Genomic data structured using the UCSC BED (Browser Extensible Data) format is designed to represent genomic intervals and annotations.

BED Format Structure

The standard BED format consists of at least three required columns, with up to 12 optional columns:

Column	Name	Description
1	chrom	Chromosome name (e.g., chr1, chrX)
2	chromStart	Start position (0-based)
3	chromEnd	End position (exclusive)
4	name	Optional feature name
5	score	Optional score (0–1000)
6	strand	Optional strand (+ or −)
7–12	Additional fields for BED12 (e.g., thickStart, blockCount, blockSizes)	

BED12 Format (for complex features like genes)

The full 12-column BED format is used for features with multiple blocks (e.g., exons):

Column	Description
7	`thickStart` – Start of coding region
8	`thickEnd` – End of coding region
9	`itemRgb` – RGB color for display
10	`blockCount` – Number of blocks (e.g., exons)
11	`blockSizes` – Comma-separated list of block sizes
12	`blockStarts` – Comma-separated list of block start positions relative to `chromStart`

☐ UCSC-Specific Enhancements

- bigBed format: A binary indexed version of BED for faster access and visualization in the UCSC Genome Browser.

- bedGraph format: Used for continuous-valued data like coverage or scores.

- Custom tracks: BED files can be uploaded to UCSC Genome Browser to create custom annotation tracks.