

```
proj_analyze("project_miceps")  
## # A tibble: 1 x 3  
##   package      N used_in  
##   <chr>      <int> <chr>  
## 1 rmarkdown      1 project_miceps/analysis.Rmd  
## # A tibble: 9 x 4  
##   file              ext      size mime  
##   <fs::path>      <chr> <fs::byt> <chr>  
## 1 Estrogen_Receptor~ docx    10.97K application/vnd.openxmlformats-officedocum~  
## 2 citrate_v_time.png png    188.45K image/png
```