

# Package: somaticflags (via r-universe)

September 5, 2024

**Title** Database of Somatic Flags

**Version** 0.1.0

**Description** Database of genes which frequently sustain somatic mutations, but are unlikely to drive cancer.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.1

**Depends** R (>= 2.10)

**Suggests** usethis, devtools

**URL** <https://github.com/CCICB/somaticflags>

**BugReports** <https://github.com/CCICB/somaticflags/issues>

**Repository** <https://ccicb.r-universe.dev>

**RemoteUrl** <https://github.com/CCICB/somaticflags>

**RemoteRef** HEAD

**RemoteSha** 37d531b1830d4d5f01815b12c737d3dd1fc5c172

## Contents

somaticflags . . . . .	2
somaticflags_df . . . . .	2

<b>Index</b>	<b>4</b>
--------------	----------

---

`somaticflags`*Somatic Flags Dataset*

---

**Description**

a list of genes which are frequently mutated in somatic cancer datasets but are unlikely to drive disease.

**Usage**

```
somaticflags
```

**Format**

A vector with 139 gene names:

**Source**

[doi:10.1038/nature12213](https://doi.org/10.1038/nature12213) and [doi:10.1186/s129200140064y](https://doi.org/10.1186/s129200140064y)

**Examples**

```
data(somaticflags)
head(somaticflags)
```

---

`somaticflags_df`*Somatic Flags Dataset*

---

**Description**

a list of genes which are frequently mutated in somatic cancer datasets but are unlikely to drive disease.

**Usage**

```
somaticflags_df
```

**Format**

A data.frame with 139 gene names:

**Gene** Genes frequently mutated in somatic cancer datasets but that are unlikely to drive disease

**Source** Supporting papers for the gene being a somatic flag

**Reason** Explanation for the gene being considered a somatic flag ...

*somaticflags\_df*

3

### **Source**

[doi:10.1038/nature12213](https://doi.org/10.1038/nature12213) and [doi:10.1186/s129200140064y](https://doi.org/10.1186/s129200140064y)

### **Examples**

```
data(somaticflags_df)  
head(somaticflags_df)
```

# Index

## \* datasets

somaticflags, [2](#)

somaticflags\_df, [2](#)

somaticflags, [2](#)

somaticflags\_df, [2](#)