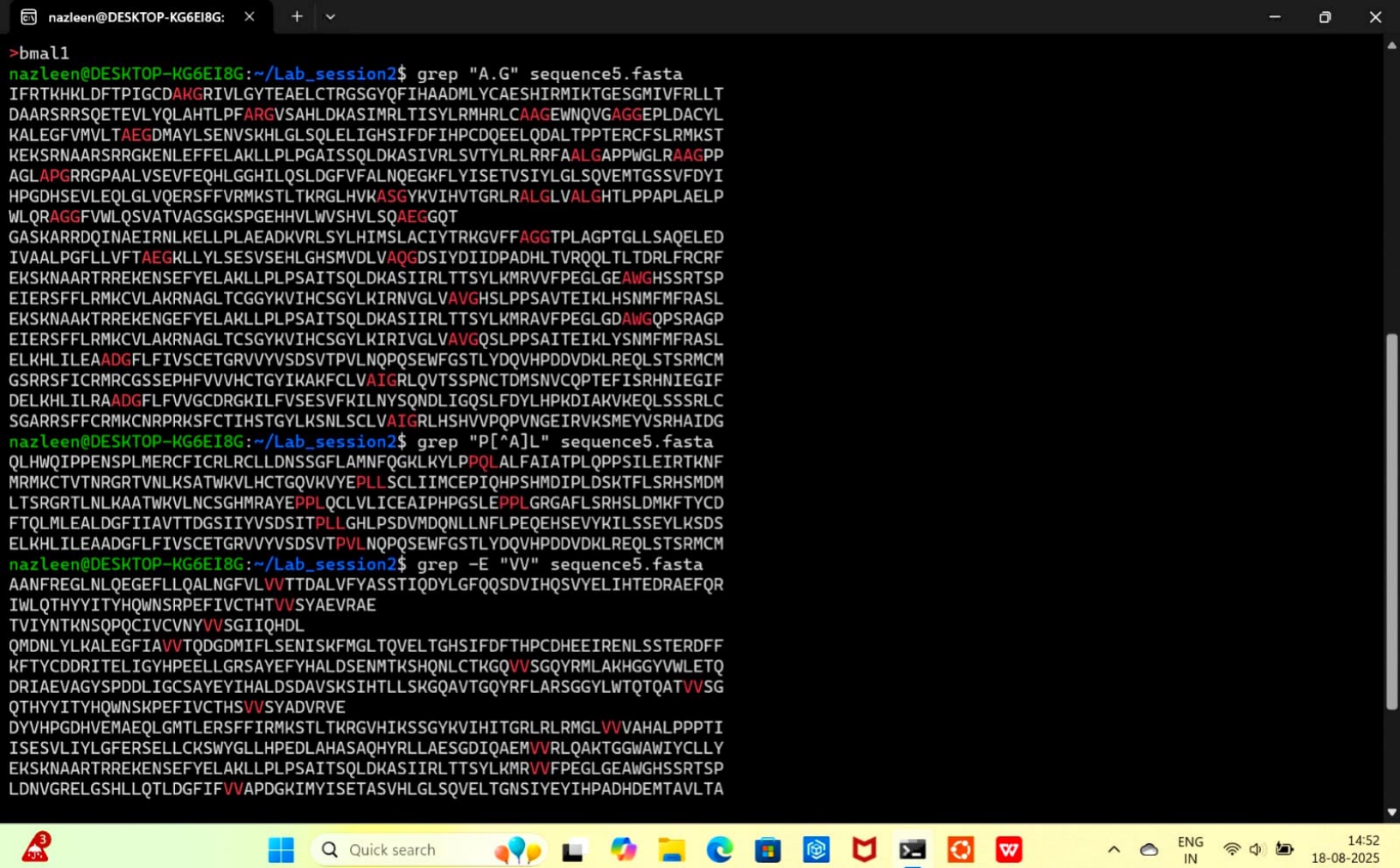


To run a command as administrator (user "root"), use "sudo <command>".
See "man sudo_root" for details.

```
nazleen@DESKTOP-KG6EI8G:~$ cd Lab_session2
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ vi
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ wc -l notes.txt
1 notes.txt
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ wc -c notes.txt
16 notes.txt
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ tail -4 sequence.fasta
TAACTACTGATAAGTTACAAAAGTGTTCCTATCCTAAAGGGCAATACAGCCCTAGACTCTCCAGGTAT
TTGACTCCTGCAGCAAAAAGGGAAATTGAGGAAATAGAGCAAGCTATTTCTCAGAGGCAACTATATCACA
TAGACACCCCG
```

```
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ grep ">" sequence5.fasta
```

```
>ahr
>clock
>hif1a
>hif2a
>hif3a
>npas1
>npas2
>npas3
>npas4
>sim1
>sim2
>arnt1
>bmal1
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ grep "A.G" sequence5.fasta
IFRTKHKLDFTPIGCDAKGRIVLGYTEAELCTRGSGYQFIHAADMLYCAESHIRMIKTGESGMIVFRLLT
DAARSRRSQETEVLYQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLCAAGEWNVGAGGEPLDACYL
KALEGFVMVLTAEGDMAYLSENVSKHLGLSQLELIGHSIFDFIHPCDQEELQDALTPPTERCFSLRMKST
KEKSRNAARSRRGKENLEFFELAKLLPLPGAISSQLDKASIVRLSVTYLRLRRFAALGAPPWGLRAAGPP
AGLAPGRRGPAALVSEVFEQHLGGHILQSLDGFVFALNQEGKFLYISETVSIYLGLSQVEMTGSSVFDYI
HPGDHSEVLEQLGLVQERSFFVRMKSTLTKRGLHVKAASGYKVIHVTGRLRALGLVALGHTLPPAPLAELP
WLQRAGGFVWLQSVATVAGSGKSPGEHHVLWVSHVLSQAEGGQT
GASKARRDQINAEIRNLKELLPLAEDKVRLSYLHIMSLACIYTRKGVFFAGGTPLAGPTGLLSAQELED
```



```
nazleen@DESKTOP-KG6E18G:~/Lab_session2$ grep -E "VV" sequence5.fasta
AANFREGFLNLQEGEFLLQALNGFVLVTTDALVFYASSTIQDYLGFQQSDVIHQSVYELIHTEDRAEFQR
IWLQTHYYITYHQWNSRPEFIVCTHTVVSVAEVRAE
TVIYNTKNSQPQCIVCVNYVVSIGIIQHDL
QMDNLYLKALEGFIAVVTQDGMIFLSENI SKFMGLTQVELTGHISFDTHPCDHEEIRENLSSTERDFF
KFTYCDDRITELIGYHPEELLGRSAYEFYHALDSENMTKSHQNLCTKGQVVSQGYRMLAKHGGYVWLETQ
DRIA EVAGYSPDDLIGCSAYEYIHALDSDAVSKSIHTLLSKGQAVTGQYRFLARSGGYLWTQTQATVVS
QTHYYITYHQWNSKPEFIVCTHSVVSADVRVE
DYVHPGDHVEMAEQLGMLTERSFIRMKSTLTKRGVHIKSSGYKVIHITGRLRLRMGLVVAHALPPPTI
ISESVLIYLGFRSELLCKSWYGLHPEDLAHASAQHYRLLAESGDIQAEMVRLQAKTGGWAWIYCLLY
EKSNAARTRREKENSEFYELAKLLPLPSAITSQLDKASIIRLTTSYLKMRVVFPEGLGEAWGHSSRTSP
LDNVGRELGSHELLQTLDFGFI VVAPDGKIMYISETASVHLGLSQVELTGNISYIEYIHPADHDEMTAVLTA
LDGVAKELGSHELLQTLDFGFVVASDGKIMYISETASVHLGLSQVELTGNISYIEYIHPSDHDEMTAVLTA
SYATVVHNSRSSRPHCIVSVNYVLTEIEYKEL
ELKHLILEAADGFLFIVSCETGRVVVS DSVTPVLNQPSQSEWFGSTLYDQVHPDDVDKREQLSTSRMCM
GSRRSFICMRGCSSEPHFVVHCTGYIKAKFCLVAIGRLQVTSSPNC DMSNVQCPTEFISRHNIEGIF
TFVDHRCVATVGYPQQLKMLIVFCHPEDDQQLRDSFQVVKLKGQVLSVMFRFRSKNQEWLWMRTSS
DELKHLILRAADGFLFVVGCDRGKILFVSESVFKILNYSQNDLIGQSLFDYLHPKDIKVKELSSSRLC
SGARRSFFCRMKNRPRKSFCTIHTSGYLKSNLSCLVAIGRLHSHVVPQPVNGEIRVKSMEYVSRHAIDG
RWF SFMNPWTKEVEYIVSTNTVV
```

```
nazleen@DESKTOP-KG6E18G:~/Lab_session2$ grep -E "AA|DD" sequence5.fasta
AANFREGFLNLQEGEFLLQALNGFVLVTTDALVFYASSTIQDYLGFQQSDVIHQSVYELIHTEDRAEFQR
IFRTKHKLDFTPIGCDAKGRIVLGYTEALCTRGSGYQFIHAADMLYCAESHIRMIKTGESGMIVFRLLT
RHSLEWKFLFLDHRAPPIIGYLPFEVLGTSGYDYHYHDDLENLAKCHEHLMQYGGKSKCYRFLTKGQQW
KEKSRDAARSRRSKSESEFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRKLLDAGDLDIEDDMAQAM
NCFYLKALDGFVMVLTDGDMIYISDNVNKYMGLTQFELTGHVSFDFTHPCDHEEMREMLTHNTQRSFFL
KEKSRDAARCRRSKETEVFYELAHQLPLPHSVSSHLDKASIMRLAISFLRTHKLLSSVCSENESEAEADQ
KFTYCDDRITELIGYHPEELLGRSAYEFYHALDSENMTKSHQNLCTKGQVVSQGYRMLAKHGGYVWLETQ
DAA SRRSQETEVLYQLAHTLPFARGSAHLDAHQPLPHNVSSHLDKASIMRLTISYLRMHRLCAAGEWNVQVAGGEPLDACYL
LTSRGRTLNLKAA TWKVLNCSGHMRAYPEPLQCLVLICEAIPHPGSLEPPLGRGAFLSRHSLDMKFTYCD
DRIA EVAGYSPDDLIGCSAYEYIHALDSDAVSKSIHTLLSKGQAVTGQYRFLARSGGYLWTQTQATVVS
KEKSRNAARSRRGKENEFFELAKLLPLPGAISSQLDKASIVRLSVTYLRRLRF AALGAPPWGLRAAGPP
AGLAPGRRGP AALVSEVFEQHLGGHTLQSLDGFVFALNQEGKFLYISETSVIYLGLSQVEMTGSSVFDYI
LEWKFLFLDHRAPPIIGYLPFEVLGTSGYDYHYHDDLELLARCHQHLMQFGKGKSCCYRFLTKGQQWIWL
SRDAARSRRGKENFEFYELAKLLPLPAITSQLDKASIIRLTISYLRMRDFANQGDPPWNLRMGPPPNNT
IV AALPGFLLVFTAEGKLLYLSVSEHLGHSMDVLVAQGDSIYDIDPADHLTVRQQLTLTDRLFRCRF
EKSNAARTRREKENSEFYELAKLLPLPSAITSQLDKASIIRLTTSYLRMRVVFPEGLGEAWGHSSRTSP
```


KFTYCDRITELIGYHPEELLGRSAEYFHYALDSEMTKSHQNLCTKGQVVSGQYRMLAKHGGYVWLEIQ
DRIAEGVAGYSPDDLIGCSAYEYIHALDSDAVSKSIHTLLSKGQAVTGQYRFLARSGGYLWTQTQATVVSG
QTHYYITYYHWNKPEFIVCTHSSVVSYADVRVE
DYVHPGDHVMAEQLGMTLERSFFIRMKSTLTKRGVHIKSSGYKVIHTGRLRLRMGLVVVAHALPPPTI
ISESVLYLGFERSELLCKSWYGLLHPEDLAHASAQHYRLLAESGDIQAEMVVRLQAKTGGWAWIYCLLY
EKSNAARTTRREKENSEFYELAKLLPLPSAITSQDKASIIRLTTSYLKMRVVFPEGLGEAWGHSSRTSP
LDNVGRELGSLLQLTLDGFIFVVPADGKIMYISETASVHLGLSQVELTGNSIYEYIHPADHDEMTAVLTA
LDGVAKELGSHLLQLTLDGFVFPVVASDVGKIMYISETASVHLGLSQVELTGNSIYEYIHPSDHDEMTAVLTA
SYATVVHNSRSSRPHCIVSVNVYLTEIEYKEL
ELKHLILEAADGFLFIVSCETGRVVVSDSVTPVLNQPQSEWFGSTLYDQVHPDDVDKLRQLSTSRMCM
GSRRSFICRMRCGSSEPHFVVVHCTGYIAKAFCLVAIGRLQVTSPPNCTDMSNVCPQTEFISRHNIEGIF
FVDHRCVATVGYQPQELLGKNIVEFCHPEDQQLLRDSFQQVVVLKGQVLSVMFRFRSKNQEWLWMRTSS
DELKHLILRAADGFLFVVGCDRGKILFVSESVFKILNYSQNDLIGQSLFDYLPKDIKAKVKEQLSSSRLC
GGARRSFFCRMKNRPRKSFCTIHSTGYLKSNSCLVAIGRLHSHVVPQPVNGEIRVKSMEYVSRHAIDG
RWFSFMNPWTKEVEYIVSTNTVVL

```
azleen@DESKTOP-KG6EI8G:~/Lab_session2$ grep -E "AA|DD" sequence5.fasta
ANFREGLNLQEGEFLQLANGFVLVTTDALVFYASSTIQDYLGQQSDVIHQSVYELIHTEDRAEFQR
FRTHKHLDFTPIGCDAKGRIVLGYTEAELCTRGSGYQFIHAADMLYCAESHIRMIKTGESGMIVFRLLT
HSLLEWKFLFLDHRAPPIIGYLPFEVLGTSGYDYYHVDDLENLAKCHEHLMQYGGKSKCYRFLTKGQQW
EKSRAARSRRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRKLLDAGDLDIEDDMKAQM
CFYLKALDGFVMVLTDGDMYISDNVNKYMGLTQFELTGHSVDFDTHPCDHEEMREMLTHNTQRSFFL
EKSRAARCRRSKETEYFELAHLEPLPHSVSSHLDKASIMRLAISFLRTHKLLSSVCSENESEAEADQ
FTYCDRITELIGYHPEELLGRSAEYFHYALDSEMTKSHQNLCTKGQVVSGQYRMLAKHGGYVWLEIQ
AARSRRSQETEVLQYLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLCAAQGEWNQVVGAGGEPLDACYL
TSRGRTLNLKAAATWKVLNCSGHMRAVEPPLQCLVLICEAIPHPGSLPEPLGRGAFLSRHSLDMKFTYCD
RIAEGVAGYSPDDLIGCSAYEYIHALDSDAVSKSIHTLLSKGQAVTGQYRFLARSGGYLWTQTQATVVSG
EKSRAARSRRGKENLEFFELAKLLPLPGAITSQDKASIVRLSVTYLRLRRFAALGAPPWGLRAAGPP
GLAPGRRGPAALVSEVFEQHLGGHILQLSDGDFVAFALNQEGKFLYISETVSIYGLSQVELTGSSVFDYI
EWKFLFLDHRAPPIIGYLPFEVLGTSGYDYYHIDDELLARCHQHLMQFGKGKSCCYRFLTKGQQWIWL
RAARSRRGKENFEFYELAKLLPLPAATISQDKASIIRLTISYLMKMRDFANQGDPPWNLRMGPPPPNT
/AAALPGFLLVFTAEGKLLYLSSEVSEHLGHSMDVLAQGDISIYDIDPADHLTVRQQLTLTDRLFRCRF
SKNAARTTRREKENSEFYELAKLLPLPSAITSQDKASIIRLTTSYLMKMRVVFPEGLGEAWGHSSRTSP
SKNAARTTRREKENGEFYELAKLLPLPSAITSQDKASIIRLTTSYLMKRAVFPGLGDAWGQPSRAGP
LKHLELAADGFLFIVSCETGRVVVSDSVTPVLNQPQSEWFGSTLYDQVHPDDVDKLRQLSTSRMCM
LKHLELAADGFLFVVGCDRGKILFVSESVFKILNYSQNDLIGQSLFDYLPKDIKAKVKEQLSSSRLC
VFDVQRATAILAYLPQELLGTSCYEYFHQDDIGHLAECRQVQLQTRKITTNCYKFKIKDGSFITLRS
azleen@DESKTOP-KG6EI8G:~/Lab_session2$
```

hazTeen@DESKTOP-HG6E18G:~/Lab_sness2\$ grep -v "" sequences.fasta | grep -v
NPZSKRHRDRNLNTELDRLASLLPFPQDVINKLDKLSVLRLSVSYLRAKSFDFVALKSSPTERNNGGDNCR
QLHWQIPPENSPLMERCFCICRLCLLDNSSGFLAMNFQGLKYLPPQLALFAIATPLQPPSILEIRTKNF
IFRTKHKLDFTPIGCDAGKRIVLGYTEAELCTRGSGYQFIHAADMLYCAESHIRMIKTGESGMIVFRLLT
KNNRWTTWVQSNARLLYKNGRPDYIIVTQRPLTDEEGTEHLR
/SRNKSEKKRRDQFNVLIKELGSMPLPGNARKMDKSTVLQKSIDFLRKHKETIQAQSDASEIRQDWKPTFLS
NEEFTQLMLEALDGFLLAIMTDGSIYVSEVSTLLEHLPSDLVDQSFNFIPGEHSEVYKILSTEYLK
SKNQLFECCHMLRGITIDPKEPSTYEVVKFIGNFKSLYEDRVCFVATVRLATPQFIKEMCTVEEPNEEFTS
RHSLEWKFLFLDHRAPPPIIGYLPFEVLGTSGYDYHVDLENLAKCHEHLMQYGGKSCYYRFLTKGQQW
IWLQTHYYITYHQWNSRPEFIVCTHTVVSVAEVRAE
KEKSRDAARSRSKESEVFYELAHQLPLPHNVSSHLDKASVMRLTISYLRVRKLLDAGDLIEDDMKAQM
NCFYLLKALDGFVMVLTDGDMYISDNVNKYMGLTQFELTGHSVDFDTHPCDHEEMREMLTHNTQRSFLL
RMKCTLTSRGRTMNIKSATWVKVLHCTGHIHVYKPPMTCLVLICEPIPHPSNIEIPLDSKTFLSRHSLDMK
FSYCDERITELMGYPEELLGRSIEYHYHALDSOHLTKTHDMFTKGQVTTGQYRMLAKRGYVWVETQA
TVIYNTKNSQPQCIVCNVYVVSIGIQHDL
KEKSRDAARCRRSKETEVFYLAEHLPLPHSVSSHLDKASIMRLAISFLRTHKLLSSVCSENESEAEADQ
QMDNLYLKALEGFIAVVTQDGMIFLSENISKFMGLTQVELTGHSIFDTHPCDHEEIRENLSSTERDFF
MRMKCTVTNRGRTVNLKSATWVKVLHCTGQVVKVEPLLSCLIIIMCEPIQHPSHMDIPLDSKTFLSRHSDM
KFTYCDRITELIGYHPEELLGRSAYEFYHALDSENMTKSHQNLCTKGQVVSQYRMLAKHGGYVWVLETQ
GTVIYNPRNLQPQCIMCVNYVLSIEIKNDV
DAARSRRSQETEVLQLAHTLPFARGVSAHLDKASIMRLTISYLRMHRLCAAGEWNVQVAGGEPDACYL
KALEGFVMVLTAEGDMAYLSENVSKHLGLSQLELIGHISIFDFIHPCDQEELQDALTPPTERCFSLRMKST
LTSRGRTLNLKAATWVKVNLCSGHHMAYEPPLQCLVLICEAIPHGSGLEPPLGRGAFLSRHSLDMKFTYCD
DRIAEVAGYSDDLIGCSAYEYIHALDSADVSKIHTLLSKGQAVTGQYRFLARSGGYLWTQTQATVVSG
GRGPQSESIVCVHFLISQVEETGV
KEKSRNAARSRRGKENLEFFELAKLLPLPGAISSQLDKASIVRLSVTYLRLRRFAALGAPPWGLRAAGPP
AGLAPGRRGPAAALVSEVFEQLGGHILQSLDGFVFALNQEKGFLYISETVSIYLGLSQVEMTGSSVFDYI
HPGDHSEVLEQLGLVQERSFFVRMKSTLTKRGLHVKASGYKVIHVTGRLRALGLVALGHTLPPAPLAELP
LHGMMIVFRLSLGLTILACESRVSDHMDLGPSELVGRSCYQFVHGQDATRIRQSHVDLLDKGQVMTGYR
WLQRAGGFVWLQSVATVAGSGKSPGEHHVLWVSHVLSQAEGGQT
NKSEKKRRDQFNVLIKELSSMLPGNTRKMDKTTVLEKVIQFLQKHNEVSAQTEICDIQDQDWKPSFLSNEE
FTQLMLEALDGFIIAVTTDGSIIYVSDSITPLLGHLPSDVMQDNLNLFPEQEHSEVYKILSSEYKSDS
DLEFYCHLLRGSLNPKFPTYEVYKIFVGNFRSYLGEVCFIATVRLATPQFLKEMCIVDEPLEEFTSRHS
LEWKFLFLDHRAPPPIIGYLPFEVLGTSGYDYHIDDELLARCHQHLMQFGKGKSCCYRFLTKGQQWIWL
QTHYYITYHQWNSKPEFIVCTHSVVSADVRVE
SRDAARSRRGKENFEFYLAKLLPLPAAITSQLDKASIRLTISYLMRDFANQGDPPWNLRMGEPPTNT
SVKVIQAQRRRSPSALAEVFEAHLGSHILQSLDGFVFALNQEKGFLYISETVSIYLGLSQVELTGSSVF



Quick search



ENG
IN



14:54
18-08-2025

```
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$
```


MSGPVPSRARVYTDVNTHRPREYWDYESHVVEWGNQDDYQLVRKLGRGKYSEVFEATINITNNEKVVVKIL
KPVKKKKIKREIKIENLRGKPNIIITLADIVKDPVSRTPAVFHEVNNITDFQQLYQTLTDYDIRFYMEI
LKALDYCKSMGIMHRDVRGPHNVIIDHEHRKRLRLTDWGLAEVFGPQGEYNNVRSVRYFKGPELLVDYQMY
YSLDMWSLGCMLASHIFRKEPFFHGHNDYDQLVRIAKELGTEDLYDYIDKYNETLDRPFNDILGRHSRKR
WERFVSHENQHLVSPEALDFDLKLRHYDQHSRLTAREAMEHPEYFTVVKDQARMGSSMPGGSTPVSSAN
MMSGTSSVPTPSPLGPLAGSPVIAAANLGMPPVAAAGA00

```
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ file="Biocomputing"
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ expoet file
expoet: command not found
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ export file
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ bash -c 'echo $file'
Biocomputing
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ vi
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ vi new_file |
```



```
#!/bin/bash
```

```
if [ -f "sequence3.fasta" ]; then
wc -l sequence3.fasta
else
echo "Missing file"
fi
```

```
#!/bin/bash
```

```
for file in *.fasta do
    echo "Processing:$file"
    echo "Sequence:$file(grep -c ">" "$file")"
    echo "File size (characters): $(wc -c < "$file")"
done
```

```
#!/bin/bash
```

```
for file in *.fasta; do
    if [ -f "$file" ]; then
        seqs=$(grep -c "^>" "$file")
        if [ "$seqs" -gt 3 ]; then
            echo "Processing:$file"
            echo "Sequences:$seqs"
            echo "File size (characters):"
        fi
    fi
done
```

```
"new_file" 32L, 487B
```

```
nazleen@DESKTOP-KG6EI8G: x + v
nazleen@DESKTOP-KG6EI8G$ export file
nazleen@DESKTOP-KG6EI8G$ bash -c 'echo $file'
Biocomputing
nazleen@DESKTOP-KG6EI8G$ vi
nazleen@DESKTOP-KG6EI8G$ vi new_file
nazleen@DESKTOP-KG6EI8G$ vi new_file
nazleen@DESKTOP-KG6EI8G$ vi new_file
nazleen@DESKTOP-KG6EI8G$ chmod +x new_file
nazleen@DESKTOP-KG6EI8G$ ./new_file
19 sequence3.fasta
./new_file: line 14: syntax error near unexpected token `echo'
./new_file: line 14: ` echo "Processing:$file"
nazleen@DESKTOP-KG6EI8G$ vi new_file
nazleen@DESKTOP-KG6EI8G$ vi new_file
nazleen@DESKTOP-KG6EI8G$ ./new_file
19 sequence3.fasta
./new_file: line 14: syntax error near unexpected token `echo'
./new_file: line 14: ` echo "Processing:$file"
nazleen@DESKTOP-KG6EI8G$ vi new_file
nazleen@DESKTOP-KG6EI8G$ ./new_file
19 sequence3.fasta
Processing:protein.fasta
File size (characters): 467
Processing:sequence.fasta
File size (characters): 79551
Processing:sequence1.fasta
File size (characters): 974
Processing:sequence2.fasta
File size (characters): 1710
Processing:sequence3.fasta
File size (characters): 1000
Processing:sequence4.fasta
File size (characters): 2374
Processing:sequence5.fasta
File size (characters): 4229
./new_file: line 28: unexpected EOF while looking for matching `''
nazleen@DESKTOP-KG6EI8G$ |
```



Quick search



15:22
18-08-2025

```
nazleen@DESKTOP-KG6EI8G: + ~  
File size (characters): 974  
Processing:sequence2.fasta  
File size (characters): 1710  
Processing:sequence3.fasta  
File size (characters): 1000  
Processing:sequence4.fasta  
File size (characters): 2374  
Processing:sequence5.fasta  
File size (characters): 4229  
./new_file: line 28: unexpected EOF while looking for matching `'  
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ vi new_file  
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ ./new_file  
19 sequence3.fasta  
Processing:protein.fasta  
File size (characters): 467  
Processing:sequence.fasta  
File size (characters): 79551  
Processing:sequence1.fasta  
File size (characters): 974  
Processing:sequence2.fasta  
File size (characters): 1710  
Processing:sequence3.fasta  
File size (characters): 1000  
Processing:sequence4.fasta  
File size (characters): 2374  
Processing:sequence5.fasta  
File size (characters): 4229  
Processing:sequence2.fasta  
Sequences:4  
File size (characters): 1710  
Processing:sequence4.fasta  
Sequences:4  
File size (characters): 2374  
Processing:sequence5.fasta  
Sequences:13  
File size (characters): 4229  
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ |
```

```
nazleen@DESKTOP-KG6EI8G: x + v
Processing:sequence2.fasta
File size (characters): 1710
Processing:sequence3.fasta
File size (characters): 1000
Processing:sequence4.fasta
File size (characters): 2374
Processing:sequence5.fasta
File size (characters): 4229
./new_file: line 28: unexpected EOF while looking for matching `"'
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ vi new_file
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ ./new_file
19 sequence3.fasta
Processing:protein.fasta
File size (characters): 467
Processing:sequence.fasta
File size (characters): 79551
Processing:sequence1.fasta
File size (characters): 974
Processing:sequence2.fasta
File size (characters): 1710
Processing:sequence3.fasta
File size (characters): 1000
Processing:sequence4.fasta
File size (characters): 2374
Processing:sequence5.fasta
File size (characters): 4229
Processing:sequence2.fasta
Sequences:4
File size (characters): 1710
Processing:sequence4.fasta
Sequences:4
File size (characters): 2374
Processing:sequence5.fasta
Sequences:13
File size (characters): 4229
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ grep -v "^>" sequence5.fasta | grep "C.*C.*C" | grep -v "^>" > cys_rich.txt
nazleen@DESKTOP-KG6EI8G:~/Lab_session2$ man sort
```


SORT(1)

User Commands

SORT(1)

NAME

sort - sort lines of text files

SYNOPSIS

```
sort [OPTION]... [FILE]...  
sort [OPTION]... --files0-from=F
```

DESCRIPTION

Write sorted concatenation of all FILE(s) to standard output.

With no FILE, or when FILE is -, read standard input.

Mandatory arguments to long options are mandatory for short options too. Ordering options:

-b, --ignore-leading-blanks
ignore leading blanks

-d, --dictionary-order
consider only blanks and alphanumeric characters

-f, --ignore-case
fold lower case to upper case characters

-g, --general-numeric-sort
compare according to general numerical value

-i, --ignore-nonprinting
consider only printable characters

-M, --month-sort
compare (unknown) < 'JAN' < ... < 'DEC'

-h, --human-numeric-sort
compare human readable numbers (e.g., 2K 1G)

Manual page sort(1) line 1 (press h for help or q to quit)



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15:28
18-08-2025