

# dGSEAvieW

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dGSEAvieW

*Function to view enrichment results in a sample-specific manner*

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## Description

dGSEAvieW is supposed to view results of gene set enrichment analysis but for a specific sample.

## Usage

```
dGSEAvieW(eTerm, which_sample = 1, top_num = 10, sortBy = c("adjp",
"gadjp", "ES", "nES", "pvalue", "FWER", "FDR", "qvalue"), decreasing =
NULL,
details = F)
```

## Arguments

eTerm	an object of class "eTerm"
which_sample	which sample will be viewed
top_num	the maximum number of gene sets will be viewed
sortBy	which statistics will be used for sorting and viewing gene sets. It can be "adjp" for adjusted p value, "gadjp" for globally adjusted p value, "ES" for enrichment score, "nES" for normalised enrichment score, "pvalue" for p value, "FWER" for family-wise error rate, "FDR" for false discovery rate, "qvalue" for q value
decreasing	logical to indicate whether to sort in a decreasing order. If it is null, it would be true for "ES" or "nES"; otherwise it would be false
details	logical to indicate whether the detail information of gene sets is also viewed. By default, it sets to false for no inclusion

## Value

a data frame with following components:

- setID: term ID
- ES: enrichment score
- nES: normalised enrichment score
- pvalue: nominal p value

- adjp: adjusted p value
- gadjp: globally adjusted p value
- FDR: false discovery rate
- qvalue: q value
- setSize: the number of genes in the set; optional, it is only appended when "details" is true
- name: term name; optional, it is only appended when "details" is true
- namespace: term namespace; optional, it is only appended when "details" is true
- distance: term distance; optional, it is only appended when "details" is true

**Note**

none

**See Also**

[dGSEA](#)

**Examples**

```
#dGSEAView(eTerm, which_sample=1, top_num=10, sortBy="adjp", decreasing=FALSE, details=TRUE)
```