

## Table Browser

Use this program to retrieve the data associated with a track in text format, to calculate intersections between tracks, and to generate reports. For more information, see the [User's Guide](#) for general information and sample queries, and the OpenHelix Table Browser [tutorial](#) for information on using the [public MySQL server](#). To examine the biological function of your set through annotation enrichments, send the data to [Gene Set Enrichment Analysis](#). Usage restrictions associated with these data. All tables can be downloaded in their entirety from the [Sequence and Annotation Browser](#).

**clade:**  **genome:**  **assembly:**

**group:**  **track:**

**table:**

**region:**  genome  ENCODE Pilot regions  position

**identifiers (names/accessions):**

**filter:**

**subtrack merge:**

**intersection:**

**correlation:**

**output format:**  Send output to  [Galaxy](#)  [GREAT](#)  [GenomeSpace](#)

**output file:**  (leave blank to keep output in browser)

**file type returned:**  plain text  gzip compressed

To reset all user cart settings (including custom tracks), [click here](#).

## Select Fields from hg19.wgEncodeGencodeCompV19

<input checked="" type="checkbox"/>	bin	
<input checked="" type="checkbox"/>	name	Name of gene (usually transcript_id from GTF)
<input checked="" type="checkbox"/>	chrom	Reference sequence chromosome or scaffold
<input checked="" type="checkbox"/>	strand	+ or - for strand
<input checked="" type="checkbox"/>	txStart	Transcription start position
<input checked="" type="checkbox"/>	txEnd	Transcription end position
<input checked="" type="checkbox"/>	cdsStart	Coding region start
<input checked="" type="checkbox"/>	cdsEnd	Coding region end
<input checked="" type="checkbox"/>	exonCount	Number of exons
<input checked="" type="checkbox"/>	exonStarts	Exon start positions
<input checked="" type="checkbox"/>	exonEnds	Exon end positions
<input checked="" type="checkbox"/>	score	score
<input checked="" type="checkbox"/>	name2	Alternate name (e.g. gene_id from GTF)
<input checked="" type="checkbox"/>	cdsStartStat	enum('none','unk','incmpl','cmpl')
<input checked="" type="checkbox"/>	cdsEndStat	enum('none','unk','incmpl','cmpl')
<input checked="" type="checkbox"/>	exonFrames	Exon frame {0,1,2}, or -1 if no frame for exon

## hg19.wgEncodeGencodeAttrsV19 fields

<input checked="" type="checkbox"/>	genelid	Gene identifier
<input checked="" type="checkbox"/>	geneName	Gene name
<input checked="" type="checkbox"/>	geneType	BioType of gene
<input checked="" type="checkbox"/>	geneStatus	Status of gene
<input checked="" type="checkbox"/>	transcriptId	Transcript identifier
<input checked="" type="checkbox"/>	transcriptName	Transcript name
<input checked="" type="checkbox"/>	transcriptType	BioType of transcript
<input checked="" type="checkbox"/>	transcriptStatus	Status of transcript
<input checked="" type="checkbox"/>	havanaGenelid	HAVANA identifier if gene is in HAVANA
<input checked="" type="checkbox"/>	havanaTranscriptId	HAVANA identifier if transcript is in HAVANA
<input checked="" type="checkbox"/>	ccdsId	CCDS identifier if transcript is in CCDS
<input checked="" type="checkbox"/>	level	GENCODE level: 1 = experimental confirmed, 2 = manual, 3 = automated
<input checked="" type="checkbox"/>	transcriptClass	high level type of transcript

## Linked Tables

<input type="checkbox"/>	hg19	wgEncodeGencodeAnnotationRemarkV19	Annotation remarks
<input checked="" type="checkbox"/>	hg19	wgEncodeGencodeAttrsV19	Basic set of attributes associated with al
<input type="checkbox"/>	hg19	wgEncodeGencodeBasicV19	A gene prediction with some additional i
<input type="checkbox"/>	hg19	wgEncodeGencodeExonSupportV19	GENCODE exon support from other dat
<input type="checkbox"/>	hg19	wgEncodeGencodeGeneSourceV19	The source of Gencode gene annotation
<input type="checkbox"/>	hg19	wgEncodeGencodePdbV19	GENCODE transcript to Protein Data Ba
<input type="checkbox"/>	hg19	wgEncodeGencodePseudoGeneV19	A gene prediction with some additional i
<input type="checkbox"/>	hg19	wgEncodeGencodePubMedV19	Gencode metadata table of PubMed ide
<input type="checkbox"/>	hg19	wgEncodeGencodeRefSeqV19	GENCODE transcript to RefSeq mRNA
<input type="checkbox"/>	hg19	wgEncodeGencodeTagV19	Tags associated with GENCODE transcr
<input type="checkbox"/>	hg19	wgEncodeGencodeTranscriptSourceV19	The source of Gencode transcript annota
<input type="checkbox"/>	hg19	wgEncodeGencodeTranscriptSupportV19	GENCODE transcript support from other
<input type="checkbox"/>	hg19	wgEncodeGencodeTranscriptionSupportLevelV19	GENCODE transcription support level, c
<input type="checkbox"/>	hg19	wgEncodeGencodeUniProtV19	GENCODE transcript to UniProt peptide