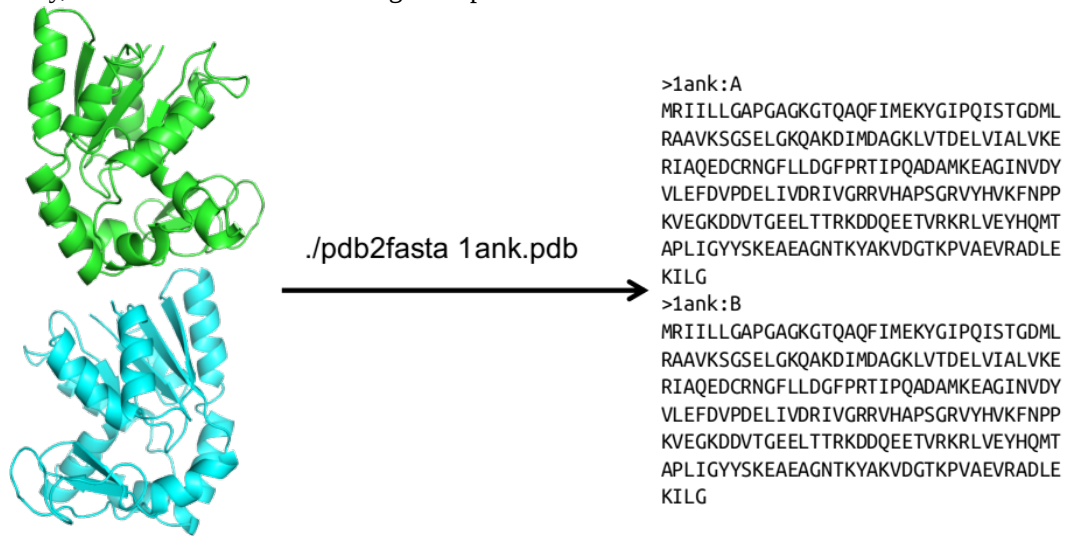Write a program to convert a PDB structure to protein sequence in FASTA format. If a PDB file contains multiple chains, you program should be able to show sequence for different chains separately, as illustrated in the following example.

./pdb2fasta 1ank.pdb

```
>1ank:A
MRIILLGAPGAGKGTQAQFIMEKYGIPQISTGDML
RAAVKSGSELGKQAKDIMDAGKLVTDELVIALVKE
RIAQEDCRNGFLLDGFPRTIPQADAMKEAGINVDY
VLEFDVPDELIVDRIVGRRVHAPSGRVYHVKFNPP
KVEGKDDVTGEELTTRKDDQEETVRKRLVEYHQMT
APLIGYYSKEAEAGNTKYAKVDGTKPVAEVRADLE
KILG
>1ank:B
MRIILLGAPGAGKGTQAQFIMEKYGIPQISTGDML
RAAVKSGSELGKQAKDIMDAGKLVTDELVIALVKE
RIAQEDCRNGFLLDGFPRTIPQADAMKEAGINVDY
VLEFDVPDELIVDRIVGRRVHAPSGRVYHVKFNPP
KVEGKDDVTGEELTTRKDDQEETVRKRLVEYHQMT
APLIGYYSKEAEAGNTKYAKVDGTKPVAEVRADLE
KILG
```

PDB structure: 1ank   FASTA sequence

If you use scripting language (Python, Perl, MATLAB, Shell, etc), you should be able to implement the program within 40 lines. If you use compiled language (C, C++, Fortran etc), you should be able to implement the program within 100 lines.

You are NOT allowed to use third-party library such as Bio++ or biopython for parsing the PDB file.

Hint: You can read about PDB format from the official PDB site at
http://www.wwpdb.org/documentation/file-format-content/format33/sect9.html#ATOM
An example application is available at
https://zhanglab.ccmb.med.umich.edu/pdb2fasta/