

gse28619

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Abstract

> Alcoholic hepatitis (AH) is the most severe form of alcoholic liver disease and occurs in p

The data has been downloaded from [GEO](#).

Packages

```
library(GEOquery)
library(affy)
library(hgu133plus2.db)
```

Downloading the dataset

```
gcel = getGEOSuppFiles("GSE28619")
system("tar xvf GSE28619/GSE28619_RAW.tar")
gse28619raw = ReadAffy()
gse28619 = rma(gse28619raw)
type = factor(rep(1:2,c(7,15)),levels=1:2,labels=c("control","alcoholic"))
pData(gse28619) = data.frame(type)
experimentdata0 = new('MIAME', name = 'Juanjo Lozano et al.',
  lab = 'CIBEREHD',
  contact = 'juanjo.lozano@ciberehd.org',
  title = 'Transcriptome analysis identifies TNF
  superfamily receptors as potential therapeutic
  targets in alcoholic hepatitis.',
  abstract = 'Alcoholic hepatitis (AH) is the most severe
  form of alcoholic liver disease and occurs in patients
  with excessive alcohol intake It is characterized by
  marked hepatocellular damage, steatosis and pericellular
  fibrosis. Patients with severe AH have a poor short-term
  prognosis. Unfortunately, current therapies (i.e.
  corticosteroids and pentoxifylline) are not effective
  in many patients and novel targeted therapies are urgently
  needed. The development of such therapies is hampered by a
  poor knowledge of the underlying molecular mechanisms.
  Based on studies from animal models, TNF alfa was proposed
  to play a pivotal role in the mechanisms of AH.
  Consequently, drugs interfering TNF alfa were tested
  in these patients. The results were disappointing due
  to an increased incidence of severe infections.
  Unluckily, there are not experimental models that
  mimic the main findings of AH in humans. To overcome
  this limitation, translational studies with human samples
  are required. We previously analyzed samples from
  patients with biopsy-proven AH. In these previous studies,
  we identified CXC chemokines as a potential therapeutic
  target for these patients. We expanded these previous
  observations by performing a high-throughout transcriptome
  analysis.',
  url = 'http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE28619')

experimentData(gse28619) = experimentdata0
```

Guardar ExpressionSet

Additional identifiers per gene.

```
a = AnnotationDbi::select(hgu133plus2.db,keys=featureNames(gse28619),
                           columns=c("ENTREZID","ENSEMBL","GO"),keytype="PROBEID")
b = BiocGenerics::match(featureNames(gse28619),a[, "PROBEID"])
fData(gse28619) = a[b,]
```

Saving the ExpressionSet.

```
save(gse28619,file="gse28619.rda")
```