Demo

Richel J.C. Bilderbeek

2019-01-03

Install

The `bbbq` package depends on the `tmhmm` package, which needs to be installed first:

```
devtools::install_github("richelbilderbeek/tmhmm")
#> Skipping install of 'tmhmm' from a github remote, the SHA1 (c7aeeabe) has not changed since last ins
#>   Use `force = TRUE` to force installation
```

The `tmhmm` package relies on TMHMM that needs to be installed:

```
tmhmm::install_tmhmm("http://www.cbs.dtu.dk/download/D3198788-0F1D-11E9-883C-84B3B9CD16B5/")
```

The URL can be obtained by requesting a download link at the TMHMM website at http://www.cbs.dtu.dk/services/TMHMM. As this URL expires after four hours, `tmhmm` cannot do this for you.

The installation of NetMHC2pan is checked, with the goal of giving a helpful error message:

```
tmhmm::check_tmhmm_installation()
```

Additionall, The `bbbq` package depends on the `netmhc2pan` package, which needs to be installed as well:

```
devtools::install_github("richelbilderbeek/netmhc2pan")
#> Skipping install of 'netmhc2pan' from a github remote, the SHA1 (2cb7ff90) has not changed since las
#>   Use `force = TRUE` to force installation
```

The `netmhc2pan` package relies on NetMHCIIpan that needs to be installed:

```
netmhc2pan::install_netmhc2pan("http://www.cbs.dtu.dk/download/33A6B0AC-0F2E-11E9-B4D1-8ABCB9CD16B5/")
```

The URL can be obtained by requesting a download link at the NetMHCIIpan website at [www.cbs.dtu.dk/services/NetMHCIIpa
As this URL expires after four hours, `netmhc2pan` cannot do this for you.

The installation of NetMHC2pan is checked, with the goal of giving a helpful error message:

```
netmhc2pan::check_netmhc2pan_installation()
```

Another dependency is the `epitopiome` package. Installing the `epitopeome` package:

```
devtools::install_github("richelbilderbeek/epitopeome")
#> Skipping install of 'epitopeome' from a github remote, the SHA1 (72ff7c38) has not changed since las
#>   Use `force = TRUE` to force installation
```

```
devtools::install_github("richelbilderbeek/bbbq")
#> Skipping install of 'bbbq' from a github remote, the SHA1 (113b34f1) has not changed since last inst
#>   Use `force = TRUE` to force installation
```

Usage

From a protein sequence, `bbbq` estimates where amino acids of transmembrane proteins are located (inside, outside, in the membrane) and which bind to an MHC2 allele with a certain strength.

We need a FASTA file with at least one protein sequence in it to work on:

```
fasta_filename <- system.file("extdata", "short.fasta", package = "bbbq")
```

This is how such a FASTA file looks like:

```
cat(head(readLines(fasta_filename, warn = FALSE)), sep = "\n")
#> >sp|A0A089QKZ7|Y155A_MYCTU Uncharacterized protein Rv1155A OS=Mycobacterium tuberculosis (strain ATC
#> MGESKSPQESSSEGETKRKFREALDRKMAQSSSGSDHKDGGGKQSRAHGPVASRREFRRK
#> SG
#> >sp|A0A089QRB9|MSL3_MYCTU Mycolipanoate synthase OS=Mycobacterium tuberculosis (strain ATCC 25618 / 
#> MRTATATSVAVIGMACRLPGGIDSPQRLWEALLRGDDLVGEIPADRWDANVYYDPEPGVP
#> >sp|E2FZM4|SOCA_MYCTU Uncharacterized protein SocA OS=Mycobacterium tuberculosis (strain ATCC 25618 
```

Different MHC2 alleles bind differently to protein epitopes. By default, `bbbq` uses only the default MHC2 allele used by NetMCHIIpan. In this demo, we'll use the first two MHC2 alleles from the complete NetMHCIIpan set of more than 5000 alleles:

```
alleles <- netmhc2pan::get_netmhc2pan_alleles()[1:2]
testit::assert(all(alleles %in% netmhc2pan::get_netmhc2pan_alleles()))
```

Select a binding strength. For example, a value of `5.0` will select those epitopes that are in the top 5 percent.

```
binding_strength_threshold <- 5.0
```

Here, the BBBQ is answered:

```
df <- bbbq::answer_bbbq(
  fasta_filename = fasta_filename,
  alleles = alleles,
  binding_strength_threshold = binding_strength_threshold
)
```

Resulting in:

```
knitr::kable(df)
```

epitopium	n
i	276
m	27
o	774
I	69
M	19
O	148

Legend:

Location	Strong binder	Weak binder
outside	O	o
membrane	M	m
inside	I	i

Appendix

This appendix shows the intermediate files created by `bbbq`.

These are:

- `tmhmm_filename`: the TMHMM results file, containing the location of the amino acids (inside, outside, in membrane)
- `netmhc2pan_filename`: the NetMHC2pan results file, containing the binding of all MHC2 alleles to all protein epitopes
- `epitopeome_filename`: the `epitopeome` results file, containing the combinated informationb

```
tmhmm_filename = tempfile(".txt")
netmhc2pan_filename = tempfile(".csv")
epitopeome_filename = tempfile(".fasta")
```

Answering the BBBQ again (and ignorening its result):

```
bbbq::answer_bbbq(
  fasta_filename = fasta_filename,
  alleles = alleles,
  binding_strength_threshold = binding_strength_threshold,
  tmhmm_filename = tmhmm_filename,
  netmhc2pan_filename = netmhc2pan_filename,
  epitopeome_filename = epitopeome_filename
)
#>   epitopium   n
#> 1         i 276
#> 2         m  27
#> 3         o 774
#> 4         I  69
#> 5         M  19
#> 6         O 148
```

The TMHMM results file:

```
cat(readLines(tmhmm_filename), sep = "\n")
#> >sp|A0A089QKZ7|Y155A_MYCTU Uncharacterized protein Rv1155A OS=Mycobacterium tuberculosis (strain ATC
#> OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
#> >sp|A0A089QRB9|MSL3_MYCTU Mycolipanoate synthase OS=Mycobacterium tuberculosis (strain ATCC 25618 / 
#> iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii
#> >sp|E2FZM4|SOCA_MYCTU Uncharacterized protein SocA OS=Mycobacterium tuberculosis (strain ATCC 25618 
#> iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii
#> >sp|E2FZM5|SOCB_MYCTU Uncharacterized protein SocB OS=Mycobacterium tuberculosis (strain ATCC 25618 
#> iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii
#> >tr|I6WX95|I6WX95_MYCTU Probable acyl carrier protein AcpA (ACP) OS=Mycobacterium tuberculosis (stra
#> iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii
#> iiiiiiiiiiiiiii
#> >tr|I6WXK4|I6WXK4_MYCTU Phosphotyrosine protein phosphatase PTPB (Protein-tyrosine-phosphatase) (PTP
#> OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
#> >tr|I6WXK8|I6WXK8_MYCTU Conserved protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv) 
#> OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
#> >sp|I6WXS6|VPB51_MYCTU Putative antitoxin VapB51 OS=Mycobacterium tuberculosis (strain ATCC 25618 / 
#> OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
#> >tr|I6WY86|I6WY86_MYCTU Uncharacterized protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H
#> iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii
#> >tr|I6WYT7|I6WYT7_MYCTU Mce-family protein Mce2D OS=Mycobacterium tuberculosis (strain ATCC 25618 / 
#> iiiiiiiiiiiiiiiiMMMMMMMMMMMMMMMMMMMMMMMMoooooooooooooooooooo
#> >tr|I6WYU2|I6WYU2_MYCTU Uncharacterized protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H
#> OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
```

```
#> >tr|I6WYY7|I6WYY7_MYCTU (3R)-hydroxyacyl-ACP dehydratase subunit HadB OS=Mycobacterium tuberculosis
#> OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
#> >tr|I6WZ26|I6WZ26_MYCTU Uncharacterized protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H
#> OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
#> >tr|I6WZ30|I6WZ30_MYCTU Conserved threonine rich protein OS=Mycobacterium tuberculosis (strain ATCC
#> OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
#> >tr|I6WZ39|I6WZ39_MYCTU Uncharacterized protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H
#> OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
#> OOOOOOOOOOOO
#> >tr|I6WZ58|I6WZ58_MYCTU Probable conserved transmembrane protein OS=Mycobacterium tuberculosis (stra
#> ooooooooooooooooooooooooooooooooMMMMMMMMMMMMMMMMMMMMMMMiiiii
#> >tr|I6WZ71|I6WZ71_MYCTU Possible D-3-phosphoglycerate dehydrogenase SerA2 (Phosphoglycerate dehydrog
#> OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
#> >tr|I6WZ83|I6WZ83_MYCTU Uncharacterized protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H
#> OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
#> >tr|I6WZD7|I6WZD7_MYCTU Conserved protein OS=Mycobacterium tuberculosis (strain ATCC 25618 / H37Rv)
#> OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
#> OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
#> >tr|I6WZD9|I6WZD9_MYCTU Probable oxidoreductase OS=Mycobacterium tuberculosis (strain ATCC 25618 / H
#> OOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOOO
```

The NetMHCIIpan results table:

```r
knitr::kable(read.csv(netmhc2pan_filename))
```

Pos	Peptide	ID	Allele	one_minus_log50k	nM	Rank
5	QITGVVLAAGRSNRL	tr|I6WY86|I6WY86_MYCTU	DRB1_0101	0.711	22.69	4.50
6	ITGVVLAAGRSNRLG	tr|I6WY86|I6WY86_MYCTU	DRB1_0101	0.727	19.14	3.00
7	TGVVLAAGRSNRLGT	tr|I6WY86|I6WY86_MYCTU	DRB1_0101	0.729	18.81	3.00
8	GVVLAAGRSNRLGTP	tr|I6WY86|I6WY86_MYCTU	DRB1_0101	0.712	22.50	4.00
45	GFDQLILTLGGAASA	tr|I6WY86|I6WY86_MYCTU	DRB1_0101	0.742	16.27	2.50
46	FDQLILTLGGAASAV	tr|I6WY86|I6WY86_MYCTU	DRB1_0101	0.762	13.15	1.20
2	STIFDIRSLRLPKLS	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0101	0.703	24.99	5.00
3	TIFDIRSLRLPKLSA	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0101	0.704	24.67	5.00
27	VVLAVVAAAAGARLY	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0101	0.735	17.66	2.50
28	VLAVVAAAAGARLYR	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0101	0.757	13.93	1.40
29	LAVVAAAAGARLYRK	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0101	0.763	13.02	1.20
30	AVVAAAAGARLYRKL	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0101	0.739	16.90	2.50
31	VVAAAAGARLYRKLT	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0101	0.704	24.67	5.00
35	AAGARLYRKLTTTTV	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0101	0.720	20.67	3.50
36	AGARLYRKLTTTTVV	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0101	0.772	11.85	0.90
37	GARLYRKLTTTTVVA	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0101	0.790	9.67	0.50
38	ARLYRKLTTTTVVAY	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0101	0.797	8.98	0.40
39	RLYRKLTTTTVVAYF	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0101	0.791	9.64	0.50
40	LYRKLTTTTVVAYFS	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0101	0.760	13.40	1.30
8	SVVLSVLLGAHPAWA	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0101	0.711	22.73	4.50
9	VVLSVLLGAHPAWAT	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0101	0.722	20.21	3.50
10	VLSVLLGAHPAWATA	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0101	0.727	19.19	3.00
11	LSVLLGAHPAWATAS	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0101	0.718	21.12	4.00
36	IKETTLRVALTRMVG	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0101	0.713	22.42	4.00
37	KETTLRVALTRMVGA	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0101	0.735	17.52	2.50
38	ETTLRVALTRMVGAG	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0101	0.730	18.50	3.00
39	TTLRVALTRMVGAGD	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0101	0.724	19.72	3.50
40	TLRVALTRMVGAGDL	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0101	0.707	23.75	4.50

Pos	Peptide	ID	Allele	one_minus_log50k	nM	Rank
13	HSRLATFALALAAAA	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0101	0.804	8.31	0.25
14	SRLATFALALAAAAL	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0101	0.828	6.46	0.06
15	RLATFALALAAAALP	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0101	0.837	5.84	0.04
16	LATFALALAAAALPL	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0101	0.838	5.78	0.03
17	ATFALALAAAALPLA	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0101	0.842	5.55	0.03
18	TFALALAAAALPLAG	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0101	0.830	6.26	0.06
19	FALALAAAALPLAGC	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0101	0.797	9.03	0.40
20	ALALAAAALPLAGCS	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0101	0.728	19.01	3.00
107	VRGVFTYRVNKAGLI	tr|I6WZD7|I6WZD7_MYCTU	DRB1_0101	0.727	19.08	3.00
108	RGVFTYRVNKAGLIT	tr|I6WZD7|I6WZD7_MYCTU	DRB1_0101	0.751	14.78	1.60
109	GVFTYRVNKAGLITN	tr|I6WZD7|I6WZD7_MYCTU	DRB1_0101	0.753	14.53	1.60
110	VFTYRVNKAGLITNM	tr|I6WZD7|I6WZD7_MYCTU	DRB1_0101	0.758	13.70	1.40
111	FTYRVNKAGLITNMR	tr|I6WZD7|I6WZD7_MYCTU	DRB1_0101	0.744	16.01	2.00
112	TYRVNKAGLITNMRG	tr|I6WZD7|I6WZD7_MYCTU	DRB1_0101	0.701	25.42	5.00
24	MGTFALHGLTHRLPS	sp|E2FZM4|SOCA_MYCTU	DRB1_0102	0.517	185.21	4.00
25	GTFALHGLTHRLPSA	sp|E2FZM4|SOCA_MYCTU	DRB1_0102	0.526	169.36	3.50
26	TFALHGLTHRLPSAS	sp|E2FZM4|SOCA_MYCTU	DRB1_0102	0.514	192.71	4.50
14	IEFFFRYLTWGLRGV	tr|I6WXK8|I6WXK8_MYCTU	DRB1_0102	0.506	210.26	5.00
15	EFFFRYLTWGLRGVE	tr|I6WXK8|I6WXK8_MYCTU	DRB1_0102	0.509	201.89	4.50
16	FFFRYLTWGLRGVET	tr|I6WXK8|I6WXK8_MYCTU	DRB1_0102	0.509	203.20	4.50
6	ITGVVLAAGRSNRLG	tr|I6WY86|I6WY86_MYCTU	DRB1_0102	0.513	193.38	4.50
7	TGVVLAAGRSNRLGT	tr|I6WY86|I6WY86_MYCTU	DRB1_0102	0.510	200.04	4.50
45	GFDQLILTLGGAASA	tr|I6WY86|I6WY86_MYCTU	DRB1_0102	0.519	182.44	4.00
46	FDQLILTLGGAASAV	tr|I6WY86|I6WY86_MYCTU	DRB1_0102	0.546	135.28	2.50
1	MSTIFDIRSLRLPKL	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.551	129.29	1.90
2	STIFDIRSLRLPKLS	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.566	109.24	1.30
3	TIFDIRSLRLPKLSA	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.580	94.01	0.90
4	IFDIRSLRLPKLSAK	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.578	96.03	1.00
5	FDIRSLRLPKLSAKV	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.555	123.16	1.70
6	DIRSLRLPKLSAKVV	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.532	157.56	3.00
7	IRSLRLPKLSAKVVV	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.534	155.43	3.00
8	RSLRLPKLSAKVVVV	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.509	202.61	4.50
27	VVLAVVAAAAGARLY	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.509	202.91	4.50
28	VLAVVAAAAGARLYR	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.543	140.74	2.50
29	LAVVAAAAGARLYRK	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.553	125.96	1.80
30	AVVAAAAGARLYRKL	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.521	177.41	4.00
36	AGARLYRKLTTTTVV	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.519	182.64	4.00
37	GARLYRKLTTTTVVA	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.543	141.03	2.50
38	ARLYRKLTTTTVVAY	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.543	140.97	2.50
39	RLYRKLTTTTVVAYF	tr|I6WYT7|I6WYT7_MYCTU	DRB1_0102	0.526	169.10	3.50
7	RSVVLSVLLGAHPAW	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0102	0.509	202.25	4.50
8	SVVLSVLLGAHPAWA	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0102	0.539	146.78	2.50
9	VVLSVLLGAHPAWAT	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0102	0.548	132.41	2.00
10	VLSVLLGAHPAWATA	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0102	0.547	133.80	2.50
11	LSVLLGAHPAWATAS	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0102	0.525	170.27	3.50
36	IKETTLRVALTRMVG	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0102	0.538	147.68	2.50
37	KETTLRVALTRMVGA	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0102	0.571	104.04	1.20
38	ETTLRVALTRMVGAG	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0102	0.565	111.27	1.40
39	TTLRVALTRMVGAGD	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0102	0.557	120.08	1.70
40	TLRVALTRMVGAGDL	tr|I6WZ26|I6WZ26_MYCTU	DRB1_0102	0.532	157.81	3.00
13	HSRLATFALALAAAA	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0102	0.566	109.00	1.30
14	SRLATFALALAAAAL	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0102	0.604	72.33	0.50

Pos	Peptide	ID	Allele	one_minus_log50k	nM	Rank
15	RLATFALALAAAALP	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0102	0.615	64.46	0.40
16	LATFALALAAAALPL	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0102	0.619	61.66	0.30
17	ATFALALAAAALPLA	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0102	0.624	58.48	0.25
18	TFALALAAAALPLAG	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0102	0.606	71.31	0.50
19	FALALAAAALPLAGC	tr|I6WZ30|I6WZ30_MYCTU	DRB1_0102	0.554	124.77	1.80
1	MTRQQLAHLLRRACA	tr|I6WZ83|I6WZ83_MYCTU	DRB1_0102	0.538	147.71	2.50
2	TRQQLAHLLRRACAV	tr|I6WZ83|I6WZ83_MYCTU	DRB1_0102	0.553	126.56	1.80
3	RQQLAHLLRRACAVV	tr|I6WZ83|I6WZ83_MYCTU	DRB1_0102	0.562	114.54	1.50
4	QQLAHLLRRACAVVG	tr|I6WZ83|I6WZ83_MYCTU	DRB1_0102	0.545	137.78	2.50
5	QLAHLLRRACAVVGD	tr|I6WZ83|I6WZ83_MYCTU	DRB1_0102	0.526	169.03	3.50
107	VRGVFTYRVNKAGLI	tr|I6WZD7|I6WZD7_MYCTU	DRB1_0102	0.509	202.53	4.50
108	RGVFTYRVNKAGLIT	tr|I6WZD7|I6WZD7_MYCTU	DRB1_0102	0.511	199.31	4.50
30	LAGRGFPVALGARRM	tr|I6WZD9|I6WZD9_MYCTU	DRB1_0102	0.518	184.00	4.00
31	AGRGFPVALGARRMD	tr|I6WZD9|I6WZD9_MYCTU	DRB1_0102	0.517	186.44	4.00
32	GRGFPVALGARRMDK	tr|I6WZD9|I6WZD9_MYCTU	DRB1_0102	0.539	146.12	2.50
33	RGFPVALGARRMDKL	tr|I6WZD9|I6WZD9_MYCTU	DRB1_0102	0.553	125.79	1.80
34	GFPVALGARRMDKLA	tr|I6WZD9|I6WZD9_MYCTU	DRB1_0102	0.517	186.30	4.00

The epitopeome results file:

```
cat(readLines(epitopeome_filename), sep = "\n")
#> >sp|A0A089QKZ7|Y155A_MYCTU
#> oooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooo
#> >sp|A0A089QRB9|MSL3_MYCTU
#> iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii
#> >sp|E2FZM4|SOCA_MYCTU
#> iiiiiiiiiiiiiiiiiiiiiiiIIIIIIIIIIIIIIIIIiiiiiiiiiiiiiiiiiiiii
#> >sp|E2FZM5|SOCB_MYCTU
#> iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii
#> >sp|I6WXS6|VPB51_MYCTU
#> oooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooo
#> >tr|I6WX95|I6WX95_MYCTU
#> iiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiiii
#> >tr|I6WXK4|I6WXK4_MYCTU
#> oooooooooooooooooooooooooooooooooooooooooooooooooooooooooooo
#> >tr|I6WXK8|I6WXK8_MYCTU
#> oooooooooooooOOOOOOOOOOOOOOOOOoooooooooooo
#> >tr|I6WY86|I6WY86_MYCTU
#> iiiiIIIIIIIIIIIIIIIIIIiiiiiiiiiiiiiiiiiiiiiiIIIIIIIIIIIIIIII
#> >tr|I6WYT7|I6WYT7_MYCTU
#> IIIIIIIIIIIIIIIIIIMMMMmmmmMMMMMMMMMMMMMMMOOOOOOOOOOOOOoooooo
#> >tr|I6WYU2|I6WYU2_MYCTU
#> oooooooooooooooooooooooooooooooooooooooooooooooooooooooooooo
#> >tr|I6WYY7|I6WYY7_MYCTU
#> oooooooooooooooooooooooooooooooooooooooooooooooooooooooooooo
#> >tr|I6WZ26|I6WZ26_MYCTU
#> ooooooOOOOOOOOOOOOOOOOOOOooooooooooOOOOOOOOOOOOOOOOOOOoooooo
#> >tr|I6WZ30|I6WZ30_MYCTU
#> ooooooooooooOOOOOOOOOOOOOOOOOOOOOOoooooooooooooooooooooooooo
#> >tr|I6WZ39|I6WZ39_MYCTU
#> oooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooo
#> >tr|I6WZ58|I6WZ58_MYCTU
```

```
#> oooooooooooooooooooooooooooooooommmmmmmmmmmmmmmmmmmmmmmiiiii
#> >tr|I6WZ71|I6WZ71_MYCTU
#> oooooooooooooooooooooooooooooooooooooooooooooooooooooooooooo
#> >tr|I6WZ83|I6WZ83_MYCTU
#> OOOOOOOOOOOOOOOOOOOooooooooooooooooooooooooooooooooooooooooo
#> >tr|I6WZD7|I6WZD7_MYCTU
#> oooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooooo
#> >tr|I6WZD9|I6WZD9_MYCTU
#> oooooooooooooooooooooooooooooOOOOOOOOOOOOOOOOOOOoooooooooooo
```