Create fasta DB

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```
library(pepfdr)
library(p1755)
```

Create db

Contaminants and mscqc1 proteins

```
rm(list=ls())
contaminants <- loadContaminantsNoMSQC1Fasta()
msqc1 <- loadMSQC1Fasta()
```

Create Reverse Sequences

```
contaminantsrev <- reverseSeq(contaminants)
msqc1rev <- reverseSeq(msqc1)
```

Prepare e-coli and human databases

```
ecoli <- readPeptideFasta("../data/fastaFiles/uniprot-taxonomy83333.fasta")
human <- readPeptideFasta("../data/fastaFiles/uniprot-taxonomyHomoSapiensHuman9606.fasta")

length(ecoli)
```

```
## [1] 6098
```

```
length(human)
```

```
## [1] 20197
```

```
ecoliRev <- reverseSeq(ecoli)
humanRev <- reverseSeq(human)
```

Create new database, with reverse and forward sequences

```
all_d <-c(msqc1, ecoli, human, contaminants,  msqc1rev, ecoliRev, humanRev , contaminantsrev)
length(all_d)/2
```

```
## [1] 26559
```

```
stopifnot(length(all_d)/2 == length(ecoli) + length(human) + length(msqc1) + length(contaminants))
writeFasta(all_d, file="../data/fastaFiles/output/p1755_db1_d_20151016_msqc1ecolihuman.fasta")

all <- c(msqc1, ecoli, human, contaminants)
stopifnot(length(all) == length(ecoli) + length(human) + length(msqc1) + length(contaminants))

writeFasta(all, file="../data/fastaFiles/output/p1755_db1_20151016_msqc1ecolihuman.fasta")
```