Fasta file splitted into individual entries

```bash
#!/bin/bash

while read line
do
    if [[ ${line:0:1} == '>' ]] # files starting with '>'
    then
        outfile=$(echo "${line#>}" | cut -d ' ' -f4).fasta
        # '${line#>}' is the enter heading,
        # 'cut' separates parts based on space
        # '-f4' picks up the fourth part
        echo $line > "$outfile"
    else
        echo $line >> "$outfile"
    fi
done < $1 # '$1' is the input file assigned after the script in the terminal
```

A fasta file

containing multiple entries

atp6_a.fasta	atp6_b.fasta
atp8-0.fasta	atp8-1.fasta
cob_a.fasta	cob_b.fasta
cox1.fasta	cox2.fasta
cox3_a.fasta	cox3_b.fasta
nad1-0.fasta	nad1-1.fasta
nad2_a.fasta	nad2_b.fasta
nad2_c.fasta	nad3-0.fasta
nad3-1.fasta	nad4_a.fasta
nad4_b.fasta	nad4l.fasta
nad5.fasta	nad6_a.fasta
nad6_b.fasta	rrnL.fasta
rrnS.fasta	trnC(tgc).fasta
trnD(gac).fasta	trnE(gaa).fasta
trnF(ttc).fasta	trnG(gga).fasta
trnH(cac).fasta	trnI(atc).fasta
trnK(aaa).fasta	trnL1(cta).fasta
trnL2(tta).fasta	trnM(ata).fasta
trnN(aac).fasta	trnP(cca).fasta
trnQ(caa).fasta	trnR(cga).fasta
trnS1(aga).fasta	trnS2(tca).fasta
trnT(aca).fasta	trnV(gta).fasta
trnW(tga).fasta	trnY(tac).fasta

Asad Prodhan

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while read line
do
   if [[ ${line:0:1} == '>' ]] # files starting with '>'
   then
      outfile=$(echo "${line#>}" | cut -d ' ' -f4).fasta # '${line#>}' is the enter heading,
                                    # 'cut' separates parts based on space
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      echo $line > "$outfile"
   else
      echo $line >> "$outfile"
   fi
done < $1 # '$1' is the input file assigned after the script in the terminal
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