

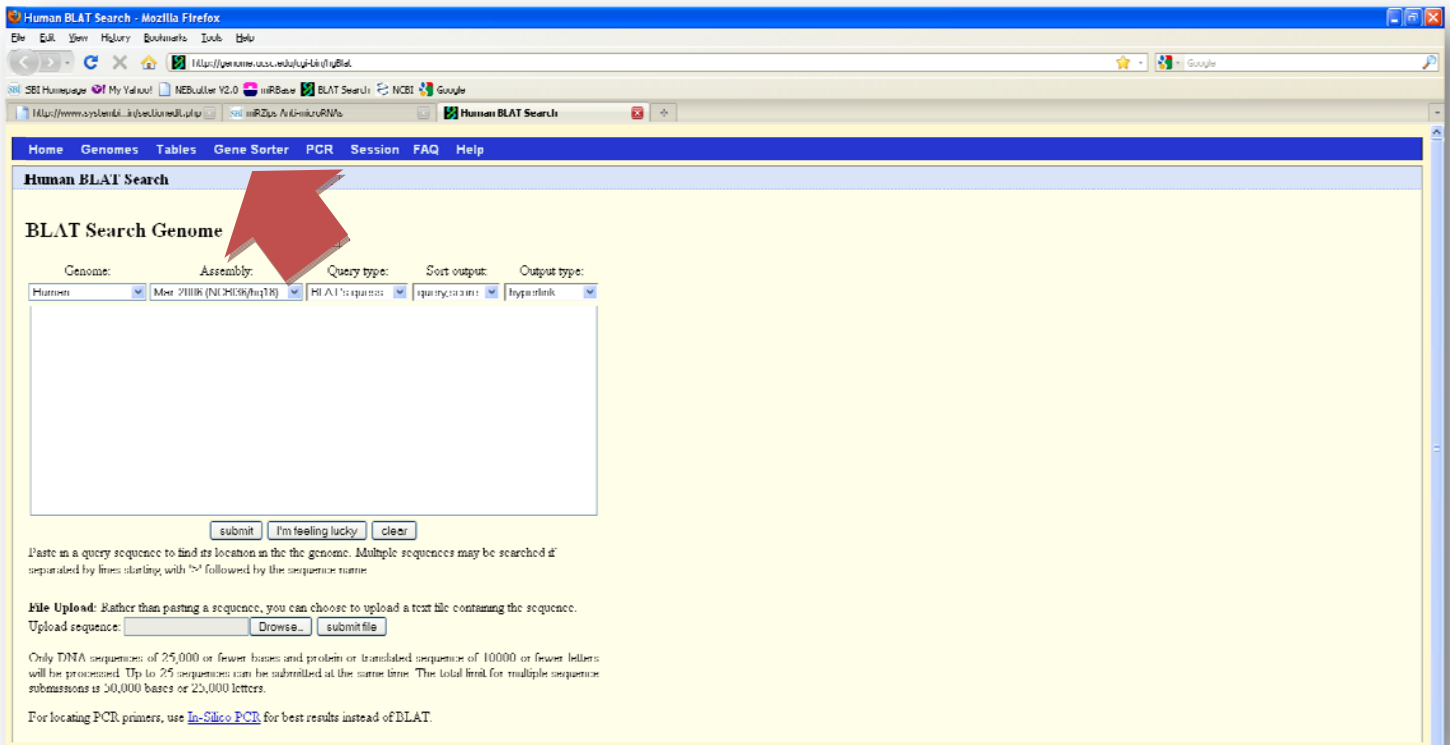
How do I find the 3' UTR sequence for my gene of interest?

START HERE:

<http://genome.ucsc.edu/cgi-bin/hgNear?org=Human&db=hg18&hgsid=160960441>

This will take you to UCSC's BLAT genome browser.

Next, click on **Gene Sorter**



Human BLAT Search - Mozilla Firefox

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Human BLAT Search

BLAT Search Genome

Genome: Assembly: Query type: Sort output: Output type:

Human Mar 2006 (NCBI36/hg18) BLAT's queries query names hyperlink

submit I'm feeling lucky clear

Paste in a query sequence to find its location in the genome. Multiple sequences may be searched if separated by lines starting with '#' followed by the sequence name.

File Upload: Rather than pasting a sequence, you can choose to upload a text file containing the sequence.
Upload sequence:

Only DNA sequences of 25,000 or fewer bases and protein or translated sequence of 10,000 or fewer letters will be processed. Up to 25 sequences can be submitted at the same time. The total limit for multiple sequence submissions is 50,000 bases or 25,000 letters.

For locating PCR primers, use [In-Silico PCR](#) for best results instead of BLAT.

Now, type in your gene of interest's name – this example shows "Slc7a1".

The screenshot shows the UCSC Human Gene Sorter web application. At the top, there are dropdown menus for 'genome' (set to 'Human') and 'assembly' (set to 'Mar 2006 (NCBI36/hu18)'). The search bar contains the text 'Slc7a1'. Below the search bar are buttons for 'sort by', 'configure', 'filter (now off)', 'display (all)', and 'output'. A red arrow points to the search bar. Below the search bar is a section titled 'About the Gene Sorter' with instructions on how to use the tool.

About the Gene Sorter

This program displays a sorted table of genes that are related to one another. The relationship can be one of several types, including protein-level homology, similarity of gene expression patterns, or genomic proximity.

To display a gene and its relatives:

1. Select a genome and assembly from the corresponding pull-down menu.
2. Type a word or phrase into the search text box to specify which gene should be displayed in the Gene Sorter. Examples of search terms include FOXA2, HOXA9, and MAP kinase.
3. Choose the gene relationship with which you would like to sort the list by selecting an option from the sort-by pull-down menu.
4. Press the Go! button to display your results.

Following a successful search, the Gene Sorter displays a table containing the specified gene, highlighted in light green, and its relatives, each on a separate line. To adjust the number of rows shown, select an option from the display pull-down menu.

The default set of table columns -- which can be expanded, reduced, and rearranged via the configure button -- shows additional information about the genes. Some of the column data, such as those in the *ELIAS* *S*-value and *%ID* columns, are calculated relative to the highlighted gene. To select a different gene in the list, click on its name. Clicking on a gene's *Genome Position* will open the UCSC Genome Browser to the location of that gene. Similarly, clicking on a gene's *Accession* will open a page showing detailed information about the gene.

One of the most powerful features of the Gene Sorter is its filtering capabilities, accessed via the filter button. Use the filter to fine-tune the list of displayed genes to a subset based on a selection of detailed and flexible criteria. For example, the filter may be used to select all human genes over-expressed in the cerebellum that have GPCR-associated G-protein-coupled receptor activity.

The Gene Sorter offers two options for displaying and downloading sequence associated with the genes in the table. Clicking on the sequence button will fetch associated protein, mRNA, promoter, or genomic sequence. To dump the table into a simple tab-delimited format suitable for import into a spreadsheet or relational database, click the text button.

The UCSC Gene Sorter was designed and implemented by Jim Kent, Fan Hou, Donna Karolich, David Haussler, and the UCSC Genome Bioinformatics Group. This work is supported by a grant from the National Human Genome Research Institute and by the Howard Hughes Medical Institute.

Search Results, click on the exact gene you want to find the 3'UTR for:

The screenshot shows the 'Simple Search Results' page of the UCSC Human Gene Sorter. The search term 'Slc7a1' has been entered, and the results are displayed under the heading 'Known Gene Names'. A red arrow points to the first entry, 'SLC7A1'.

Simple Search Results

Known Gene Names

SLC7A1 - solute carrier family 7 (cationic amino acid)
SLC7A10 - solute carrier family 7, member 10
SLC7A11 - solute carrier family 7, (cationic amino acid)
SLC7A13 - solute carrier family 7, (cationic amino acid)
SLC7A14 - solute carrier family 7 (cationic amino acid)

Under the Description field, click the gene name (highlighted in green):

UCSC Human Gene Sorter

genome: human assembly: M10 (NCBI36/hg18) search: slc7a1

sort by: Expression (ZNF Atlas) | configure | filter (row off) | display: 50 | output: sequence | text

Name	Visualize	5' UTR	3' UTR	BLAST	Genomic Position	Description
1. SLC7A1	181022			0	chr13:29,024,636	solute carrier family 7 (cationic amino acid)
2. ZNFPR2	n/a			n/a	chr13:114,104,308	zinc finger protein 208
3. PRPS1	77042			n/a	chrX:106,769,611	phosphoribosyl pyrophosphate synthetase 1
4. BBOX1D	176289			n/a	chr2:197,790,221	box protein 15

The official gene information page is now located – scroll down to the 5'UTR and 3'UTR annotation box near bottom of web page.

Human Gene SLC7A1 (uc001iso.1) Description and Page Index - Mozilla Firefox

http://genome.ucsc.edu/cgi-bin/hGeneTable?db=hg18hg18gene=uc001iso.1&hg18chr=chr13&hg18start=29015200&hg18end=2907721

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Human Gene SLC7A1 (uc001iso.1) Description and Page Index

Description: solute carrier family 7 (cationic amino acid)
Strand: - Genomic Size: 16571 Exon Count: 15 Coding Exon Count: 11

Page Index	Sequence and Links	UniProtKB	Comments	Genetic Associations	CTD	Microarray
3D Structure	Protein Structure	Other Species	GO Annotations	miRNA Descriptions	Pathways	
Other Names	Model Information	Methods				

Sequence and Links to Tools and Databases

Genomic Sequence (chr13:29,081,511-29,067,721)	mRNA (may differ from genome)	Protein (629 aa)			
Gene Sorter	Genome Browser	Protein FASTA	Protein BLAST	ViewGene	Table Schema
OSAP	Ensembl	Ensembl Gene	Ensembl Transcript	Gene Ontology	Gene Network
Capit Tissue	TI-TRV	TCMNC	TPPRD	ThiTR	Jackson Lab
QBLM	PubMed	Reactome	Stanford SOURCE	Treefam	UniProtKB

Comments and Description Text from UniProtKB

ID: [SLC7A1_HUMAN](#)

DESCRIPTION: RecName: Full=High affinity cationic amino acid transporter 1; Short=CAT-1; Short=CAT1; AltName: Full=System Y+ basic amino acid transporter 1; Short=SLC7A1; AltName: Full=Solute carrier family 7 member 1; AltName: Full=Protoporphyrin oxidase receptor homolog; AltName: Full=Urotropic retinoid receptor homolog; Short=URR.

FUNCTION: Endo-lysosomal, low capacity putrescine involved in the transport of the cationic amino acids (arginine, lysine and ornithine) in non-hepatic tissues.

SUBCELLULAR LOCATION: Membrane. Multi-pass membrane protein

TISSUE SPECIFICITY: Ubiquitous.

SIMILARITY: Belongs to the amino acid-polyamine-organization (APC) superfamily. Cationic amino acid transporter (CAT) (TC 2.A.1.3) family.

Genetic Association Studies of Complex Diseases and Disorders

Genetic Association Database: [SLC7A1](#)

