



[Course](#) > [Section 2: Biocondu...](#) > [IRanges and GRang...](#) > Assessment: Setup ...

### Audit Access Expires Jun 2, 2020

You lose all access to this course, including your progress, on Jun 2, 2020.

Upgrade by May 19, 2020 to get unlimited access to the course as long as it exists on the site. [Upgrade now](#)

## Assessment: Setup and GRanges

This week we are using two sets of genomic regions as examples. These are the reported ESRRA binding sites obtained for a ENCODE ChIP-seq experiment on two cell lines: HepG2 and GM12878. We have put these regions into an R package for your convenience. If you have not done so already, please download and install the **ERBS** package:

```
BiocManager::install("genomicsclass/ERBS")
```

### Q1: Classes for genomic ranges

2/2 points (graded)

Load the **ERBS** library and then the `HepG2` object.

```
library(ERBS)
data(HepG2)
```

What is the class of `HepG2` ?

Hint: use the `class()` function.

GRanges



What package is this class defined in?

GenomicRanges



Submit

You have used 1 of 5 attempts

## Q2: Counting regions

1/1 point (graded)

Explore the `HepG2` object.

How many regions are represented?

303



Submit

You have used 1 of 5 attempts

## Discussion

**Topic:** Section 2 / Setup and GRanges

Show Discussion

Learn About Verified Certificates

© All Rights Reserved