In order to run DISOPRED on human sequence, you need to extract the human sequence from <all_seqs_with_latin_names$genename.fasta> files.

All you need is the path to sequence file directory.

Following is the screenshot of terminal command line.

```
python extract_human_unalignedseq.py /Users/xiaowang/Desktop/program_code_tested/extract_human_seq/example_seqfile/
```

For further questions, send me an email:
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