

## Cancer Biomarker Finder

### Results Report

#### Error: Unable to read Sequences

Error occurred on Line 36 of FASTA file "[p30241.fasta](#)"

This error most likely occurred because one of the fasta sequences provided has strange characters in the sequence segment of the file, unwanted spaces between sequences or does not match the standard FASTA format. Please check the validity of your FASTA file and try again.