

# What gets sanitized

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## 1 Notes are sanitized

```
x <- ptdata() %>% st_new(notes = "EDA_summary = TRUE") %>%  
  st_make(inspect = TRUE) %>%  
  get_stable_data()
```

```
x$notes
```

```
## [1] "EDA\\_summary = TRUE"
```

## 2 File names are sanitized

```
x <- ptdata() %>% st_new() %>%  
  st_files(r = "my_script.R") %>%  
  st_make(inspect = TRUE) %>%  
  get_stable_data()  
  
x$notes  
  
## [1] "Source code: my\\_script.R"
```

## 3 Column names are sanitized

```
out <-  
  tibble(a_1 = 5) %>%  
  stable(inspect = TRUE) %>%  
  get_stable_data()  
  
out$cols_new  
  
## [1] "a\\_1"
```

## 4 Data are sanitized

```
out <-  
  tibble(a = "5_2") %>%  
  stable(inspect = TRUE) %>%  
  get_stable_data()  
  
out$tab  
  
## [1] "5\\_2 \\\\"
```

## 5 Span titles - sanitized

```
out <-  
  ptdata() %>%  
  stable(inspect = TRUE, span = colgroup("foo_this", WT:SCR)) %>%  
  get_stable_data()  
  
out$span_data  
  
## $tex  
## [1] "\\multicolumn{4}{c}{} & \\multicolumn{5}{c}{\\textbf{foo\\_this}}\\\\"  
## [2] "\\cmidrule{1r}{5-9}"  
##  
## $cols  
## [1] "STUDY" "DOSE" "FORM" "N" "WT" "CRCL" "AGE" "ALB" "SCR"
```

```
##
## $span
## $span$`1`
## # A tibble: 9 x 7
##   coln col   newcol title      level   flg align
##   <int> <chr> <chr>   <chr>      <dbl> <dbl> <chr>
## 1     1 STUDY STUDY   ""          1     1 c
## 2     2 DOSE DOSE    ""          1     1 c
## 3     3 FORM FORM    ""          1     1 c
## 4     4 N     N      ""          1     1 c
## 5     5 WT    WT     "foo_this"  1     2 c
## 6     6 CRCL CRCL   "foo_this"  1     2 c
## 7     7 AGE   AGE    "foo_this"  1     2 c
## 8     8 ALB   ALB    "foo_this"  1     2 c
## 9     9 SCR   SCR    "foo_this"  1     2 c
```

## 6 Panel names

```
data <- tibble(a = c("a_1", "a_1", "a_1", "a_2", "a_2"),
               b = letters[1:5])

out <- stable(data, panel = "a")
out[grepl("multicolumn", out)]

## [1] "\\multicolumn{1}{l}{\\textbf{a\\_1}}\\\\"
## [2] "\\hline \\multicolumn{1}{l}{\\textbf{a\\_2}}\\\\"
```