```
> library(dplyr)
> library(lmerTest)
> library(SwipProteomics)

> data(msstats_prot)

> washc_prots = c('Q8C2E7', 'Q6PGL7', 'Q3UMB9', 'Q9CR27', 'Q8VDD8')

# fit the LMM

> fx <- Abundance ~ 0 + Genotype:BioFraction + (1|Mixture) + (1|Protein)

> fm <- lmer(fx, data=msstats_prot %>% filter(Protein %in% washc_prots))

> 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