Q81728	Q8B046
Q57307	Q8AVF7	Q50W44	Q81604	Q8B441
Q67388	Q8AUB8	Q00W45	Q8B5UB	Q8B442
Q28335	Q8WPD6	Q91078	Q9B0G5	Q9U083

Ensembl *Danio rerio* peptides

ENSDFARP00000016716	ENSDFARP00000016584
-------------------------------------	-------------------------------------

Ensembl *Mus musculus* peptides

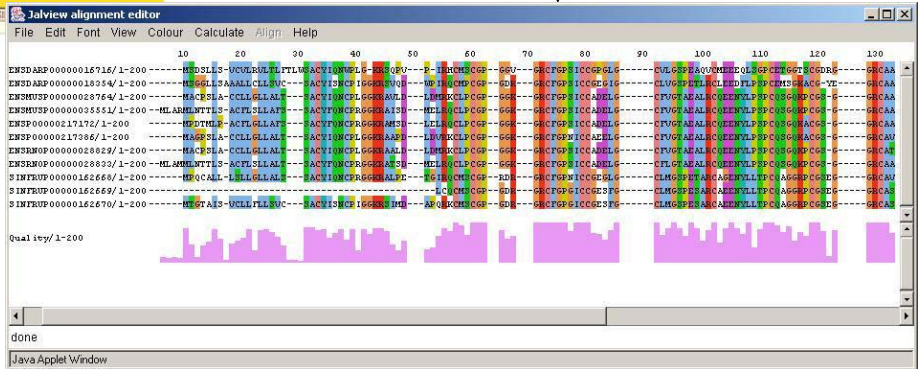
ENSMUSP00000003764	ENSMUSP00000003551
------------------------------------	------------------------------------

Ensembl *Rattus norvegicus* peptides

ENSRRNOP00000028828	ENSRRNOP00000028833
-------------------------------------	-------------------------------------

Ensembl *Fugu rubripes* peptides

SINFRUP000000162669	SINFRUP000000162669
-------------------------------------	-------------------------------------



STEP 18
Use browser BACK button to return to GeneView, then click on 'Export gene data in EMBL, GenBank or FASTA'

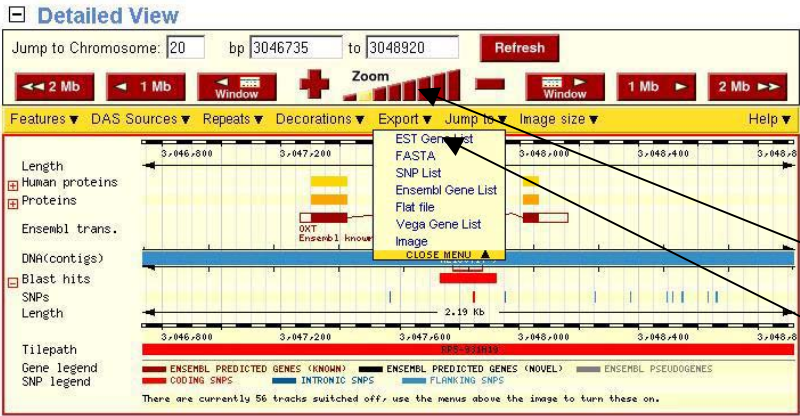
STEP 22
 Paste the sequence, select the databases *Homo sapiens* & *Peptides*; select **BLASTX** as search tool; then click 'Run'

Status of query: Job queued

STEP 23
 Click to retrieve results – repeat till see that query is completed – then click 'view'

Display options – use default

Status of query: Completed



STEP 25

After viewing BLAST hits, zoom out several steps, then use 'Export' pull-down menu to export an Ensembl gene list

View the BLAST hits

Ensmart page, ready to export gene feature list for the region

OUTPUT START FILTER OUTPUT export

Features SNPs Structures Sequences

REGION:

Chromosome Attributes:

Chromosome Name End Position (bp)

Start Position (bp) Start

Band

GENE:

Ensembl Attributes:

Ensembl Gene ID Description

Ensembl Transcript ID Ensembl Peptide ID

External Gene ID External Gene DB

Ensembl CDS length Ensembl cDNA length

Ensembl Peptide length Transcript count

External Reference Attributes (max 3):

Protein ID HUGO ID

GO ID GO Description

GO Evidence Code SPTSEMBL ID

EMBL ID SWISSPROT ID

PDB ID MIM ID

RefSeq ID LocusLink ID

GKB ID

Microarray Attributes

Include

AFFY HG U133 all AFFY HG U133A

AFFY HG U133B AFFY HG U95 all

AFFY HG U95A AFFY HG U95A2

AFFY HG U95B AFFY HG U95C

AFFY HG U95D AFFY HG U95E

Disease Attributes

Disease OMIM ID Disease Description

EXPRESSION:

Source of expression data

eGenetics/SANBI GNF (AFFY-HG-U95)

MULTI SPECIES COMPARISONS

Fugu Homolog Attributes

Fugu Ensembl Gene ID Fugu External ID

Fugu External DB Fugu Chromosome

Fugu Chr Start (bp) Fugu Chr End (bp)

Orthology Type Ensembl Peptide ID

% Coverage % Identity

Fugu Ensembl Peptide ID Fugu % Coverage

Fugu % Identity

MULTI SPECIES COMPARISONS

Fugu Homolog Attributes

Fugu Ensembl Gene ID Fugu External ID

Fugu External DB Fugu Chromosome

Fugu Chr Start (bp) Fugu Chr End (bp)

Orthology Type Ensembl Peptide ID

% Coverage % Identity

Fugu Ensembl Peptide ID Fugu % Coverage

Fugu % Identity

Mouse Homolog Attributes

Mouse Ensembl Gene ID Mouse External ID

Mouse External DB Mouse Chromosome

Mouse Chr Start (bp) Mouse Chr End (bp)

Orthology Type dN/dS

dN dS

Ensembl Peptide ID % Coverage

% Identity Mouse Ensembl Peptide ID

Mouse % Coverage Mouse % Identity

Rat Homolog Attributes

Rat Ensembl Gene ID Rat External ID

Rat External DB Rat Chromosome

Rat Chr Start (bp) Rat Chr End (bp)

Orthology Type dN/dS

dN dS

Ensembl Peptide ID % Coverage

% Identity Rat Ensembl Peptide ID

Rat % Coverage Rat % Identity

Zebrafish Homolog Attributes

Zebrafish Ensembl Gene ID Zebrafish External ID

Zebrafish External DB Zebrafish Chromosome

Zebrafish Chr Start (bp) Zebrafish Chr End (bp)

Orthology Type Ensembl Peptide ID

% Coverage % Identity

Zebrafish Ensembl Peptide ID Zebrafish % Coverage

Zebrafish % Identity

Homo sapiens Regions Matching Mouse Genome

Distance Upstream (match with Mouse) Length of Match (match with Mouse)

Percentage Identity (match with Mouse) Chromosome Start (match with Mouse)

Chromosome End (match with Mouse)

Homo sapiens Regions Matching Rat Genome

Distance Upstream (match with Rat) Length of Match (match with Rat)

Percentage Identity (match with Rat) Chromosome Start (match with Rat)

Chromosome End (match with Rat)

PROTEIN:

Interpro Attributes

InterPro ID InterPro Description

InterPro Short Description

Family Attributes

Ensembl Family ID Family Description

Domain Attributes

Include

PFAM ID PRINTS ID

Prosite ID

Select the output format:

HTML Text, fixed width

Text, comma separated Text, tab separated

MS Excel

File compression:

None gzip (.gz)

Enter a name for this result set:

Name:

Enter a value to open results in a new browser window, or to provide a name for file download.

back export

STEP 26
Request positional data and external gene ID

Summary

start

- Focus: Ensembl Genes
- Species: Homo sapiens
- 21787 Entries Total

filter

- Chromosome: 20
- From base: 3046735
- To base: 3048920
- 1 Entries pass Filters

output

Not yet initialised

Select Excel output format, and click 'export'

Output in Excel format

	A	B	C	D	E	F
1	Chromosome Name	Start Position (bp)	Band	Ensembl Gene ID	External Gene ID	
2	20	2972268	p13	ENSG00000125787.1	GNRH2	
3	20	2974708	p13	ENSG00000125901.1	Q9H273	
4	20	3000261	p13	ENSG00000101405.1	OXT	
5	20	3011186	p13	ENSG00000101200.1	AVP	
6	20	3035553	p13	ENSG00000178560.1		
7	20	3036220	p13	ENSG00000125819.1	U7I5_HUMAN	
8	20	3091273	p13	ENSG00000088899.1	Y552_HUMAN	
9						
10						
11						

Output in HTML format



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Chromosome Name	Start Position (bp)	Band	Ensembl Gene ID	External Gene ID
20	2972268	p13	ENSG00000125787.1	GNRH2
20	2974708	p13	ENSG00000125901.1	Q9H273
20	3000261	p13	ENSG00000101405.1	OXT
20	3011186	p13	ENSG00000101200.1	AVP
20	3035553	p13	ENSG00000178560.1	
20	3036220	p13	ENSG00000125819.1	U7I5_HUMAN
20	3091273	p13	ENSG00000088899.1	Y552_HUMAN
20	3119012	p13	ENSG00000101205.1	C2Oorf116
20	3138094	p13	ENSG00000125877.1	ITPA
20	3156063	p13	ENSG00000088836.1	SLC4A11
20	3179792	p13	ENSG00000088854.1	C2Oorf194