

#Discover if there are any overlapping ranges in ABCD1 Gene:

```
> overlapsAny(ABCD1, hg_chrX)
```

```
[1] TRUE
```

```
#####
```

```
> # Store the overlapping range in rangefound
```

```
> rangefound <- subsetByOverlaps(hg_chrX, ABCD1)
```

```
>
```

```
> # Check names of rangefound
```

```
> names(rangefound)
```

```
[1] "215"
```

```
>
```

```
> # Check the geneOfInterest
```

```
> ABCD1
```

```
GRanges object with 1 range and 1 metadata column:
```

```
  seqnames      ranges strand |   gene_id  
    <Rle>      <IRanges> <Rle> | <character>  
  215  chrX [153724868, 153744762] + |    215
```

```
-----
```

```
seqinfo: 1 sequence from hg38 genome
```

```
>
```

```
> # Check rangefound
```

```
> rangefound
```

```
GRanges object with 1 range and 1 metadata column:
```

```
  seqnames      ranges strand |   gene_id  
    <Rle>      <IRanges> <Rle> | <character>  
  215  chrX [153724868, 153744762] + |    215
```

```
-----
```

```
seqinfo: 1 sequence from hg38 genome
```

Gene_id = 215 which is an ENTREZ id

Location: chrX: 153724868, 153744762

```
#####
```

How many transcripts in gene?

```
> # load the human transcripts DB to hg
```

```
> library(TxDb.Hsapiens.UCSC.hg38.knownGene)
```

```
> hg <- TxDb.Hsapiens.UCSC.hg38.knownGene
```

```
>
```

```
> # prefilter chromosome X "chrX" using seqlevels()
```

```
> seqlevels(hg) <- c("chrX")
```

```
>
```

```

> # get all transcripts by gene and print it
> hg_chrXt <- transcriptsBy(hg, by = "gene")
> hg_chrXt
GRangesList object of length 985:
$10009
GRanges object with 2 ranges and 2 metadata columns:
  seqnames      ranges strand | tx_id  tx_name
  <Rle>         <IRanges> <Rle> | <integer> <character>
[1] chrX [120250752, 120258398] + | 178656 uc004esn.2
[2] chrX [120250755, 120255434] + | 178657 uc010nqm.2

```

```

$100093698
GRanges object with 1 range and 2 metadata columns:
  seqnames      ranges strand | tx_id  tx_name
  <Rle>         <IRanges> <Rle> | <integer> <character>
[1] chrX [13310652, 13319933] + | 176971 uc031tgt.1

```

```

$100124540
GRanges object with 1 range and 2 metadata columns:
  seqnames      ranges strand | tx_id  tx_name
  <Rle>         <IRanges> <Rle> | <integer> <character>
[1] chrX [47388649, 47388777] + | 177448 uc010nhr.2

```

```

...
<982 more elements>

```

```

-----
seqinfo: 1 sequence from hg38 genome
>

```

```

> # select gene `215` from the transcripts
> hg_chrXt$`215`
GRanges object with 3 ranges and 2 metadata columns:
  seqnames      ranges strand | tx_id  tx_name
  <Rle>         <IRanges> <Rle> | <integer> <character>
[1] chrX [153724868, 153744762] + | 179161 uc004fif.2
[2] chrX [153725817, 153729897] + | 179162 uc065bvz.1
[3] chrX [153735344, 153740604] + | 179163 uc065bwa.1

```

```

-----
seqinfo: 1 sequence from hg38 genome

```