```r
library(dplyr)
library(lmerTest)
library(SwipProteomics)

data(msstats_prot)

washc_prots <- c("Q8C2E7", "Q6PGL7", "Q3UMB9", "Q9CR27", "Q8VDD8")

# the formula to be fit:
fx <- Abundance ~ 0 + Genotype:BioFraction + (1 | Mixture) + (1 | Protein)

# fit a model to WASH complex proteins:
fm <- lmer(fx, data = msstats_prot %>% filter(Protein %in% washc_prots))

# compute Satterthwaite degrees of freedom
model_summary <- summary(fm,ddf="Satterthwaite")
```

Term	Estimate	SE	DF	Tvalue	Pvalue
Control:BioFractionF4	6.884	0.151	6.909	45.686	2.776e-09
Control:BioFractionF5	7.168	0.151	6.909	47.570	7.845e-10
Control:BioFractionF6	7.465	0.151	6.909	49.548	2.183e-09
Control:BioFractionF7	7.495	0.151	6.909	49.745	5.939e-10
Control:BioFractionF8	7.327	0.151	6.909	48.629	1.922e-09
Control:BioFractionF9	7.138	0.151	6.909	47.377	4.486e-10
Control:BioFractionF10	7.756	0.151	6.909	51.478	1.839e-09
Mutant:BioFractionF4	5.729	0.151	6.909	38.025	4.364e-10
Mutant:BioFractionF5	5.933	0.151	6.909	39.377	2.197e-09
Mutant:BioFractionF6	6.044	0.151	6.909	40.113	5.103e-10
Mutant:BioFractionF7	6.083	0.151	6.909	40.370	2.275e-09
Mutant:BioFractionF8	5.927	0.151	6.909	39.339	6.108e-10
Mutant:BioFractionF9	5.897	0.151	6.909	39.141	1.898e-09
Mutant:BioFractionF10	6.055	0.151	6.909	40.186	3.447e-10

```r
# define a contrast
contrast <- lme4::fixef(fm)
contrast[] <- 0
contrast[grep("Mutant",names(contrast))] <- +1/7
contrast[grep("*Control*",names(contrast))] <- -1/7

# test contrast with lmerTestContrast
results <- lmerTestContrast(fm,contrast)

results %>% mutate(Contrast = "Mutant-Control") %>% unique() %>% knitr::kable()
```

Contrast	log2FC	percentControl	Pvalue	Tstatistic	SE	DF
Mutant-Control	-1.366434	0.3878488	0	-36.93673	0.0369939	190