C-IMMSIM simulation results

June 13, 2025

Abstract

This document includes the plots relative to the simulation and the outcome of the epitope/peptide prediction used.

Produced by the C-IMMSIM Online server available at
`http://c-immsim.iac.rm.cnr.it (alias to http://kraken.iac.rm.cnr.it/C-IMMSIM)`

CITATIONS: For publication of results, please cite the following:

Nicolas Rapin, Ole Lund, Massimo Bernaschi, Filippo Castiglione. Computational Immunology Meets Bioinformatics: The Use of Prediction Tools for Molecular Binding in the Simulation of the Immune System. PLoS ONE 5(4): e9862
tt doi:10.1371/journal.pone.0009862, 2010

A retrospective validation

In-silico evaluation of adenoviral COVID-19 vaccination protocols: Assessment of immunological memory up to 6 months after the third dose. P. Stolfi, F. Castiglione, E. Mastrostefano, I. Di Biase, S. Di Biase, G. Palmieri, A. Prisco. Frontiers in Immunology, 13 (2022) doi: 10.3389/fimmu.2022.998262
`https://www.frontiersin.org/articles/10.3389/fimmu.2022.998262i`

An in vivo validation

Identification and validation of viral antigens sharing sequence and structural homology with tumor associated antigens (TAAs). C. Ragone, C. Manolio, B. Cavalluzzo, A. Petrizzo, A. Mauriello, M-L. Tornesello, F. M. Buonaguro, F. Castiglione, L. Vitagliano, M. Ruvo, M. Tagliamonte, L. Buonaguro. Journal for ImmunoTherapy of Cancer. 9:e002694 (2021)
`https://jitc.bmj.com/content/9/5/e002694`

Original C-IMMSIM model: `www.iac.cnr.it/∼filippo/c-immsim`

GETTING HELP:
Scientific problems: Filippo Castiglione (filippo dot castiglione at cnr dot it)
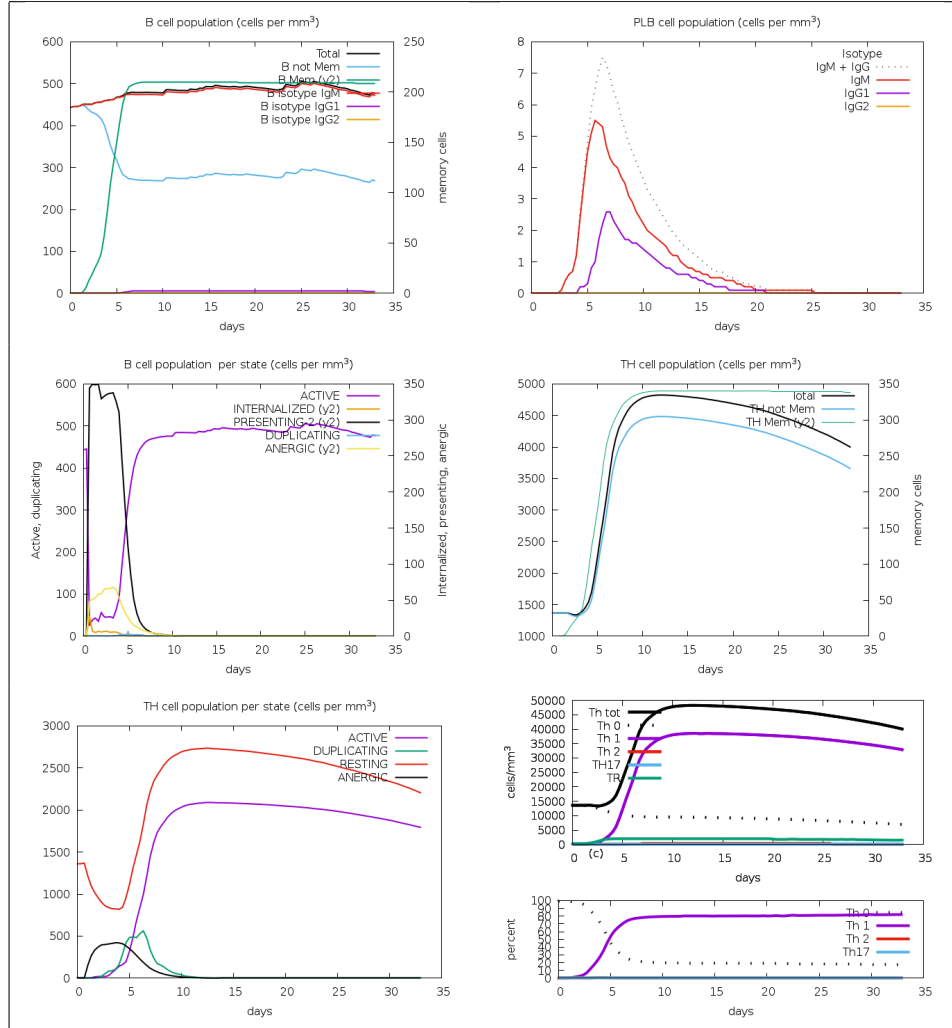Technical problems: Ilaria Gonnella (ilaria dot gonnella at cnr dot it)

Figure 1: Cell counts shown. Legend: Act=active, Intern=internalized the Ag, Pres II = presenting on MHC II, Dup = in the mitotic cycle, Anergic = anergic, Resting = not active.
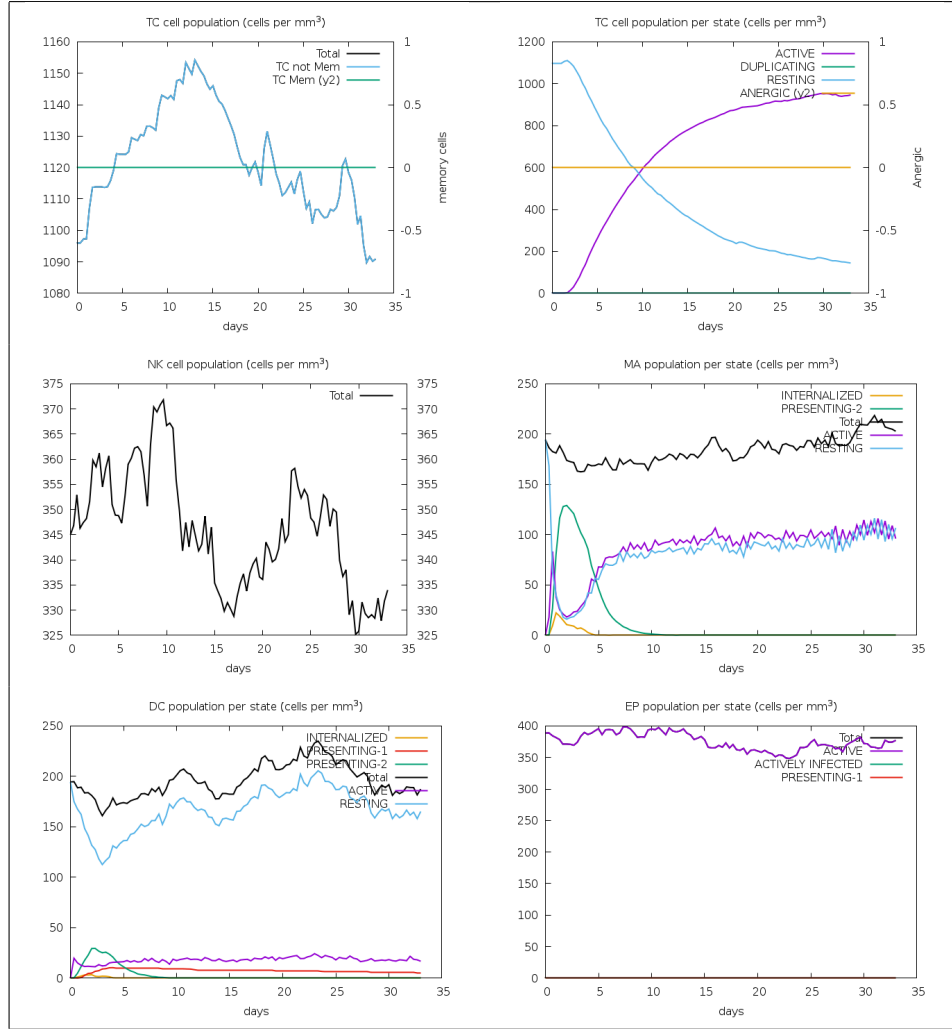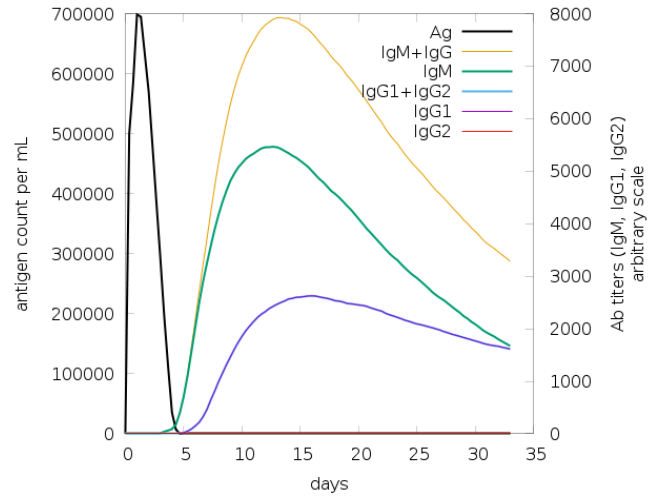
Figure 2: Legend: symbols as figure above.

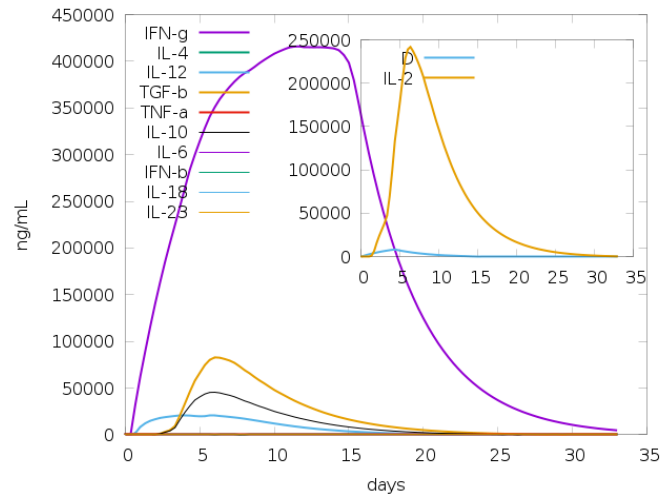Figure 3: The virus, the immunoglobulins and the immunocomplexes.

Figure 4: Concentration of cytokines and interleukins. Inset plot shows danger signal together with leukocyte growth factor IL-2.

4

Parker_B_scale_epitope_find
Use Parker's propensity scale, takes an antigen block as input,
and creates a list of residues that are possible epitopes.

Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/37044_20250613-051710_5_WxEvsyjYD47M.FSA_1_001

GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKAKFVAAWTLKAAAGPGPGFISFIIVEKKRN
TYSGPGPGISFIIVEKKRNTYSRGPGPGITFISFIIVEKKRNTGPGPGSFIIVEKKRNTYSRLGPGPGTFISFIIVEKKR
NTYGPGPGGVTRKYKIKSNPLTKGPGPGAVGFLVRTEFKYNDSGPGPGDRINWISAGVFLDSNGPGPGDTLYFPAVGFLV
RTEGPGPGGDTLYFPAVGFLVRTGPGPGGDVLTVNPLVVNWRNGPGPGGFLVRTEFKYNDSNCGPGPGKKVRFENTTSDK
GKIGPGPGIKTEMRAVIKNSQKPGPGPGIKWAFEIHHRRPRGRGPGPGISTEFSINETLTLDVGPGPGKTEMRAVIKNSQ
KPKGPGPGPHNHYKSDNTEAAVLAAYAQITAGVALYAAYSIVPNFILVAAYAQITAGVALAAYRTLGYATEDFAAYAIGP
PVFTDKAAYGIAIGPPVFAAYDAFLIDRINWAAYAFLIDRINWAAYTITIPANIGLAAYAMDEGYFAYAAYQTAENPVFT
VAAYLAMDEGYFAYAAYHTEFNPHNHYAAYLETDDYNGIYAAYHLISIAINVAAYSMIEPLVLAAAYTEIILNPNLAAYK
SSELYHIKKKSLYILRQSKQGDYIRNKKSVGILHYEKLKKNTYSRLEDRRVRPTSSGDLYYKKSNGGGYNQHQLALRSIE
KGHHHHHH

00000000000000000000000000001111001111111111111100000000000000000000000000000111
11111000000000000111111101000000000000001111111100000000111100000000000000000011
11110101000000000000000000000000001011111101000000000000000011111000000000000000
0011111100000000000000001111000000000000000011000000000001111111111010000011111
11000000000000000000001111110000000000000011111100010000000000000010111110000000001
1111111110001111111100000000000000000000000000000000000000000000000000000000000000
000000010000000000000000000000000000000000000000000000000000000000000011100000
00000000000000000000000000000000111000000000000000000000000000000000000000000001
00000000000000000011000000010000000000010010000100110111100000011111111100000000000
00100000
Epitopes of protein 0 ------------
1]   pos=27 len=4   EQIG
2]   pos=33 len=14   STRGRKCCRRKKEA
3]   pos=77 len=8   KRNTYSGP
4]   pos=96 len=7   KRNTYSR
5]   pos=119 len=7   KRNTGPG
6]   pos=135 len=4   KRNT
7]   pos=158 len=6   KRNTYG
8]   pos=201 len=6   DSGPGP
9]   pos=222 len=5   NGPGP
10]   pos=242 len=6   EGPGPG
11]   pos=264 len=4   PGPG
12]   pos=297 len=10   YNDSNCGPGP
13]   pos=314 len=8   NTTSDKGK
14]   pos=340 len=5   QKPGP
15]   pos=359 len=6   PRGRGP
16]   pos=386 len=5   PGKTE
17]   pos=399 len=10   QKPKGPGPGP
18]   pos=412 len=7   YKSDNTE
19]   pos=692 len=4   PTSS
20]   pos=702 len=8   KSNGGGYN

_____

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DoPeptideList_I:
       Given the antigen injected creates the list of peptides for all the
       NumAgProts proteins and for all i.e., 4 MHCI molecules

       Read class I peptide list from file? NO

```
================================================================

Allele: A0101
Pseudo sequence: KAVHAEQRNKAQTRA
Threshold: 9.456400
Max score: 29.236000


----------------------------------
Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/37044_20250613-051710_5_WxEvsyjYD47M.FSA_1_001
----------------------------------

GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKAKFVAAWTLKAAAGPGPGFISFIIVEKKRN
TYSGPGPGISFIIVEKKRNTYSRGPGPGITFISFIIVEKKRNTGPGPGSFIIVEKKRNTYSRLGPGPGTFISFIIVEKKR
NTYGPGPGGVTRKYKIKSNPLTKGPGPGAVGFLVRTEFKYNDSGPGPGDRINWISAGVFLDSNGPGPGDTLYFPAVGFLV
RTEGPGPGGDTLYFPAVGFLVRTGPGPGGDVLTVNPLVVNWRNGPGPGGFLVRTEFKYNDSNCGPGPGKKVRFENTTSDK
GKIGPGPGIKTEMRAVIKNSQKPGPGPGIKWAFEIHHRRPRGRGPGPGISTEFSINETLTLDVGPGPGKTEMRAVIKNSQ
KPKGPGPGPHNHYKSDNTEAAVLAAYAQITAGVALYAAYSIVPNFILVAAYAQITAGVALAAYRTLGYATEDFAAYAIGP
PVFTDKAAYGIAIGPPVFAAYDAFLIDRINWAAYAFLIDRINWAAYTITIPANIGLAAYAMDEGYFAYAAYQTAENPVFT
VAAYLAMDEGYFAYAAYHTEFNPHNHYAAYLETDDYNGIYAAYHLISIAINVAAYSMIEPLVLAAAYTEIILNPNLAAYK
SSELYHIKKKSLYILRQSKQGDYIRNKKSVGILHYEKLKKNTYSRLEDRRVRPTSSGDLYYKKSNGGGYNQHQLALRSIE
KGHHHHHH


Epitopes of protein 0 ------------
0]        pos= 459 score=0.006877 unnormalised=0.9316000000       LAAYRTLGY
1]        pos= 467 score=0.007962 unnormalised=1.0786000000       YATEDFAAY
2]        pos= 539 score=0.044406 unnormalised=6.0156000000       AMDEGYFAY
3]        pos= 565 score=0.044406 unnormalised=6.0156000000       AMDEGYFAY
4]        pos= 591 score=0.056025 unnormalised=7.5896000000       ETDDYNGIY
5]        pos= 636 score=0.011609 unnormalised=1.5726000000       AAYKSSELY
6]        pos= 692 score=0.054807 unnormalised=7.4246000000       PTSSGDLYY
7]        pos=  -1 score=0.773910 unnormalised=104.8410000000        non-binding event

================================================================

Allele: A0101
Pseudo sequence: KAVHAEQRNKAQTRA
Threshold: 9.456400
Max score: 29.236000


----------------------------------
Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/37044_20250613-051710_5_WxEvsyjYD47M.FSA_1_001
----------------------------------

GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKAKFVAAWTLKAAAGPGPGFISFIIVEKKRN
TYSGPGPGISFIIVEKKRNTYSRGPGPGITFISFIIVEKKRNTGPGPGSFIIVEKKRNTYSRLGPGPGTFISFIIVEKKR
NTYGPGPGGVTRKYKIKSNPLTKGPGPGAVGFLVRTEFKYNDSGPGPGDRINWISAGVFLDSNGPGPGDTLYFPAVGFLV
RTEGPGPGGDTLYFPAVGFLVRTGPGPGGDVLTVNPLVVNWRNGPGPGGFLVRTEFKYNDSNCGPGPGKKVRFENTTSDK
GKIGPGPGIKTEMRAVIKNSQKPGPGPGIKWAFEIHHRRPRGRGPGPGISTEFSINETLTLDVGPGPGKTEMRAVIKNSQ
KPKGPGPGPHNHYKSDNTEAAVLAAYAQITAGVALYAAYSIVPNFILVAAYAQITAGVALAAYRTLGYATEDFAAYAIGP
PVFTDKAAYGIAIGPPVFAAYDAFLIDRINWAAYAFLIDRINWAAYTITIPANIGLAAYAMDEGYFAYAAYQTAENPVFT
VAAYLAMDEGYFAYAAYHTEFNPHNHYAAYLETDDYNGIYAAYHLISIAINVAAYSMIEPLVLAAAYTEIILNPNLAAYK
SSELYHIKKKSLYILRQSKQGDYIRNKKSVGILHYEKLKKNTYSRLEDRRVRPTSSGDLYYKKSNGGGYNQHQLALRSIE
KGHHHHHH


Epitopes of protein 0 ------------
0]        pos= 459 score=0.006877 unnormalised=0.9316000000       LAAYRTLGY
1]        pos= 467 score=0.007962 unnormalised=1.0786000000       YATEDFAAY
2]        pos= 539 score=0.044406 unnormalised=6.0156000000       AMDEGYFAY
3]        pos= 565 score=0.044406 unnormalised=6.0156000000       AMDEGYFAY
4]        pos= 591 score=0.056025 unnormalised=7.5896000000       ETDDYNGIY
5]        pos= 636 score=0.011609 unnormalised=1.5726000000       AAYKSSELY
6]        pos= 692 score=0.054807 unnormalised=7.4246000000       PTSSGDLYY
```

```
7]         pos=  -1 score=0.773910 unnormalised=104.8410000000        non-binding event


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Allele: B0702
Pseudo sequence: KAAREEQQIKAQTRE
Threshold: 8.702800
Max score: 28.406000



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Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/37044_20250613-051710_5_WxEvsyjYD47M.FSA_1_001
----------------------------------

GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKAKFVAAWTLKAAAGPGPGFISFIIVEKKRN
TYSGPGPGISFIIVEKKRNTYSRGPGPGITFISFIIVEKKRNTGPGPGSFIIVEKKRNTYSRLGPGPGTFISFIIVEKKR
NTYGPGPGGVTRKYKIKSNPLTKGPGPGAVGFLVRTEFKYNDSGPGPGDRINWISAGVFLDSNGPGPGDTLYFPAVGFLV
RTEGPGPGGDTLYFPAVGFLVRTGPGPGGDVLTVNPLVVNWRNGPGPGGFLVRTEFKYNDSNCGPGPGKKVRFENTTSDK
GKIGPGPGIKTEMRAVIKNSQKPGPGPGIKWAFEIHHRRPRGRGPGPGISTEFSINETLTLDVGPGPGKTEMRAVIKNSQ
KPKGPGPGPHNHYKSDNTEAAVLAAYAQITAGVALYAAYSIVPNFILVAAYAQITAGVALAAYRTLGYATEDFAAYAIGP
PVFTDKAAYGIAIGPPVFAAYDAFLIDRINWAAYAFLIDRINWAAYTITIPANIGLAAYAMDEGYFAYAAYQTAENPVFT
VAAYLAMDEGYFAYAAYHTEFNPHNHYAAYLETDDYNGIYAAYHLISIAINVAAYSMIEPLVLAAAYTEIILNPNLAAYK
SSELYHIKKKSLYILRQSKQGDYIRNKKSVGILHYEKLKKNTYSRLEDRRVRPTSSGDLYYKKSNGGGYNQHQLALRSIE
KGHHHHHH


Epitopes of protein 0 -----------
0]         pos= 243 score=0.005883 unnormalised=0.6722000000        GPGPGGDTL
1]         pos= 263 score=0.003608 unnormalised=0.4122000000        GPGPGGDVL
2]         pos= 358 score=0.027519 unnormalised=3.1442000000        RPRGRGPGP
3]         pos= 383 score=0.006023 unnormalised=0.6882000000        GPGPGKTEM
4]         pos= 529 score=0.039361 unnormalised=4.4972000000        IPANIGLAA
5]         pos=  -1 score=0.917605 unnormalised=104.8410000000        non-binding event


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Allele: B0702
Pseudo sequence: KAAREEQQIKAQTRE
Threshold: 8.702800
Max score: 28.406000



----------------------------------
Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/37044_20250613-051710_5_WxEvsyjYD47M.FSA_1_001
----------------------------------

GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKAKFVAAWTLKAAAGPGPGFISFIIVEKKRN
TYSGPGPGISFIIVEKKRNTYSRGPGPGITFISFIIVEKKRNTGPGPGSFIIVEKKRNTYSRLGPGPGTFISFIIVEKKR
NTYGPGPGGVTRKYKIKSNPLTKGPGPGAVGFLVRTEFKYNDSGPGPGDRINWISAGVFLDSNGPGPGDTLYFPAVGFLV
RTEGPGPGGDTLYFPAVGFLVRTGPGPGGDVLTVNPLVVNWRNGPGPGGFLVRTEFKYNDSNCGPGPGKKVRFENTTSDK
GKIGPGPGIKTEMRAVIKNSQKPGPGPGIKWAFEIHHRRPRGRGPGPGISTEFSINETLTLDVGPGPGKTEMRAVIKNSQ
KPKGPGPGPHNHYKSDNTEAAVLAAYAQITAGVALYAAYSIVPNFILVAAYAQITAGVALAAYRTLGYATEDFAAYAIGP
PVFTDKAAYGIAIGPPVFAAYDAFLIDRINWAAYAFLIDRINWAAYTITIPANIGLAAYAMDEGYFAYAAYQTAENPVFT
VAAYLAMDEGYFAYAAYHTEFNPHNHYAAYLETDDYNGIYAAYHLISIAINVAAYSMIEPLVLAAAYTEIILNPNLAAYK
SSELYHIKKKSLYILRQSKQGDYIRNKKSVGILHYEKLKKNTYSRLEDRRVRPTSSGDLYYKKSNGGGYNQHQLALRSIE
KGHHHHHH


Epitopes of protein 0 -----------
0]         pos= 243 score=0.005883 unnormalised=0.6722000000        GPGPGGDTL
1]         pos= 263 score=0.003608 unnormalised=0.4122000000        GPGPGGDVL
2]         pos= 358 score=0.027519 unnormalised=3.1442000000        RPRGRGPGP
3]         pos= 383 score=0.006023 unnormalised=0.6882000000        GPGPGKTEM
4]         pos= 529 score=0.039361 unnormalised=4.4972000000        IPANIGLAA
5]         pos=  -1 score=0.917605 unnormalised=104.8410000000        non-binding event
```

DoPeptideList_II:
        Given the antigen injected creates the list of peptides for all the
        NumAgProts proteins and for all i.e., 2 MHCII molecules

        Read class II peptide list from file? NO

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Allele: DRB1_0101
Pseudo sequence: KAFAHVEQRKAQTRV
Threshold: 2.392440
Max score: 26.461000

Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/37044_20250613-051710_5_WxEvsyjYD47M.FSA_1_001

GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKAKFVAAWTLKAAAGPGPGFISFIIVEKKRN
TYSGPGPGISFIIVEKKRNTYSRGPGPGITFISFIIVEKKRNTGPGPGSFIIVEKKRNTYSRLGPGPGTFISFIIVEKKR
NTYGPGPGGVTRKYKIKSNPLTKGPGPGAVGFLVRTEFKYNDSGPGPGDRINWISAGVFLDSNGPGPGDTLYFPAVGFLV
RTEGPGPGGDTLYFPAVGFLVRTGPGPGGDVLTVNPLVVNWRNGPGPGGFLVRTEFKYNDSNCGPGPGKKVRFENTTSDK
GKIGPGPGIKTEMRAVIKNSQKPGPGPGIKWAFEIHHRRPRGRGPGPGISTEFSINETLTLDVGPGPGKTEMRAVIKNSQ
KPKGPGPGPHNHYKSDNTEAAVLAAYAQITAGVALYAAYSIVPNFILVAAYAQITAGVALAAYRTLGYATEDFAAYAIGP
PVFTDKAAYGIAIGPPVFAAYDAFLIDRINWAAYAFLIDRINWAAYTITIPANIGLAAYAMDEGYFAYAAYQTAENPVFT
VAAYLAMDEGYFAYAAYHTEFNPHNHYAAYLETDDYNGIYAAYHLISIAINVAAYSMIEPLVLAAAYTEIILNPNLAAYK
SSELYHIKKKSLYILRQSKQGDYIRNKKSVGILHYEKLKKNTYSRLEDRRVRPTSSGDLYYKKSNGGGYNQHQLALRSIE
KGHHHHHH

Epitopes of protein 0 ------------
0]   pos=   9 score=0.013185 unnormalised=3.2015600000   YCRVRGGRC
1]   pos= 52 score=0.013939 unnormalised=3.3845600000   FVAAWTLKA
2]   pos= 81 score=0.006283 unnormalised=1.5255600000   YSGPGPGIS
3]   pos= 100 score=0.032390 unnormalised=7.8645600000   YSRGPGPGI
4]   pos= 139 score=0.035211 unnormalised=8.5495600000   YSRLGPGPG
5]   pos= 173 score=0.021307 unnormalised=5.1735600000   YKIKSNPLT
6]   pos= 180 score=0.005451 unnormalised=1.3235600000   LTKGPGPGA
7]   pos= 197 score=0.007502 unnormalised=1.8215600000   FKYNDSGPG
8]   pos= 231 score=0.024911 unnormalised=6.0485600000   YFPAVGFLV
9]   pos= 252 score=0.024911 unnormalised=6.0485600000   YFPAVGFLV
10]   pos= 259 score=0.003388 unnormalised=0.8225600000   LVRTGPGPG
11]   pos= 270 score=0.004664 unnormalised=1.1325600000   VLTVNPLVV
12]   pos= 280 score=0.015521 unnormalised=3.7685600000   WRNGPGPGG
13]   pos= 295 score=0.012794 unnormalised=3.1065600000   FKYNDSNCG
14]   pos= 372 score=0.010237 unnormalised=2.4855600000   FSINETLTL
15]   pos= 412 score=0.002346 unnormalised=0.5695600000   YKSDNTEAA
16]   pos= 421 score=0.013470 unnormalised=3.2705600000   VLAAYAQIT
17]   pos= 425 score=0.030417 unnormalised=7.3855600000   YAQITAGVA
18]   pos= 428 score=0.002576 unnormalised=0.6255600000   ITAGVALYA
19]   pos= 432 score=0.003462 unnormalised=0.8405600000   VALYAAYSI
20]   pos= 438 score=0.029783 unnormalised=7.2315600000   YSIVPNFIL
21]   pos= 444 score=0.032105 unnormalised=7.7955600000   FILVAAYAQ
22]   pos= 446 score=0.022542 unnormalised=5.4735600000   LVAAYAQIT
23]   pos= 450 score=0.030417 unnormalised=7.3855600000   YAQITAGVA
24]   pos= 453 score=0.009351 unnormalised=2.2705600000   ITAGVALAA
25]   pos= 456 score=0.006283 unnormalised=1.5255600000   GVALAAYRT
26]   pos= 475 score=0.026587 unnormalised=6.4555600000   YAIGPPVFT
27]   pos= 488 score=0.016966 unnormalised=4.1195600000   YGIAIGPPV
28]   pos= 490 score=0.008247 unnormalised=2.0025600000   IAIGPPVFA
29]   pos= 497 score=0.007259 unnormalised=1.7625600000   FAAYDAFLI
30]   pos= 508 score=0.002412 unnormalised=0.5855600000   INWAAYAFL

```
31]          pos= 525 score=0.014437 unnormalised=3.5055600000        YTITIPANI
32]          pos= 538 score=0.014483 unnormalised=3.5165600000        YAMDEGYFA
33]          pos= 544 score=0.025565 unnormalised=6.2075600000        YFAYAAYQT
34]          pos= 545 score=0.009635 unnormalised=2.3395600000        FAYAAYQTA
35]          pos= 550 score=0.008210 unnormalised=1.9935600000        YQTAENPVF
36]          pos= 557 score=0.027390 unnormalised=6.6505600000        VFTVAAYLA
37]          pos= 558 score=0.008066 unnormalised=1.9585600000        FTVAAYLAM
38]          pos= 570 score=0.018832 unnormalised=4.5725600000        YFAYAAYHT
39]          pos= 580 score=0.009714 unnormalised=2.3585600000        FNPHNHYAA
40]          pos= 595 score=0.012218 unnormalised=2.9665600000        YNGIYAAYH
41]          pos= 602 score=0.001917 unnormalised=0.4655600000        YHLISIAIN
42]          pos= 605 score=0.007407 unnormalised=1.7985600000        ISIAINVAA
43]          pos= 607 score=0.003697 unnormalised=0.8975600000        IAINVAAYS
44]          pos= 614 score=0.039749 unnormalised=9.6515600000        YSMIEPLVL
45]          pos= 622 score=0.000109 unnormalised=0.0265600000        LAAAYTEII
46]          pos= 629 score=0.018671 unnormalised=4.5335600000        IILNPNLAA
47]          pos= 638 score=0.000620 unnormalised=0.1505600000        YKSSELYHI
48]          pos= 682 score=0.030858 unnormalised=7.4925600000        YSRLEDRRV
49]          pos=  -1 score=0.272508 unnormalised=66.1680000000         non-binding event

========================================================================

Allele: DRB1_0101
Pseudo sequence: KAFAHVEQRKAQTRV
Threshold: 2.392440
Max score: 26.461000


----------------------------------
Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/37044_20250613-051710_5_WxEvsyjYD47M.FSA_1_001
----------------------------------

GIINTLQKYYCRVRGGRCAVLSCLPKEEQIGKCSTRGRKCCRRKKEAAAKAKFVAAWTLKAAAGPGPGFISFIIVEKKRN
TYSGPGPGISFIIVEKKRNTYSRGPGPGITFISFIIVEKKRNTGPGPGSFIIVEKKRNTYSRLGPGPGTFISFIIVEKKR
NTYGPGPGGVTRKYKIKSNPLTKGPGPGAVGFLVRTEFKYNDSGPGPGDRINWISAGVFLDSNGPGPGDTLYFPAVGFLV
RTEGPGPGGDTLYFPAVGFLVRTGPGPGGDVLTVNPLVVNWRNGPGPGGFLVRTEFKYNDSNCGPGPGKKVRFENTTSDK
GKIGPGPGIKTEMRAVIKNSQKPGPGPGIKWAFEIHHRRPRGRGPGPGISTEFSINETLTLDVGPGPGKTEMRAVIKNSQ
KPKGPGPGPHNHYKSDNTEAAVLAAYAQITAGVALYAAYSIVPNFILVAAYAQITAGVALAAYRTLGYATEDFAAYAIGP
PVFTDKAAYGIAIGPPVFAAYDAFLIDRINWAAYAFLIDRINWAAYTITIPANIGLAAYAMDEGYFAYAAYQTAENPVFT
VAAYLAMDEGYFAYAAYHTEFNPHNHYAAYLETDDYNGIYAAYHLISIAINVAAYSMIEPLVLAAAYTEIIILNPNLAAYK
SSELYHIKKKSLYILRQSKQGDYIRNKKSVGILHYEKLKKNTYSRLEDRRVRPTSSGDLYYKKSNGGGYNQHQLALRSIE
KGHHHHHH


Epitopes of protein 0 ------------
0]           pos=   9 score=0.013185 unnormalised=3.2015600000        YCRVRGGRC
1]           pos=  52 score=0.013939 unnormalised=3.3845600000        FVAAWTLKA
2]           pos=  81 score=0.006283 unnormalised=1.5255600000        YSGPGPGIS
3]           pos= 100 score=0.032390 unnormalised=7.8645600000        YSRGPGPGI
4]           pos= 139 score=0.035211 unnormalised=8.5495600000        YSRLGPGPG
5]           pos= 173 score=0.021307 unnormalised=5.1735600000        YKIKSNPLT
6]           pos= 180 score=0.005451 unnormalised=1.3235600000        LTKGPGPGA
7]           pos= 197 score=0.007502 unnormalised=1.8215600000        FKYNDSGPG
8]           pos= 231 score=0.024911 unnormalised=6.0485600000        YFPAVGFLV
9]           pos= 252 score=0.024911 unnormalised=6.0485600000        YFPAVGFLV
10]          pos= 259 score=0.003388 unnormalised=0.8225600000        LVRTGPGPG
11]          pos= 270 score=0.004664 unnormalised=1.1325600000        VLTVNPLVV
12]          pos= 280 score=0.015521 unnormalised=3.7685600000        WRNGPGPGG
13]          pos= 295 score=0.012794 unnormalised=3.1065600000        FKYNDSNCG
14]          pos= 372 score=0.010237 unnormalised=2.4855600000        FSINETLTL
15]          pos= 412 score=0.002346 unnormalised=0.5695600000        YKSDNTEAA
16]          pos= 421 score=0.013470 unnormalised=3.2705600000        VLAAYAQIT
17]          pos= 425 score=0.030417 unnormalised=7.3855600000        YAQITAGVA
18]          pos= 428 score=0.002576 unnormalised=0.6255600000        ITAGVALYA
19]          pos= 432 score=0.003462 unnormalised=0.8405600000        VALYAAYSI
20]          pos= 438 score=0.029783 unnormalised=7.2315600000        YSIVPNFIL
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21]        pos=  444 score=0.032105 unnormalised=7.7955600000        FILVAAYAQ
22]        pos=  446 score=0.022542 unnormalised=5.4735600000        LVAAYAQIT
23]        pos=  450 score=0.030417 unnormalised=7.3855600000        YAQITAGVA
24]        pos=  453 score=0.009351 unnormalised=2.2705600000        ITAGVALAA
25]        pos=  456 score=0.006283 unnormalised=1.5255600000        GVALAAYRT
26]        pos=  475 score=0.026587 unnormalised=6.4555600000        YAIGPPVFT
27]        pos=  488 score=0.016966 unnormalised=4.1195600000        YGIAIGPPV
28]        pos=  490 score=0.008247 unnormalised=2.0025600000        IAIGPPVFA
29]        pos=  497 score=0.007259 unnormalised=1.7625600000        FAAYDAFLI
30]        pos=  508 score=0.002412 unnormalised=0.5855600000        INWAAYAFL
31]        pos=  525 score=0.014437 unnormalised=3.5055600000        YTITIPANI
32]        pos=  538 score=0.014483 unnormalised=3.5165600000        YAMDEGYFA
33]        pos=  544 score=0.025565 unnormalised=6.2075600000        YFAYAAYQT
34]        pos=  545 score=0.009635 unnormalised=2.3395600000        FAYAAYQTA
35]        pos=  550 score=0.008210 unnormalised=1.9935600000        YQTAENPVF
36]        pos=  557 score=0.027390 unnormalised=6.6505600000        VFTVAAYLA
37]        pos=  558 score=0.008066 unnormalised=1.9585600000        FTVAAYLAM
38]        pos=  570 score=0.018832 unnormalised=4.5725600000        YFAYAAYHT
39]        pos=  580 score=0.009714 unnormalised=2.3585600000        FNPHNHYAA
40]        pos=  595 score=0.012218 unnormalised=2.9665600000        YNGIYAAYH
41]        pos=  602 score=0.001917 unnormalised=0.4655600000        YHLISIAIN
42]        pos=  605 score=0.007407 unnormalised=1.7985600000        ISIAINVAA
43]        pos=  607 score=0.003697 unnormalised=0.8975600000        IAINVAAYS
44]        pos=  614 score=0.039749 unnormalised=9.6515600000        YSMIEPLVL
45]        pos=  622 score=0.000109 unnormalised=0.0265600000        LAAAYTEII
46]        pos=  629 score=0.018671 unnormalised=4.5335600000        IILNPNLAA
47]        pos=  638 score=0.000620 unnormalised=0.1505600000        YKSSELYHI
48]        pos=  682 score=0.030858 unnormalised=7.4925600000        YSRLEDRRV
49]        pos=   -1 score=0.272508 unnormalised=66.1680000000         non-binding event
```