BIOINFORMATICS
SESSION 10. PRACTICE

2023-11-06

Royal blood and order In the sequence universe

Basic Shell Commands

```
$ cd 2023123456_HyunWoo
$ mkdir session10
$ cd session10
```

Unix commands

** 반드시 여러분의 working directory에서 아래 명령어를 수행하세요!

```
$ ln -s /home/biguser/tutor/session10/tax.txt .
$ ln -s /home/biguser/tutor/session10/mito.fa .

$ less tax.txt
```

```
1       root            other sequences
2       Bacteria        eubacteria      Bacteria
6       Azorhizobium            Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Xanthobacteraceae
7       Azorhizobium caulinodans                Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Xanthobacteraceae; Azorhizobium
9       Buchnera aphidicola             Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Buchnera
10      Cellvibrio              Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae
11      Cellvibrio gilvus               Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Cellvibrio
13      Dictyoglomus            Bacteria; Dictyoglomi; Dictyoglomales; Dictyoglomaceae
14      Dictyoglomus thermophilum               Bacteria; Dictyoglomi; Dictyoglomales; Dictyoglomaceae; Dictyoglomus
16      Methylophilus           Bacteria; Proteobacteria; Betaproteobacteria; Methylophilales; Methylophilaceae
17      Methylophilus methylotrophus            Bacteria; Proteobacteria; Betaproteobacteria; Methylophilales; Methylophilaceae; Methylophilus
18      Pelobacter              Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales; Pelobacteraceae
19      Pelobacter carbinolicus         Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales; Pelobacteraceae; Pelobacter
20      Phenylobacterium                Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae
21      Phenylobacterium immobile               Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae; Phenylobacterium
22      Shewanella              Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae
23      Shewanella colwelliana          Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella
24      Shewanella putrefaciens         Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella
25      Shewanella hanedai              Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales; Shewanellaceae; Shewanella
27      halophilic eubacterium NRCC 41227               Bacteria
```

Unix commands

```
$ less mito.fa
```

```
>Dasyurus_hallucatus
GCCTTA-CTGTTAATTTTTATTAAACCTACACATGCAAGT
TTCCGCAATCCAGTGAGT-ACGCCCTTTTAACT-TGTCTA
-----GAGCATAAAGGAGCTGGTATCAGGCACACT-CGAT
TGAGCAGCCCATGACACCTTGTCCAACCACA-CCCCCACG
GGTTACAGCAGTGACTAACATTGAGCTATAAACGAAAGTT
TGA-CTAAATTATAATAAAC--AAGGGTTGGTAAATCTCG
TGCCAGCCACCGCGGTCATACGATTAACCCAAATTAACAG
AAAAACGGCGTAAAGGGTGTTTAAGCAT---AAACCTTGC
AA-TAAAGTTAAAGCTCAACTACGCTGTAATACGCCACAG
TTGATATTAAAATAAGCAACTTACGTGACTTTATTAAC--
GCTGAAGACACTAAAACTAAGGTACAAACTGGGATTAGAG
ACCCCACTATGCTTAGTCGTAAACCTAGGTAATTAAA-TA
ACAAAATTACTCGCCAGAGAACTACTAGCTACTGCTTAAA
ACTCAAAGGACTTGGCGGTGCCCTAGACCCTCCTAGAGGA
GCCTGTTCTATAATCGATAAACCCCGATAGACCTCACCCC
TCCTCGCTC-AACAGTCTATATACCGCCATCGTCAGCTCA
CCCCAATAGGGCTTAAAAGTGAGCAAAA-TCATCAAAC-C
ATAAAAACGTTAGGTCAAGGTGTAGCATATGGAGGGGGAA
GTGATGGGCTACATTTTCTATACTAGAACAT--AACGGAT
TGTCTACTGAAAT----AAAGACATGAAGGAGGATTTAGT
AGTAAATTAAGAATAGAGAGCTTAATTGAAATAGGCAATA
```

• • •

```
>Phascogale_tapoatafa
GCCTTA-CTGTTAATTTTTATTAGACCTACACATGCAAGT
TTCCGCTACCCAGTGAGT-ATGCCCTTTTAGCT-TTCTTA
-----GAGTATAAAGGAGTAGGTATCAGGCACACTTCTGT
GAAGTAGCCCATGACACCTAGTTTGACCACA-CCCCCACG
GGCTACAGCAGTGACTAACATTGAGCTATAAACGAAAGTT
TGA-CTAAATCATAATAAA---AAGGGTTGGTAAATTTCG
TGCCAGCCACCGCGGTCATACGATTAACCCGAATTAACAG
AAGAACGGCGTAAAGTGTGTTTAAGCAATAAGAATTTTCC
AAATAAGGTTAAAGATCAACTAAGCTGTAATACGCTCAGG
TTGATGTTAAAATACGCAACTTACGTGACTTTACCCCCT-
GCTGAAGACATTAAAGCTAAGGTACAAACTGGGATTAGAG
ACCCCACTATGCTTAGCCGTAAACCGAGGTAGTTATA-TA
ACAAGACTATCCGCCAGAGAACTACGAGCCACTGCTTAAA
ACTCAAAGGACTTGGCGGTGCCCTAGACCCTCCTAGAGGA
GCCTGTTCTGTAATCGATAAACCCCGATATACCTCACCTC
TCCTGGCT--GTCAGTCTATATACCGCCATCGTCAGCTCA
CCCCAATAGGGTACAAAAGTGAGCAAGA-TCATGAAAC-C
ATAAAAACGTTAGGTCAAGGTGTAGCATATGGAAAGGGAA
GTAATGGGCTACATTTTCTATATTAGAACAT--AACGGAT
```

Unix commands

```
$ cat tax.txt
$ cat mito.fa

## 아래 명령어는 실제로 실행하지는 마세요. 단순 예시입니다!
$ cat tax.txt mito.fa > taxmito.txt


*cat = concatenate
*cat file1 file2 fil3 … > merged_file
```

Unix commands

```
$ grep --help
```

```
[biguser@biglab-master session10]$ grep --help
Usage: grep [OPTION]... PATTERN [FILE]...
Search for PATTERN in each FILE or standard input.
PATTERN is, by default, a basic regular expression (BRE).
Example: grep -i 'hello world' menu.h main.c

Regexp selection and interpretation:
  -E, --extended-regexp     PATTERN is an extended regular expression (ERE)
  -F, --fixed-strings       PATTERN is a set of newline-separated fixed strings
  -G, --basic-regexp        PATTERN is a basic regular expression (BRE)
  -P, --perl-regexp         PATTERN is a Perl regular expression
  -e, --regexp=PATTERN      use PATTERN for matching
  -f, --file=FILE           obtain PATTERN from FILE
  -i, --ignore-case         ignore case distinctions
  -w, --word-regexp         force PATTERN to match only whole words
  -x, --line-regexp         force PATTERN to match only whole lines
  -z, --null-data           a data line ends in 0 byte, not newline
```

Unix commands

```
$ grep --help
```

```
- -c : 패턴이 일치하는 행의 수를 출력한다.
- -i : 비교시 대소문자를 구별하지 않는다.
- -v : 지정한 패턴과 일치하지 않는 행만 출력한다.
- -n : 행의 번호를 함께 출력한다.
- -l : 패턴이 포함된 파일의 이름을 출력한다.
- -w : 패턴이 전체 단어와 일치하는 행만 출력한다.
```

http://www.incodom.kr/Linux/기본명령어/grep

Unix commands

```
$ grep –e “>” mito.fa
##-e, --regexp=PATTERN, use PATTERN for matching
```

```
[biguser@biglab-master session10]$ grep -e ">" mito.fa
>Dasyurus_hallucatus
>Phascogale_tapoatafa
>Sminthopsis_crassicaudata
>Myrmecobius_fasciatus
>Thylacinus_cynocephalus
>Isoodon_macrourus
>Echymipera_rufescens_australis
>Monodelphis_domestica
>Trichosurus_vulpecula
>Phalanger_interpositus
>Vombatus_ursinus
>Macropus_robustus
```

```
$ grep –c “>” mito.fa
## -c, --count, print only a count of matching lines per
FILE
```

```
[biguser@biglab-master session10]$ grep -c ">" mito.fa
16
```

Unix commands

```
$ cut --help
```

```
[biguser@biglab-master session10]$ cut --help
Usage: cut OPTION... [FILE]...
Print selected parts of lines from each FILE to standard output.

Mandatory arguments to long options are mandatory for short options too.
  -b, --bytes=LIST        select only these bytes
  -c, --characters=LIST   select only these characters
  -d, --delimiter=DELIM   use DELIM instead of TAB for field delimiter
  -f, --fields=LIST       select only these fields;  also print any line
                            that contains no delimiter character, unless
                            the -s option is specified
  -n                      with -b: don't split multibyte characters
      --complement        complement the set of selected bytes, characters
                            or fields
  -s, --only-delimited    do not print lines not containing delimiters
      --output-delimiter=STRING  use STRING as the output delimiter
                            the default is to use the input delimiter
      --help     display this help and exit
      --version  output version information and exit

Use one, and only one of -b, -c or -f.  Each LIST is made up of one
range, or many ranges separated by commas.  Selected input is written
in the same order that it is read, and is written exactly once.
Each range is one of:

  N     N'th byte, character or field, counted from 1
  N-    from N'th byte, character or field, to end of line
  N-M   from N'th to M'th (included) byte, character or field
  -M    from first to M'th (included) byte, character or field

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

Report cut bugs to bug-coreutils@gnu.org
GNU coreutils home page: <http://www.gnu.org/software/coreutils/>
General help using GNU software: <http://www.gnu.org/gethelp/>
For complete documentation, run: info coreutils 'cut invocation'
```

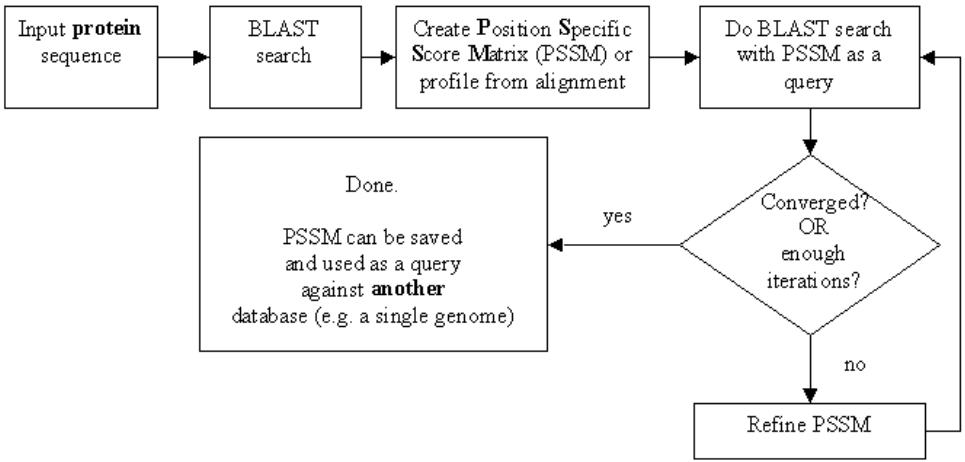
Unix commands

```
$ cut –f 1-4 tax.txt
##-f, --fields=LIST        select only these fields
```

1	ro
2	Ba
6	Az
7	Az
9	Bu
10	C
11	C
13	D
14	D
16	M
17	M
18	P
19	P
20	P

1	root	other sequences	
2	Bacteria	eubacteria	Bacteria
6	Azorhizobium	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Xanthobacteraceae	
7	Azorhizobium caulinodans	Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Xanthobacteraceae; Azorhizobium	
9	Buchnera aphidicola	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Buchnera	
10	Cellvibrio	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae	
11	Cellvibrio gilvus	Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales; Pseudomonadaceae; Cellvibrio	
13	Dictyoglomus	Bacteria; Dictyoglomi; Dictyoglomales; Dictyoglomaceae	
14	Dictyoglomus thermophilum	Bacteria; Dictyoglomi; Dictyoglomales; Dictyoglomaceae; Dictyoglomus	
16	Methylophilus	Bacteria; Proteobacteria; Betaproteobacteria; Methylophilales; Methylophilaceae	
17	Methylophilus methylotrophus	Bacteria; Proteobacteria; Betaproteobacteria; Methylophilales; Methylophilaceae; Methylophilus	
18	Pelobacter	Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales; Pelobacteraceae	
19	Pelobacter carbinolicus	Bacteria; Proteobacteria; Deltaproteobacteria; Desulfuromonadales; Pelobacteraceae; Pelobacter	
20	Phenylobacterium	Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales; Caulobacteraceae	

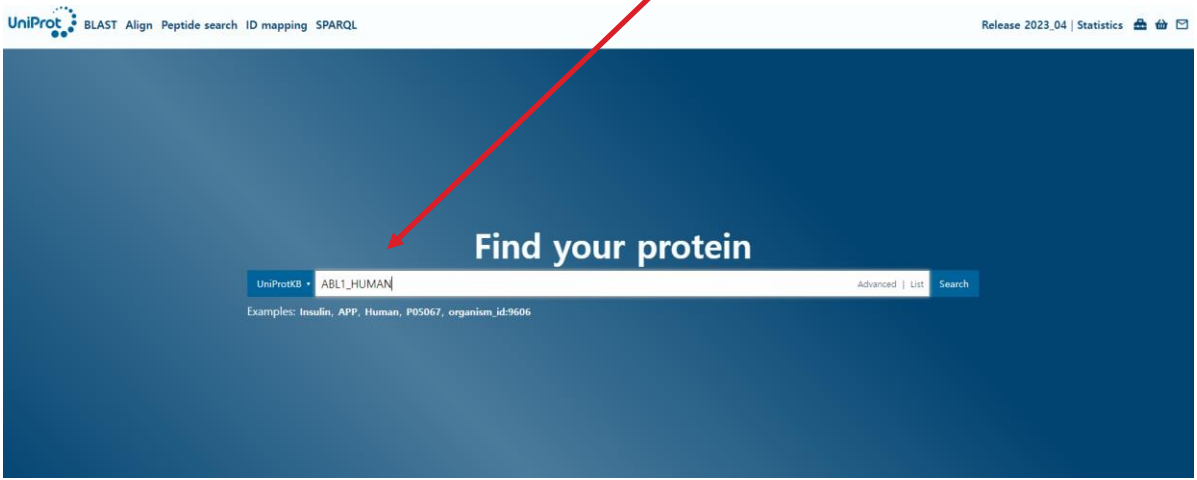
PSI-BLAST workflow



Get sequence from UniProt

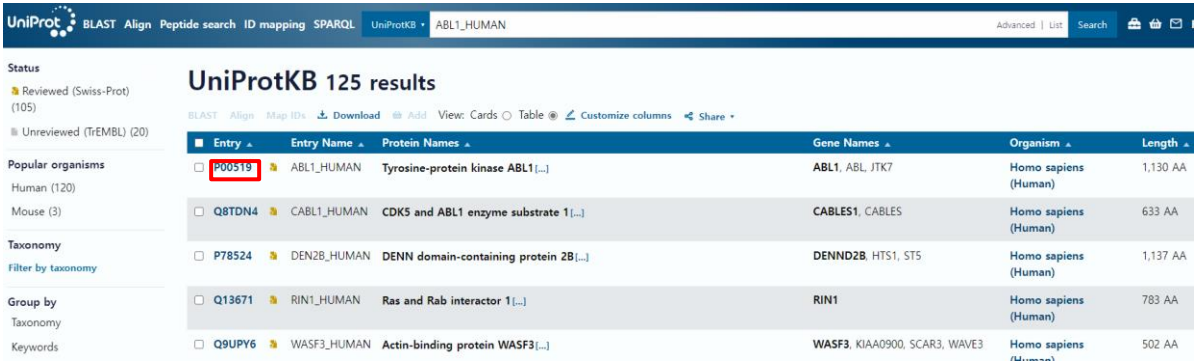
- Input: ABL1 (ABL1_HUMAN) – SH domain

“ABL1_HUMAN” and press search

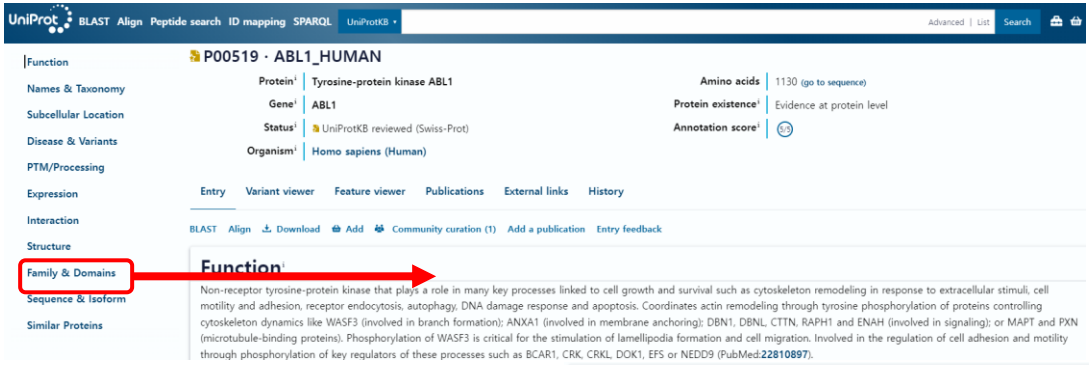


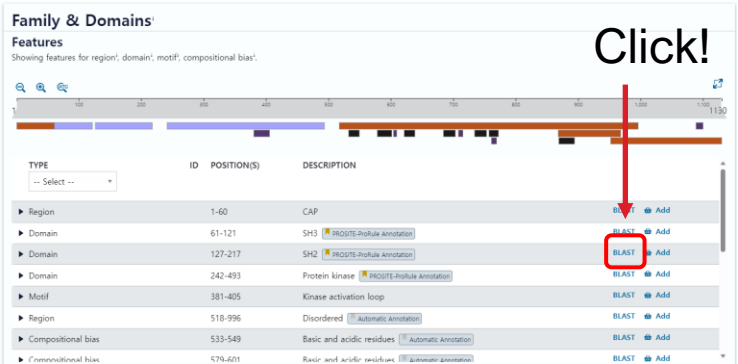
Get sequence from UniProt

- Input: ABL1 (ABL1_HUMAN) – SH domain



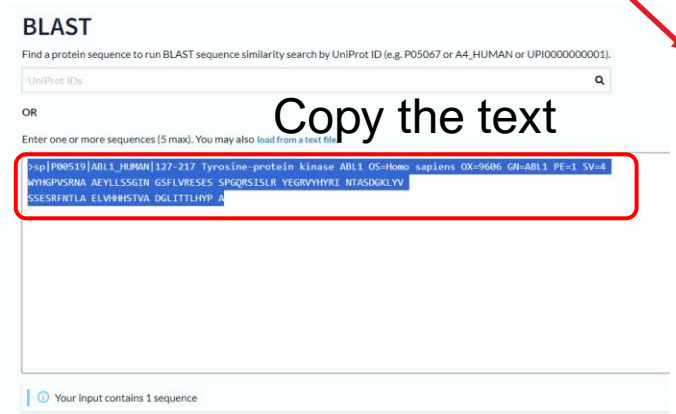
Get sequence from UniProt



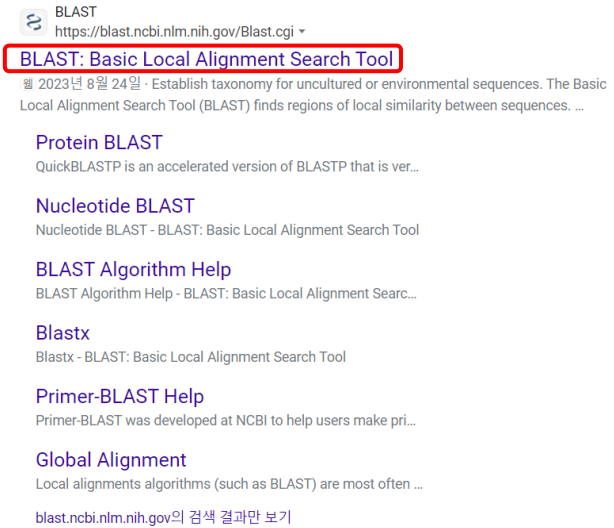


Get sequence from UniProt

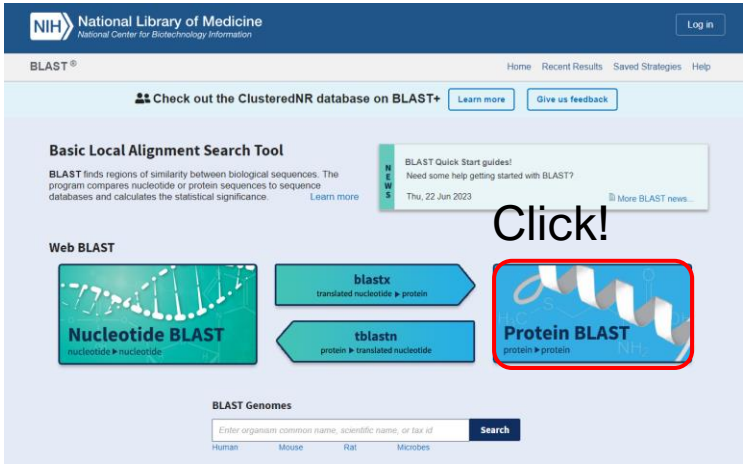
Click!



Copy the text

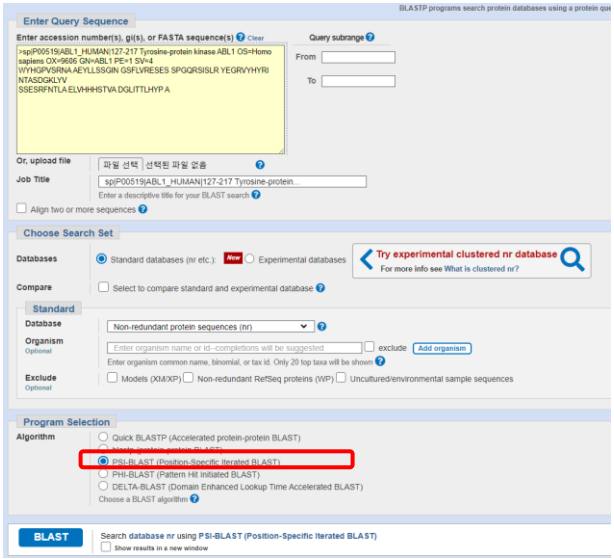


PSI-BLAST



Click!

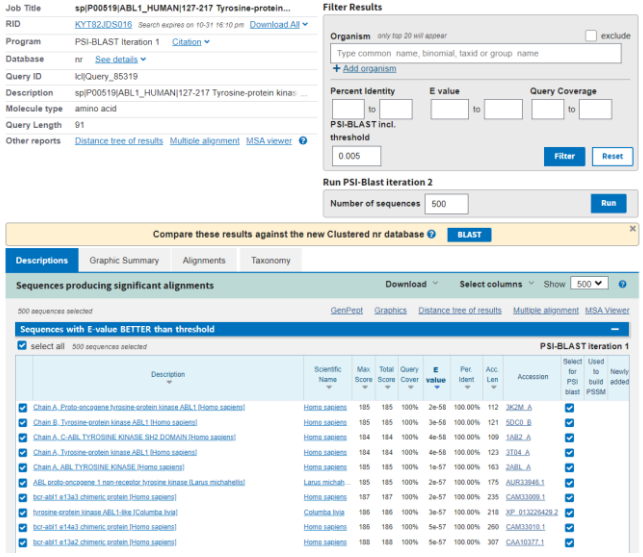
1. Paste the copied sequence of SH2

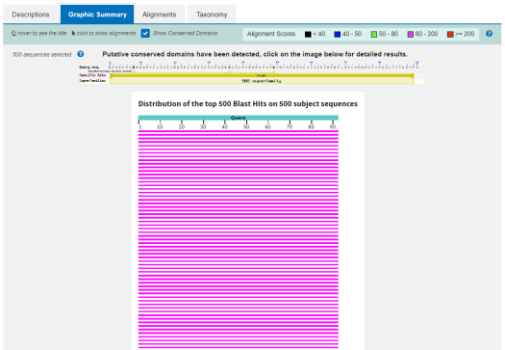


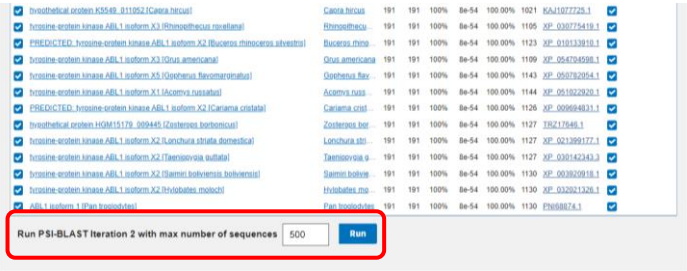
2. Check PSI-BLAST

3. Run BLAST

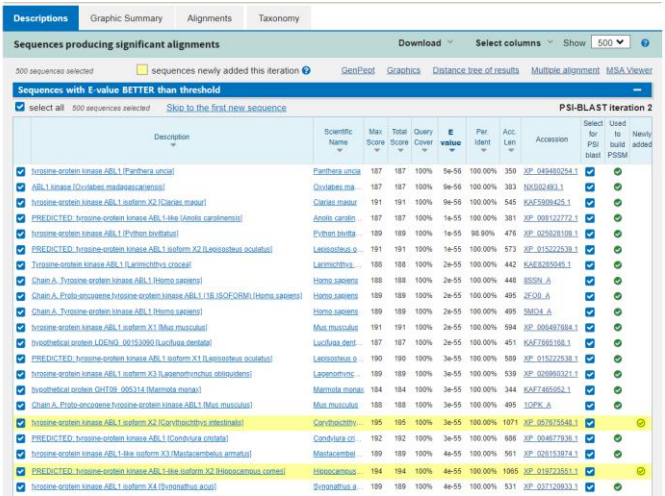
PSI-BLAST

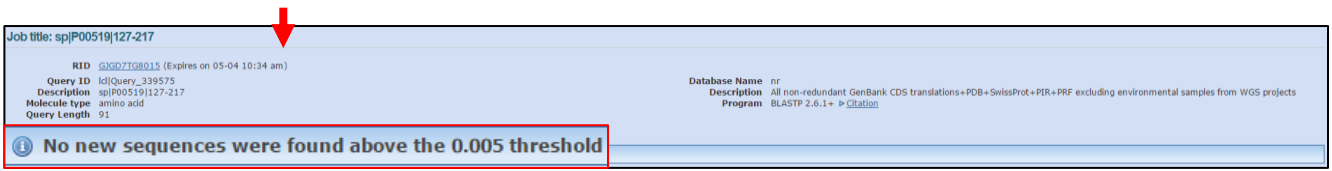

Job Title
sp|P00519|ABL1_HUMAN|127-217 Tyrosine-protein...
RID
KYT82JDS016
Search expires on 10-31 16:10 pm
Download All
Program
PSI-BLAST Iteration 1
Citation
Database
nr
See details
Query ID
lcl|Query_85319
Description
sp|P00519|ABL1_HUMAN|127-217 Tyrosine-protein kinas...
Molecule type
amino acid
Query Length
91
Other reports
Distance tree of results
Multiple alignment
MSA viewer
Filter Results
Organism
only top 20 will appear
exclude
Type common name, binomial, taxid or group name
Add organism
Percent Identity
E value
Query Coverage
PSI-BLAST incl. threshold
0.005
Filter
Reset
Run PSI-Blast iteration 2
Number of sequences
500
Run
Compare these results against the new Clustered nr database
BLAST
Descriptions
Graphic Summary
Alignments
Taxonomy
Sequences producing significant alignments
Download
Select columns
Show
500
500 sequences selected
GenPept
Graphics
Distance tree of results
Multiple alignment
MSA Viewer
Sequences with E-value BETTER than threshold
select all
500 sequences selected
PSI-BLAST iteration 1
Description
Scientific Name
Max Score
Total Score
Query Cover
E value
Per. Ident
Acc. Len
Accession
Select for PSI blast
Used to build PSSM
Newly added
Chain A, Proto-oncogene tyrosine-protein kinase ABL1 [Homo sapiens]
Homo sapiens
185
185
100%
2e-58
100.00%
112
3K2M_A
Chain B, Tyrosine-protein kinase ABL1 [Homo sapiens]
Homo sapiens
185
185
100%
3e-58
100.00%
121
5DC0_B
Chain A, C-ABL TYROSINE KINASE SH2 DOMAIN [Homo sapiens]
Homo sapiens
184
184
100%
4e-58
100.00%
109
1AB2_A
Chain A, Tyrosine-protein kinase ABL1 [Homo sapiens]
Homo sapiens
184
184
100%
4e-58
100.00%
123
3T04_A
Chain A, ABL TYROSINE KINASE [Homo sapiens]
Homo sapiens
185
185
100%
1e-57
100.00%
163
2ABL_A
ABL proto-oncogene 1 non-receptor tyrosine kinase [Larus michahellis]
Larus michah...
185
185
100%
2e-57
100.00%
175
AUR33946.1
bcr-abl1 e13a3 chimeric protein [Homo sapiens]
Homo sapiens
187
187
100%
2e-57
100.00%
235
CAM33009.1
tyrosine-protein kinase ABL1-like [Columba livia]
Columba livia
186
186
100%
3e-57
100.00%
218
XP_013226429.2
bcr-abl1 e14a3 chimeric protein [Homo sapiens]
Homo sapiens
186
186
100%
5e-57
100.00%
260
CAM33010.1
bcr-abl1 e13a2 chimeric protein [Homo sapiens]
Homo sapiens
188
188
100%
5e-57
100.00%
307
CAA10377.1


Descriptions
Graphic Summary
Alignments
Taxonomy
Alignment Scores
< 40
40 - 50
50 - 80
80 - 200
>= 200
500 sequences selected
Putative conserved domains have been detected, click on the image below for detailed results.
Distribution of the top 500 Blast Hits on 500 subject sequences

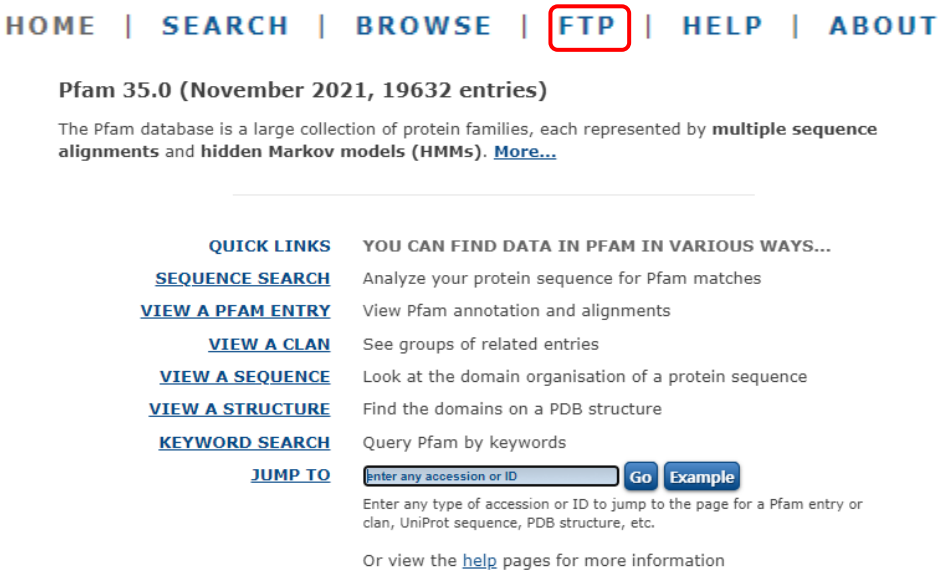

hypothetical protein K5549_011052 [Capra hircus]
Capra hircus
191
191
100%
8e-54
100.00%
1021
KAJ1077725.1
tyrosine-protein kinase ABL1 isoform X3 [Rhinopithecus roxellana]
Rhinopithecu...
191
191
100%
8e-54
100.00%
1105
XP_030775419.1
PREDICTED: tyrosine-protein kinase ABL1 isoform X2 [Buceros rhinoceros silvestris]
Buceros rhino...
191
191
100%
8e-54
100.00%
1123
XP_010133910.1
tyrosine-protein kinase ABL1 isoform X3 [Grus americana]
Grus americana
191
191
100%
8e-54
100.00%
1109
XP_054704598.1
tyrosine-protein kinase ABL1 isoform X5 [Gopherus flavomarginatus]
Gopherus flav...
191
191
100%
8e-54
100.00%
1143
XP_050782054.1
tyrosine-protein kinase ABL1 isoform X1 [Acomys russatus]
Acomys russ...
191
191
100%
8e-54
100.00%
1144
XP_051022920.1
PREDICTED: tyrosine-protein kinase ABL1 isoform X2 [Cariama cristata]
Cariama crist...
191
191
100%
8e-54
100.00%
1126
XP_009694831.1
hypothetical protein HGM15179_009445 [Zosterops borbonicus]
Zosterops bor...
191
191
100%
8e-54
100.00%
1127
TRZ17646.1
tyrosine-protein kinase ABL1 isoform X2 [Lonchura striata domestica]
Lonchura stri...
191
191
100%
8e-54
100.00%
1127
XP_021399177.1
tyrosine-protein kinase ABL1 isoform X2 [Taeniopygia guttata]
Taeniopygia g...
191
191
100%
8e-54
100.00%
1127
XP_030142343.3
tyrosine-protein kinase ABL1 isoform X2 [Saimiri boliviensis boliviensis]
Saimiri bolivie...
191
191
100%
8e-54
100.00%
1130
XP_003920918.1
tyrosine-protein kinase ABL1 isoform X2 [Hylobates moloch]
Hylobates mo...
191
191
100%
8e-54
100.00%
1130
XP_032021326.1
ABL1 isoform 1 [Pan troglodytes]
Pan troglodytes
191
191
100%
8e-54
100.00%
1130
PNI68874.1
Run PSI-BLAST Iteration 2 with max number of sequences
500
Run

PSI-BLAST


Descriptions
Graphic Summary
Alignments
Taxonomy
Sequences producing significant alignments
Download
Select columns
Show 500
500 sequences selected
sequences newly added this iteration
GenPept
Graphics
Distance tree of results
Multiple alignment
MSA Viewer
Sequences with E-value BETTER than threshold
select all 500 sequences selected
Skip to the first new sequence
PSI-BLAST iteration 2
Description
Scientific Name
Max Score
Total Score
Query Cover
E value
Per. Ident
Acc. Len
Accession
Select for PSI blast
Used to build PSSM
Newly added
tyrosine-protein kinase ABL1 [Panthera uncia] Panthera uncia 187 187 100% 5e-56 100.00% 350 XP_049480254.1
ABL1 kinase [Oryzias madagascariensis] Oryzias ma... 187 187 100% 9e-56 100.00% 393 NXD02493.1
tyrosine-protein kinase ABL1 isoform X2 [Cariacus magur] Cariacus magur 191 191 100% 9e-56 100.00% 545 KAF5909425.1
PREDICTED: tyrosine-protein kinase ABL1-like [Anolis carolinensis] Anolis carolin... 187 187 100% 1e-55 100.00% 381 XP_008122772.1
tyrosine-protein kinase ABL1 [Python bivittatus] Python bivitta... 189 189 100% 1e-55 98.90% 476 XP_025028109.1
PREDICTED: tyrosine-protein kinase ABL1 isoform X2 [Lepisosteus oculatus] Lepisosteus o... 191 191 100% 1e-55 100.00% 573 XP_015222539.1
Tyrosine-protein kinase ABL1 [Larimichthys crocea] Larimichthys... 188 188 100% 2e-55 100.00% 442 KAE8285045.1
Chain A, Tyrosine-protein kinase ABL1 [Homo sapiens] Homo sapiens 188 188 100% 2e-55 100.00% 448 8SSN_A
Chain A, Proto-oncogene tyrosine-protein kinase ABL1 (1B ISOFORM) [Homo sapiens] Homo sapiens 189 189 100% 2e-55 100.00% 495 2F00_A
Chain A, Tyrosine-protein kinase ABL1 [Homo sapiens] Homo sapiens 189 189 100% 2e-55 100.00% 495 5MO4_A
tyrosine-protein kinase ABL1 isoform X1 [Mus musculus] Mus musculus 191 191 100% 2e-55 100.00% 594 XP_006497684.1
hypothetical protein LDENG_00153090 [Lucifuga dentata] Lucifuga dent... 187 187 100% 2e-55 100.00% 451 KAF7665168.1
PREDICTED: tyrosine-protein kinase ABL1 isoform X1 [Lepisosteus oculatus] Lepisosteus o... 190 190 100% 3e-55 100.00% 589 XP_015222538.1
tyrosine-protein kinase ABL1 isoform X3 [Lagenorhynchus obliquidens] Lagenorhync... 189 189 100% 3e-55 100.00% 539 XP_026969321.1
hypothetical protein GHT09_005314 [Marmota monax] Marmota monax 184 184 100% 3e-55 100.00% 344 KAF7465052.1
Chain A, Proto-oncogene tyrosine-protein kinase ABL1 [Mus musculus] Mus musculus 188 188 100% 3e-55 100.00% 495 1OPK_A
tyrosine-protein kinase ABL1 isoform X2 [Corythoichthys intestinalis] Corythoichthy... 195 195 100% 3e-55 100.00% 1071 XP_057675548.1
PREDICTED: tyrosine-protein kinase ABL1 [Condylura cristata] Condylura cri... 192 192 100% 3e-55 100.00% 686 XP_004677936.1
tyrosine-protein kinase ABL1-like isoform X3 [Mastacembelus armatus] Mastacembel... 189 189 100% 4e-55 100.00% 561 XP_026153974.1
PREDICTED: tyrosine-protein kinase ABL1-like isoform X2 [Hippocampus comes] Hippocampus... 194 194 100% 4e-55 100.00% 1065 XP_019723551.1
tyrosine-protein kinase ABL1 isoform X4 [Gynuthus acus] Gynuthus a... 189 189 100% 4e-55 100.00% 531 XP_037120933.1


Job title: sp|P00519|127-217
RID GJGD7TG8015 (Expires on 05-04 10:34 am)
Query ID lcl|Query_339575
Description sp|P00519|127-217
Molecule type amino acid
Query Length 91
Database Name nr
Description All non-redundant GenBank CDS translations+PDB+SwissProt+PIR+PRF excluding environmental samples from WGS projects
Program BLASTP 2.6.1+ Citation
No new sequences were found above the 0.005 threshold

Data download



ftp://ftp.ebi.ac.uk/pub/databases/Pfam/releases/Pfam32.0/

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Index of /pub/databases/Pfam

Name	Last modified	Size	Description
Parent Directory		-	
AntiFam/	2021-09-01 14:43	-	
RoseTTAfold_aln/	2021-11-11 15:16	-	
Tools/	2017-03-08 09:16	-	
current_release/	2023-09-12 14:14	-	
mappings/	2023-10-25 03:00	-	
papers/	2021-04-01 13:25	-	
releases/	2023-09-14 11:22	-	
vm/	2013-05-22 06:25	-	

Index of /pub/databases/Pfam/current_release

Name	Last modified	Size	Description
Parent Directory		-	
Pfam-A.clans.tsv.gz	2023-09-12 13:30	377K	
Pfam-A.dead.gz	2023-09-12 13:30	24K	
Pfam-A.fasta.gz	2023-09-12 13:31	4.8G	
Pfam-A.full.gz	2023-09-12 13:32	18G	
Pfam-A.full.uniprot.gz	2023-09-12 13:36	33G	
Pfam-A.hmm.dat.gz	2023-09-12 13:36	540K	
Pfam-A.hmm	2023-09-12 13:36	286M	
Pfam-A.regic	:36	3.5G	
Pfam-A.regic	:37	9.6G	
Pfam-A.rp15	:38	1.2G	
Pfam-A.rp35	:38	4.0G	
Pfam-A.rp55	:39	8.2G	
Pfam-A.rp75	:40	13G	
Pfam-A.seed	:40	144M	
Pfam-B.tgz	:41	2.5G	
Pfam-C.gz	:41	178K	
Pfam.version	:41	115	
active_site.da	:41	12K	
database_files/	06:58	-	
diff.gz	2023-09-12 13:41	250K	
md5_checksums	2023-09-12 13:41	1.4K	
pdbmap.gz	2023-09-12 13:41	4.9M	
pfamseq.gz	2023-09-12 13:43	19G	
proteomes/	2023-09-12 14:54	-	
relnotes.txt	2023-09-12 13:43	25K	
swisspfam.gz	2023-09-12 13:43	3.3G	
trees.tgz	2023-09-12 13:43	24M	
uniprot.gz	2023-09-12 13:52	51G	
uniprot_reference_proteomes.dat.gz	2023-09-12 13:58	51G	
uniprot_sprot.dat.gz	2023-09-12 13:58	615M	
uniprot_trembl.dat.gz	2023-09-12 14:14	150G	
userman.txt	2023-09-12 14:14	17K	

Data download

```
$ wget [copy the URL link]
```
→ 실제로 실행하지는 말고 아래 link 명령어를 사용하세요

```
[biguser@R440 session10]$ wget http://ftp.ebi.ac.uk/pub/databases/Pfam/current_release/Pfam-A.hmm.gz
--2023-10-30 17:25:13--  http://ftp.ebi.ac.uk/pub/databases/Pfam/current_release/Pfam-A.hmm.gz
Resolving ftp.ebi.ac.uk (ftp.ebi.ac.uk)... 193.62.193.165
Connecting to ftp.ebi.ac.uk (ftp.ebi.ac.uk)|193.62.193.165|:80... connected.
HTTP request sent, awaiting response... 200 OK
Length: 299797995 (286M) [application/x-gzip]
Saving to: 'Pfam-A.hmm.gz'

 1% [>                                                    ] 5,829,145    677KB/s  eta 8m 37s
```

```
$ ln -s /home/biguser/tutor/session10/Pfam-A.hmm .
```

Build Pfam-A

```
$ less Pfam-A.hmm
```

```
HMMER3/f [3.1b2 | February 2015]
NAME  1-cysPrx_C
ACC   PF10417.11
DESC  C-terminal domain of 1-Cys peroxiredoxin
LENG  40
ALPH  amino
RF    no
MM    no
CONS  yes
CS    yes
MAP   yes
DATE  Wed Feb 24 18:37:46 2021
NSEQ  40
EFFN  17.426758
CKSUM 4086680297
GA    21.10 21.10;
TC    21.10 21.10;
NC    21.00 21.00;
BM    hmmbuild HMM.ann SEED.ann
SM    hmmsearch -Z 57096847 -E 1000 --cpu 4 HMM pfamseq
STATS LOCAL MSV       -7.5463  0.71948
STATS LOCAL VITERBI   -7.8624  0.71948
STATS LOCAL FORWARD   -4.3303  0.71948
HMM          A        C        D        E        F        G        H        I        K        L        M        N        P        Q        R        S        T        V        W        Y

            m->m     m->i     m->d     i->m     i->i     d->m     d->d
  COMPO   2.28046  4.31208  2.83393  2.63913  3.90855  2.69988  3.89812  3.33401  2.56310  2.85023  3.99954  3.22924  2.52123  2.90328  3.31238  2.94055  2.70512  2.59551  3.49266  3.8271
5
          2.68618  4.42225  2.77519  2.73123  3.46354  2.40513  3.72494  3.29354  2.67741  2.69355  4.24690  2.90347  2.73739  3.18146  2.89801  2.37887  2.77519  2.98518  4.58477  3.6150
3
          0.00226  6.48754  7.20989  0.61958  0.77255  0.00000        *
      1   0.29666  6.14436  6.78514  6.79783  7.06332  2.55785  7.22049  6.57837  6.66651  6.27638  3.28757  5.91223  5.83978  6.69238  6.58162  2.20136  4.83343  5.59959  8.41086  7.4310
7      1 A - - H
          2.68618  4.42225  2.77519  2.73123  3.46354  2.40513  3.72494  3.29354  2.67741  2.69355  4.24690  2.90347  2.73739  3.18146  2.89801  2.37887  2.77519  2.98518  4.58477  3.6150
3
          0.00226  6.48754  7.20989  0.61958  0.77255  0.48576  0.95510
      2   4.59591  5.92009  6.57211  5.96147  1.92899  5.81035  6.10135  2.33093  5.75927  0.69439  2.86149  5.97820  6.07717  5.78793  5.72916  5.13924  4.81708  2.59612  3.18569  3.3584
2      2 l - - H
          2.68618  4.42225  2.77519  2.73123  3.46354  2.40513  3.72494  3.29354  2.67741  2.69355  4.24690  2.90347  2.73739  3.18146  2.89801  2.37887  2.77519  2.98518  4.58477  3.6150
3
          0.00226  6.48754  7.20989  0.61958  0.77255  0.48576  0.95510
      3   4.81290  7.05274  3.71696  4.47757  6.60126  5.41623  3.72993  5.92180  2.06538  3.59487  6.10993  4.89014  5.75663  0.42291  2.54802  4.76779  4.95656  5.56452  7.24472  6.0861
5      3 Q - - H
          2.68618  4.42225  2.77519  2.73123  3.46354  2.40513  3.72494  3.29354  2.67741  2.69355  4.24690  2.90347  2.73739  3.18146  2.89801  2.37887  2.77519  2.98518  4.58477  3.6150
3
          0.00226  6.48754  7.20989  0.61958  0.77255  0.48576  0.95510
      4   2.64100  5.28125  5.84007  3.33362  1.80025  5.06896  2.72827  3.71332  5.01717  1.75203  2.65498  5.22280  5.43290  5.15329  5.03455  4.37913  1.80041  2.31249  5.90246  2.6329
8      4 l - - H
          2.68618  4.42225  2.77519  2.73123  3.46354  2.40513  3.72494  3.29354  2.67741  2.69355  4.24690  2.90347  2.73739  3.18146  2.89801  2.37887  2.77519  2.98518  4.58477  3.6150
```

Get sequence from swissprot

```
$ cp /home/biguser/tutor/session10/bc_seqid.txt .
```

```
$ less bc_seqid.txt
```

```
FA7_HUMAN
FA8_HUMAN
FA9_HUMAN
FA10_HUMAN
FA11_HUMAN
FA12_HUMAN
TF_HUMAN
PLMN_HUMAN
TPA_HUMAN
UROK_HUMAN
THRB_HUMAN
KLKB1_HUMAN
HGF_HUMAN
HGFA_HUMAN
bc_seqid.txt (END)
```

```
$ ln -s /home/biguser/your_directory/session6/swissprot* .

$ blastdbcmd -entry_batch bc_seqid.txt -db swissprot -long_seqids > clotting.fa
```

hmmscan from Pfam-A.hmm

HMM profile indexing

```
$ hmmpress Pfam-A.hmm
```

```
[biguser@R440 session10]$ hmmpress Pfam-A.hmm
Working...    done.
Pressed and indexed 19179 HMMs (19179 names and 19179 accessions).
Models pressed into binary file:   Pfam-A.hmm.h3m
SSI index for binary model file:   Pfam-A.hmm.h3i
Profiles (MSV part) pressed into:  Pfam-A.hmm.h3f
Profiles (remainder) pressed into: Pfam-A.hmm.h3p
```

hmmscan from Pfam-A.hmm

```
[biguser@R440 session10]$ hmmscan -h
# hmmscan :: search sequence(s) against a profile database
# HMMER 3.3.2 (Nov 2020); http://hmmer.org/
# Copyright (C) 2020 Howard Hughes Medical Institute.
# Freely distributed under the BSD open source license.
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
Usage: hmmscan [-options] <hmmdb> <seqfile>

Basic options:
  -h : show brief help on version and usage

Options controlling output:
  -o <f>           : direct output to file <f>, not stdout
  --tblout <f>     : save parseable table of per-sequence hits to file <f>
  --domtblout <f>  : save parseable table of per-domain hits to file <f>
  --pfamtblout <f> : save table of hits and domains to file, in Pfam format <f>
  --acc            : prefer accessions over names in output
  --noali          : don't output alignments, so output is smaller
  --notextw        : unlimit ASCII text output line width
  --textw <n>      : set max width of ASCII text output lines  [120]  (n>=120)
```

Searching HMM profile with a query sequence

```
$ hmmscan --domtblout clotting.tab Pfam-A.hmm clotting.fa
```

```
[biguser@R440 session10]$ hmmscan --domtblout clotting.tab Pfam-A.hmm clotting.fa
# hmmscan :: search sequence(s) against a profile database
# HMMER 3.3.2 (Nov 2020); http://hmmer.org/
# Copyright (C) 2020 Howard Hughes Medical Institute.
# Freely distributed under the BSD open source license.
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -
# query sequence file:             clotting.fa
# target HMM database:             Pfam-A.hmm
# per-dom hits tabular output:     clotting.tab
# - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - - -

Query:       sp|P08709|FA7_HUMAN  [L=466]
Description: Coagulation factor VII OS=Homo sapiens OX=9606 GN=F7 PE=1 SV=1
Scores for complete sequence (score includes all domains):
   --- full sequence ---   --- best 1 domain ---    -#dom-
    E-value  score  bias    E-value  score  bias    exp  N  Model          Description
    -------  -----  ----    -------  -----  ----    ---  -  --------       -----------
    3.2e-59  200.5   0.1    4.7e-59  200.0   0.1    1.3  1  Trypsin        Trypsin
    8.3e-19   67.6   6.3    8.8e-19   67.5   4.9    1.7  2  Gla            Vitamin K-dependent carboxylation/gamma-carbo
    9.4e-09   35.8   0.0    1.7e-08   35.0   0.0    1.4  1  DUF1986        Domain of unknown function (DUF1986)
    5.6e-08   33.0  11.4    5.6e-08   33.0  11.4    2.9  2  FXa_inhibition  Coagulation Factor Xa inhibitory site
     6e-05   23.4   4.9      6e-05   23.4   4.9    2.9  2  EGF            EGF-like domain
   0.00012   22.0   1.2   0.00012   22.0   1.2    3.7  4  cEGF           Complement Clr-like EGF-like
    0.0012   19.5   2.1    0.0012   19.5   2.1    3.5  2  hEGF           Human growth factor-like EGF
  ------ inclusion threshold ------
       0.8   10.2  24.5       0.21   12.1   8.8    3.2  2  EGF_2          EGF-like domain
       8.8    6.7  25.7        1.4    9.2  11.1    2.7  2  EGF_3          EGF domain


Domain annotation for each model (and alignments):
>> Trypsin  Trypsin
   #    score  bias  c-Evalue  i-Evalue hmmfrom  hmm to    alifrom  ali to    envfrom  env to     acc
 ---  ------ ----- --------- --------- ------- -------    -------  -------  -------  -------    ----
   1 !  200.0   0.1   2.2e-62   4.7e-59       1     221 []     213     447 ..     213     447 .. 0.94
```

Result of hmmscan

```
$ less clotting.tab
```

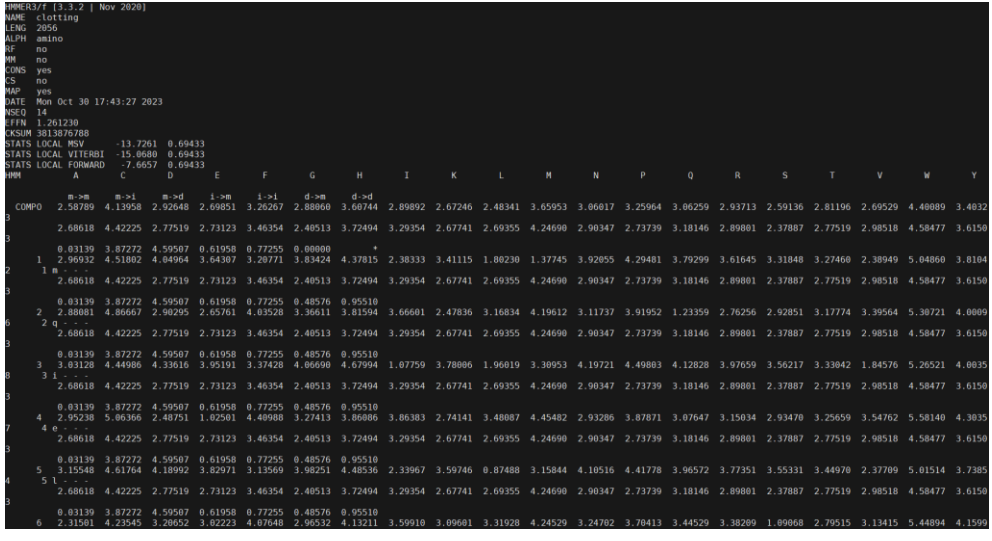
```
#                                                                            --- full sequence ---   --------------- this domain ---------------   hmm coord   ali coord   env coord
# target name        accession   tlen query name           accession   qlen   E-value  score  bias   #  of  c-Evalue  i-Evalue  score  bias  from    to  from    to  from    to  acc
#------------------- ---------- ----- -------------------- ---------- -----  --------- ------ -----  ---  --  --------- ---------  -----  ----- -----  -----  -----  -----  -----  ----
Trypsin              PF00089.28   221 sp|P08709|FA7_HUMAN  -            466   3.2e-59  200.5    0.1    1   1   2.2e-62   4.7e-59  200.0   0.1     1    221    213    447    213    447 0.94
Gla                  PF00594.22    41 sp|P08709|FA7_HUMAN  -            466   8.3e-19   67.6    6.3    1   2       2.4   5.2e+03   -2.2   0.0    20     36     48     64     46     64 0.87
Gla                  PF00594.22    41 sp|P08709|FA7_HUMAN  -            466   8.3e-19   67.6    6.3    2   2   4.1e-22   8.8e-19   67.5   4.9     1     40     65    104     65    105 0.98
DUF1986              PF09342.13   116 sp|P08709|FA7_HUMAN  -            466   9.4e-09   35.8    0.0    1   1   7.8e-12   1.7e-08   35.0   0.0     1    100    224    327    224    335 0.78
FXa_inhibition       PF14670.8     36 sp|P08709|FA7_HUMAN  -            466   5.6e-08   33.0   11.4    1   2       1.2   2.5e+03   -1.0   6.0     8     29    115    138    108    147 0.74
FXa_inhibition       PF14670.8     36 sp|P08709|FA7_HUMAN  -            466   5.6e-08   33.0   11.4    2   2   2.6e-11   5.6e-08   33.0  11.4     1     36    151    187    151    187 0.94
EGF                  PF00008.29    32 sp|P08709|FA7_HUMAN  -            466     6e-05   23.4    4.9    1   2   2.8e-08     6e-05   23.4   4.9     1     31    110    139    110    140 0.90
EGF                  PF00008.29    32 sp|P08709|FA7_HUMAN  -            466     6e-05   23.4    4.9    2   2       0.1   2.1e+02    2.4   7.2     8     29    155    179    151    180 0.82
cEGF                 PF12662.9     24 sp|P08709|FA7_HUMAN  -            466  0.00012   22.0    1.2    1   4      0.99   2.1e+03   -1.2   0.3    15     21    117    123    111    123 0.83
cEGF                 PF12662.9     24 sp|P08709|FA7_HUMAN  -            466  0.00012   22.0    1.2    2   4      0.14     3e+02    1.5   1.0     1      8    127    134    127    142 0.77
cEGF                 PF12662.9     24 sp|P08709|FA7_HUMAN  -            466  0.00012   22.0    1.2    3   4   5.8e-08  0.00012   22.0   1.2     3     20    171    188    170    189 0.95
cEGF                 PF12662.9     24 sp|P08709|FA7_HUMAN  -            466  0.00012   22.0    1.2    4   4       3.5   7.5e+03   -2.9   0.2     8     19    390    400    390    401 0.54
hEGF                 PF12661.9     22 sp|P08709|FA7_HUMAN  -            466   0.0012   19.5    2.1    1   2   5.5e-07   0.0012   19.5   2.1     1     20    115    134    115    136 0.96
hEGF                 PF12661.9     22 sp|P08709|FA7_HUMAN  -            466   0.0012   19.5    2.1    2   2      0.12   2.6e+02    2.6   4.8     7     22    162    178    150    178 0.90
EGF_2                PF07974.15    32 sp|P08709|FA7_HUMAN  -            466      0.8   10.2   24.5    1   2    0.0001      0.21   12.1   8.8     1     32    110    141    110    141 0.85
EGF_2                PF07974.15    32 sp|P08709|FA7_HUMAN  -            466      0.8   10.2   24.5    2   2     0.092     2e+02    2.6   7.7     5     28    148    179    144    187 0.70
EGF_3                PF12947.9     36 sp|P08709|FA7_HUMAN  -            466      8.8    6.7   25.7    1   2     0.069   1.5e+02    2.8   6.6     6     31    113    138    110    141 0.86
EGF_3                PF12947.9     36 sp|P08709|FA7_HUMAN  -            466      8.8    6.7   25.7    2   2   0.00068       1.4    9.2  11.1     1     36    151    187    151    187 0.89
F5_F8_type_C         PF00754.27   127 sp|P00451|FA8_HUMAN  -           2351   8.5e-55  184.4    0.3    1   2   6.5e-28   1.8e-24   86.4   0.0     1    127   2055   2185   2055   2185 0.88
F5_F8_type_C         PF00754.27   127 sp|P00451|FA8_HUMAN  -           2351   8.5e-55  184.4    0.3    2   2   1.2e-30   3.3e-27   95.2   0.2     1    127   2208   2342   2208   2342 0.94
Cu-oxidase_3         PF07732.17   119 sp|P00451|FA8_HUMAN  -           2351   3.5e-16   59.4    0.0    1   3   8.5e-08   0.00023   21.2   0.0    24    114     90    197     88    202 0.78
Cu-oxidase_3         PF07732.17   119 sp|P00451|FA8_HUMAN  -           2351   3.5e-16   59.4    0.0    2   3   3.3e-08   9.2e-05   22.6   0.0    11    114    454    572    444    577 0.76
Cu-oxidase_3         PF07732.17   119 sp|P00451|FA8_HUMAN  -           2351   3.5e-16   59.4    0.0    3   3   0.00015       0.4   10.8   0.0    24     90   1777   1841   1772   1880 0.77
Cu-oxidase_2         PF07731.16   137 sp|P00451|FA8_HUMAN  -           2351   3.2e-15   56.1    7.5    1   4       0.3   8.1e+02   -0.2   0.0    35     78     95    136     82    149 0.65
Cu-oxidase_2         PF07731.16   137 sp|P00451|FA8_HUMAN  -           2351   3.2e-15   56.1    7.5    2   4    0.0021       5.7    6.8   3.3    39    133    268    345    230    347 0.80
Cu-oxidase_2         PF07731.16   137 sp|P00451|FA8_HUMAN  -           2351   3.2e-15   56.1    7.5    3   4   1.3e-05     0.035   14.0   0.0    86    133    680    727    660    730 0.88
Cu-oxidase_2         PF07731.16   137 sp|P00451|FA8_HUMAN  -           2351   3.2e-15   56.1    7.5    4   4   8.7e-11   2.4e-07   30.7   0.0     6    134   1920   2036   1915   2039 0.83
Cu-oxidase           PF00394.24   159 sp|P00451|FA8_HUMAN  -           2351   2.7e-10   40.7    0.0    1   2   8.3e-10   2.3e-06   27.9   0.0     7    158    224    348    218    349 0.81
Cu-oxidase           PF00394.24   159 sp|P00451|FA8_HUMAN  -           2351   2.7e-10   40.7    0.0    2   2   0.00031      0.84    9.8   0.0     7     94   1905   1984   1900   2037 0.85
CytadhesinP1         PF12378.10   260 sp|P00451|FA8_HUMAN  -           2351    0.0019   18.1    0.1    1   1   1.8e-06    0.0049   16.7   0.1    81    175    954   1050    948   1068 0.83
```

Searching with custome HMM profiles

Building HMM profile

```
$ clustalw2 clotting.fa
$ hmmbuild clotting.hmm clotting.aln
```

```
$ less clotting.hmm
```



```
HMMER3/f [3.3.2 | Nov 2020]
NAME  clotting
LENG  2056
ALPH  amino
RF    no
MM    no
CONS  yes
CS    no
MAP   yes
DATE  Mon Oct 30 17:43:27 2023
NSEQ  14
EFFN  1.261230
CKSUM 3813876788
STATS LOCAL MSV      -13.7261  0.69433
STATS LOCAL VITERBI  -15.0680  0.69433
STATS LOCAL FORWARD   -7.6657  0.69433
HMM          A        C        D        E        F        G        H        I        K        L        M        N        P        Q        R        S        T        V        W        Y
            m->m     m->i     m->d     i->m     i->i     d->m     d->d
  COMPO   2.58789  4.13958  2.92648  2.69851  3.26267  2.88060  3.60744  2.89892  2.67246  2.48341  3.65953  3.06017  3.25964  3.06259  2.93713  2.59136  2.81196  2.69529  4.40089  3.4032
3
          2.68618  4.42225  2.77519  2.73123  3.46354  2.40513  3.72494  3.29354  2.67741  2.69355  4.24690  2.90347  2.73739  3.18146  2.89801  2.37887  2.77519  2.98518  4.58477  3.6150
3
          0.03139  3.87272  4.59507  0.61958  0.77255  0.00000        *
      1   2.96932  4.51802  4.04964  3.64307  3.20771  3.83424  4.37815  2.38333  3.41115  1.80230  1.37745  3.92055  4.29481  3.79299  3.61645  3.31848  3.27460  2.38949  5.04860  3.8104
2     1 m - - -
          2.68618  4.42225  2.77519  2.73123  3.46354  2.40513  3.72494  3.29354  2.67741  2.69355  4.24690  2.90347  2.73739  3.18146  2.89801  2.37887  2.77519  2.98518  4.58477  3.6150
3
          0.03139  3.87272  4.59507  0.61958  0.77255  0.48576  0.95510
      2   2.88081  4.86667  2.90295  2.65761  4.03528  3.36611  3.81594  3.66601  2.47836  3.16834  4.19612  3.11737  3.91952  1.23359  2.76256  2.92851  3.17774  3.39564  5.30721  4.0009
6     2 q - - -
          2.68618  4.42225  2.77519  2.73123  3.46354  2.40513  3.72494  3.29354  2.67741  2.69355  4.24690  2.90347  2.73739  3.18146  2.89801  2.37887  2.77519  2.98518  4.58477  3.6150
3
          0.03139  3.87272  4.59507  0.61958  0.77255  0.48576  0.95510
      3   3.03128  4.44986  4.33616  3.95191  3.37428  4.06690  4.67994  1.07759  3.78006  1.96019  3.30953  4.19721  4.49803  4.12828  3.97659  3.56217  3.33042  1.84576  5.26521  4.0035
8     3 i - - -
          2.68618  4.42225  2.77519  2.73123  3.46354  2.40513  3.72494  3.29354  2.67741  2.69355  4.24690  2.90347  2.73739  3.18146  2.89801  2.37887  2.77519  2.98518  4.58477  3.6150
3
          0.03139  3.87272  4.59507  0.61958  0.77255  0.48576  0.95510
      4   2.95238  5.06366  2.48751  1.02501  4.40988  3.27413  3.86086  3.86383  2.74141  3.48087  4.45482  2.93286  3.87871  3.07647  3.15034  2.93470  3.25659  3.54762  5.58140  4.3035
7     4 e - - -
          2.68618  4.42225  2.77519  2.73123  3.46354  2.40513  3.72494  3.29354  2.67741  2.69355  4.24690  2.90347  2.73739  3.18146  2.89801  2.37887  2.77519  2.98518  4.58477  3.6150
3
          0.03139  3.87272  4.59507  0.61958  0.77255  0.48576  0.95510
      5   3.15548  4.61764  4.18992  3.82971  3.13569  3.98251  4.48536  2.33967  3.59746  0.87488  3.15844  4.10516  4.41778  3.96572  3.77351  3.55331  3.44970  2.37709  5.01514  3.7385
4     5 l - - -
          2.68618  4.42225  2.77519  2.73123  3.46354  2.40513  3.72494  3.29354  2.67741  2.69355  4.24690  2.90347  2.73739  3.18146  2.89801  2.37887  2.77519  2.98518  4.58477  3.6150
3
          0.03139  3.87272  4.59507  0.61958  0.77255  0.48576  0.95510
      6   2.31501  4.23545  3.20652  3.82223  4.07648  2.96532  4.13211  3.59910  3.09601  3.31928  4.24529  3.24702  3.70413  3.44529  3.38209  1.09068  2.79515  3.13415  5.44894  4.1599
```

Searching with custome HMM profiles

HMM profile indexing

```
hmmpress clotting.hmm
```

```
[biguser@R440 session10]$ hmmpress clotting.hmm
Working...    done.
Pressed and indexed 1 HMMs (1 names).
Models pressed into binary file:   clotting.hmm.h3m
SSI index for binary model file:   clotting.hmm.h3i
Profiles (MSV part) pressed into:  clotting.hmm.h3f
Profiles (remainder) pressed into: clotting.hmm.h3p
```

Searching HMM profile with a query sequence

```
hmmscan --domtblout query.tab clotting.hmm query.fa
```

Code 1 parse_hmmscan.ipynb

```
import re
import sys

print('protein_name₩tlen₩tdomain₩tbegin₩tend₩tEvalue')

for line in open("clotting.tab", 'r'):
    if not re.search('^##', line): # avoid all lines beginning
                                   # with the '#' character
        col = re.split(' +', line)
        domname = col[0]
        protname = col[3]
        protname = re.sub('.*₩|', '', protname)
        length = col[5]
        evalue = float(col[12])
        begin = col[17]
        end = col[18]
        if evalue < 1e-5:
            print(protname, '₩t', length, '₩t', domname, end = '')
            print('₩t', begin, '₩t', end, '₩t', str(evalue))
            pass
    else:
        pass
```

Code 1 parse_hmmscan.ipynb

protein_name	len	domain	begin	end	Evalue
FA7_HUMAN	466	Trypsin		213	447	4.7e-59
FA7_HUMAN	466	Gla	65	104	8.8e-19
FA7_HUMAN	466	DUF1986		224	327	1.7e-08
FA7_HUMAN	466	FXa_inhibition	151	187	5.6e-08
FA8_HUMAN	2351	F5_F8_type_C	2055	2185	1.8e-24
FA8_HUMAN	2351	F5_F8_type_C	2208	2342	3.3e-27
FA8_HUMAN	2351	Cu-oxidase_2	1920	2036	2.4e-07
FA8_HUMAN	2351	Cu-oxidase	224	348	2.3e-06
FA9_HUMAN	461	Trypsin		227	454	1.3e-69
FA9_HUMAN	461	Gla	52	92	1.1e-20
FA9_HUMAN	461	FXa_inhibition	134	170	2.2e-09
FA9_HUMAN	461	EGF	97	127	7.5e-06
FA10_HUMAN	488	Trypsin		235	462	7e-70
FA10_HUMAN	488	Gla	45	85	2e-21
FA10_HUMAN	488	FXa_inhibition	129	164	6.9e-09
FA10_HUMAN	488	EGF	90	120	3.1e-07
FA11_HUMAN	625	Trypsin		388	618	4e-73
FA11_HUMAN	625	PAN_1	21	103	2e-07
FA11_HUMAN	625	PAN_1	119	193	3.4e-08
FA11_HUMAN	625	PAN_1	203	283	2.7e-08
FA11_HUMAN	625	PAN_1	296	371	3.5e-08
FA11_HUMAN	625	PAN_4	299	349	4.3e-07
FA12_HUMAN	615	Trypsin		373	609	3.6e-63
FA12_HUMAN	615	Kringle		217	295	5.7e-24
FA12_HUMAN	615	fn2	47	88	6.8e-17
FA12_HUMAN	615	EGF	98	129	6.2e-06
FA12_HUMAN	615	EGF	178	207	5.5e-08
FA12_HUMAN	615	fn1	135	170	1.7e-10

Exercise

- Merge the BCR_HUMAN.fa, ABL1_HUMAN.fa, BCR_ABL1_fusion_HUMAN.fa into single file using “cat” command. Then run “hmmscan” to search for the similar proteins (domains) of query proteins. After obtaining the output file named as “bcr_abl1.tab”, run the “parse_hmmscan.py” to get summary of the hmmscan search.

아래 명령어를 실행해서 BCR_HUMAN.fa, ABL1_HUMAN.fa, BCR_ABL1_fusion_HUMAN.fa 파일들을 여러분들의 directory에 복사해 가세요

```
$ cp /home/biguser/tutor/session10/bcr_abl_sequences/* .
```