

```
1 |$faa = $ARGV[0];
2 |$feature = $ARGV[1];
3
4 |open (FEATURE, "< $feature");
5
6 |while (<FEATURE>) {
7 |    if (/^CDS/) {
8 |        @a = split /\t/;
9 |        $chromosomeOrPlasmid = $a[4];
10 |        $start = $a[7];
11 |        $end = $a[8];
12 |        $accession = $a[10];
13
14 |        if ($chromosomeOrPlasmid eq "chromosome") {
15 |            $position{$accession} = $start;
16 |        }
17 |    }
18 |}
19 |close (FEATURE);
20 |open (FAA, "< $faa");
21
22 |while (<FAA>) {
23 |    if (/^>(\S+)/) {
24 |        $accession = $1;
25
26 |        if ($position{$accession}) {
27 |            print ">$position{$accession}\n";
28 |            $sequence = 1;
29 |        }
30 |        else {
31 |            $sequence = 0;
32 |        }
33 |    }
34 |    elsif ($sequence == 1) {
35 |        print $_;
36 |    }
37 |}
38 |close (FAA);
39
```