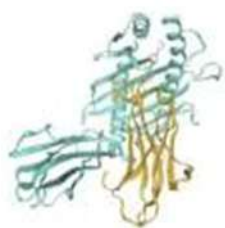


# LAMPIRAN

## Lampiran 1. Epitop MHC-II.

Epitop	Alel	Antigenitas	Energi Ikatan (kcal/mol)
<b>MFIFLLFLTLTSGSD</b>	HLA-DPA1*01, DPB1*04:01, DPA1*01:03, DPB1*02:01, DPA1*02:01, DPB1*05:01, DPA1*03:01, DPB1*04:02, DRB1*04:01, HLA-DRB1*04:05, DRB1*11:01	0,6167	-264,53
<b>AYFVGYLKPTTFMLK</b>	HLA-DPA1*02:01, DPB1*01:01, DPA1*02:01, DPB1*05:01	0,7088	-258,58
<b>LYLTQDLFLPFYSNV</b>	HLA-DPA1*01:03, DPB1*02:01, DPA1*02:01, DPB1*05:01	0,4189	-257,25
<b>GYQPYRVVLSFELL</b>	HLA-DPA1*01, DPB1*04:01, DPA1*01:03, DPB1*02:01, DPA1*02:01, DPB1*01:01	1,0740	-219,76
<b>RVVVLSFELLNAPAT</b>	HLA-DPA1*01, DPB1*04:01, DPA1*01:03, DPB1*02:01, DPA1*02:01, DPB1*01:01, DPA1*02:01, DPB1*05:01, DRB1*01:0	0,7089	-216,39
<b>DEIFRSDTLYLTQDL</b>	HLA-DRB1*04:01, HLA- DRB3*01:01, HLA-DPA1*02:01, DPB1*01:01	0,3818	-210,94

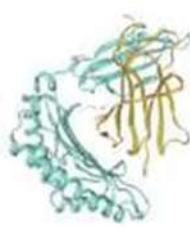
## Lampiran 2. Gambaran Penambatan Molekuler Epitop MHC-I dan alel HLA.



QYIKWPWYV



AEIRASANL



QIAPGQTGV

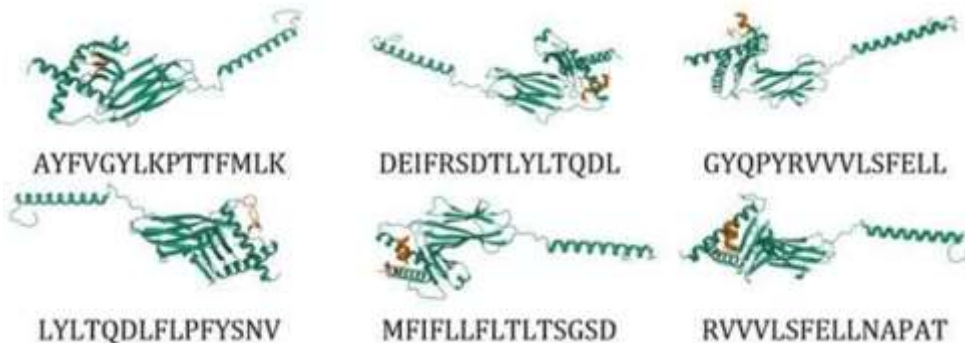


GQTGVIADY



GVIADYNYK

### Lampiran 3. Gambaran Penambatan Molekuler Epitop MHC-II dan alel HLA.



### Lampiran 4. Hasil Sel B

Epitop	Antigenitas	Toksistas	Alerginitas
<b>PIDVRDLPSGFN</b>	1,5139	Non Toksik	Non Alergen
<b>RNFFSPQITTD</b>	0,2816	Non Toksik	Non Alergen
<b>TLIHAEQLTPAW</b>	0,6664	Non Toksik	Non Alergen
<b>TGVIADYNYKLP</b>	0,9990	Non Toksik	Non Alergen
<b>VSATKLNLCFS</b>	2,2210	Non Toksik	Non Alergen

### Lampiran 5. Hasil ProtParam

Formula:  $C_{1945}H_{2958}N_{496}O_{557}S_{18}$   
 Total number of atoms: 5966

Extinction coefficients:

Extinction coefficients are in units of  $M^{-1} cm^{-1}$ , at 280 nm measured in water.

Ext. coefficient      62828  
 Abs 0.1% (=1 g/l)    1.459, assuming all pairs of Cys residues form cystines

Ext. coefficient      61770  
 Abs 0.1% (=1 g/l)    1.453, assuming all Cys residues are reduced

Estimated half-life:

The N-terminal of the sequence considered is M (Met).

<https://web.expasy.org/cgi-bin/protparam/protparam>

4/26/22, 5:01 AM

ExpASY ProtParam tool

The estimated half-life is: 30 hours (mammalian reticulocytes, in vitro).  
 >20 hours (yeast, in vivo).  
 >10 hours (Escherichia coli, in vivo).

Instability index:

The instability index (II) is computed to be 34.28  
 This classifies the protein as stable.

Aliphatic index: 88.79

Grand average of hydropathicity (GRAVY): -0.056

## Lampiran 6. Hasil Alerginitas.

Bioinformatics tool for allergenicity prediction.

[Home](#)   [Data sets](#)   [Method description](#)   [Contact](#)

# AllerTOP v. 2.0

Bioinformatics tool for allergenicity prediction

Your sequence is:

**PROBABLE NON-ALLERGEN**

The nearest protein is:

[UniProtKB accession number O9HCU4](#)  
defined as non-allergen



```

MISKLSLSLMAVAADVDVAASANNK
VMVDLQSLVQVLRGKNTLQSDAN
QNTKQKQVQSLVQVLRGKNTLQSDAN
MKCPYKGGQYDQYVQVLRGKNTLQSDAN
VTVYKLGNGVQVLRGKNTLQSDAN
1000100011011011011011011010000
0010010001010101010101010100001
001001101001000100100100000100000
100100010001100100100100100100101
  
```

## Lampiran 7. Hasil Antigenitas

Model selected: **virus**

Threshold for this model: **0.4**

Your Sequence:

```

MTETIKVSESLELHAVAESHVTPLYQLICKN
RTWLQQS LNWPQPVQSEEDTRKTVQGNVMLH
QRGYAKMFMI FKEDELIGVISFNRIEPLNKT
AEIGYWLDESHQGGIISQALQALIHHYAQS
GELRRFVIKCRVDNPFQSNQVALRNGFILEGC
LKQAEFLNDAYDDVNLYARIIDSEAAKQYI
KWPWYVAAYAEIRASANLAAYQIAPGQTGVA
AYGQTGVIADYAAAGVIADYNYRGPGPGMFI
FLFLTLTSGSDGPGPGAYFVGYLKPTTFML
GPGPGLYLTQDLFLPFVSNVGPFGGYQPYR
VVVLSFELLGPGPGRVVLSFELLNAPATGP
GPGVSATKLNLCFSGPGPGPIDVRDLPSGF
  
```

#vaxjen/scripts/Model\_scripts/vaxjen3.pl

1/2

---

VaxJen - predicting protective antigens

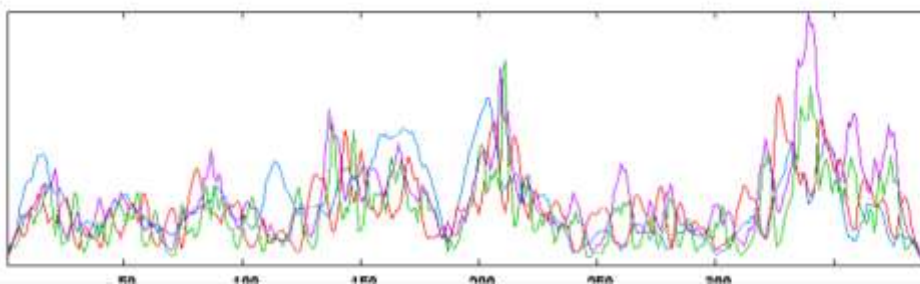
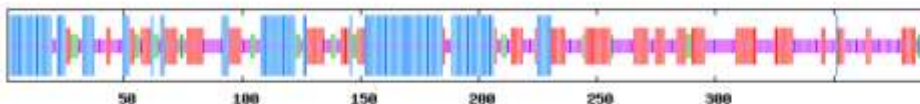
NGPGPGTGVADYNYKLP

Overall Prediction for the Protective Antigen = **0.5114** ( Probable **ANTIGEN** ).

## Lampiran 8. Hasil SOPMA.

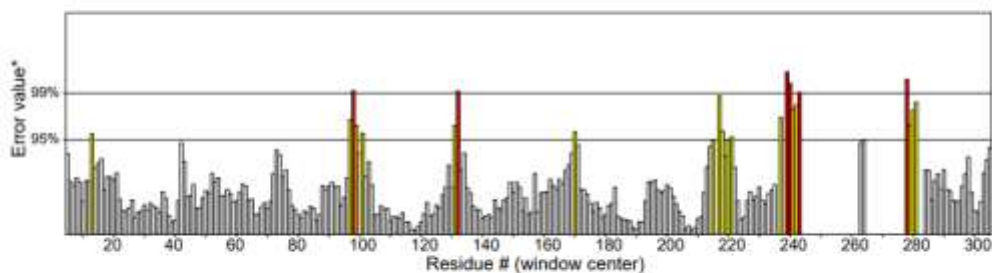
SOPMA :

Alpha helix (Hh)	:	114 is	29.23%
3 <sub>10</sub> helix (Gg)	:	0 is	0.00%
Pi helix (Ti)	:	0 is	0.00%
Beta bridge (Bb)	:	0 is	0.00%
Extended strand (Ee)	:	116 is	29.74%
Beta turn (Tt)	:	25 is	6.41%
Bend region (Ss)	:	0 is	0.00%
Random coil (Cc)	:	135 is	34.62%
Ambiguous states (?)	:	0 is	0.00%
Other states	:	0 is	0.00%



## Lampiran 9. Hasil ERRAT

Program: ERRAT2  
 File: model1.pdb  
 Chain#:A  
 Overall quality factor\*\*: 86.154



\*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

\*\*Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3Å) the average overall quality factor is around 91%.

## Lampiran 10. Hasil Swiss Model

MolProbity Results		
MolProbity Score	2.61	
<input type="checkbox"/> Clash Score	139.06	(A60 MET-A60 MET), (A157 LYS-A157 LYS), (A62 HIS-A68 LYS), (A89 PRO-A92 LYS), (A361 GLY-A362 PRO), (A157 LYS-A168 ASP), (A280 GLY-A281 PRO), (A243 GLY-A244 PRO), (A150

<https://swissmodel.expasy.org/assess/5zyJRA/01>

4/26/22, 8:25 PM

model1.pdb | Structure Assessment

Ramachandran Favoured	98.71%	
Ramachandran Outliers	0.00%	
Rotamer Outliers	0.00%	
C-Beta Deviations	0	
<input type="checkbox"/> Bad Bonds	1 / 3093	A331 PHE
<input type="checkbox"/> Bad Angles	2 / 4217	A84 PHE, A150 PHE

## Lampiran 11. Hasil Residu TLR 3




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**RESULTS from consPPISP job ID=020000200**

1 pesan

<pi2pe.fsu@gmail.com>  
 Kepada: firmansyahm0@gmail.com

Sel, 8 Mar 2022 pukul 12.03

Submission name: TLR  
 Job submitted : Tue Mar 8 04:57:25 UTC 2022  
 Job done : Tue Mar 8 05:03:46 UTC 2022

Prediction by cons-PPISP : consensus Protein-Protein Interaction Site Predictor

Column 1: AA (Amino Acid code)

Column 2: Ch (Chain ID)

Column 3: AA# (Amino Acid number)

Column 4: Score (neural network score)

Column 5: Prediction of whether the residue contacts

(P = Positive; N = Negative; - = Burried and not predicted)

\*\*\*\*\*

AA	Ch	AA#	Score	Prediction
E	X	1	0.036	N
P	X	2	0.088	N
C	X	3	0.000	-
V	X	4	0.878	P
E	X	5	0.817	P
V	X	6	0.087	N
V	X	7	0.005	N
P	X	8	0.045	N
N	X	9	0.004	N
I	X	10	0.005	N
T	X	11	0.015	N
Y	X	12	0.000	-
Q	X	13	0.932	P

---

## Lampiran 12. Hasil Residu Desain Vaksin



### RESULTS from consPPISP job ID=020000199

1 pesan

<pi2pe.fsu@gmail.com>  
Kepada: firmansyahm0@gmail.com

Sel, 8 Mar 2022 pukul 11.44

Submission name: Ribosomal  
Job submitted : Tue Mar 8 04:42:00 UTC 2022  
Job done : Tue Mar 8 04:44:48 UTC 2022

Prediction by cons-PPISP : consensus Protein-Protein Interaction Site Predictor

Column 1: AA (Amino Acid code)

Column 2: Ch (Chain ID)

Column 3: AA# (Amino Acid number)

Column 4: Score (neural network score)

Column 5: Prediction of whether the residue contacts

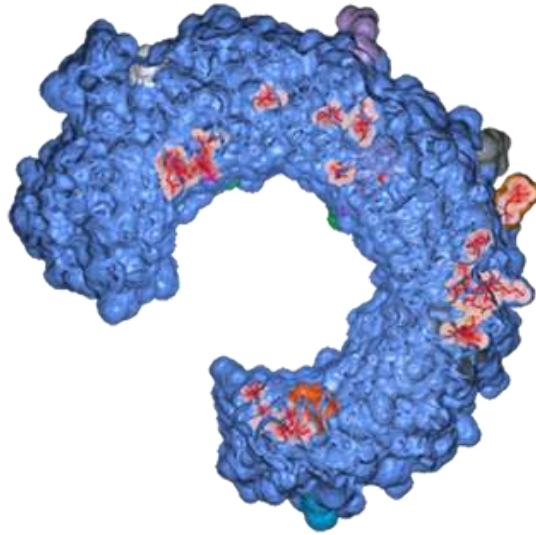
(P = Positive; N = Negative; - = Burried and not predicted)

\*\*\*\*\*

AA	Ch	AA#	Score	Prediction
M	A	1	0.953	P
T	A	2	0.931	P
E	A	3	0.982	P
T	A	4	0.985	P
I	A	5	0.986	P
K	A	6	0.361	N
V	A	7	0.073	N
S	A	8	0.009	N
E	A	9	0.058	N
S	A	10	0.097	N
L	A	11	0.000	-
E	A	12	0.041	N
L	A	13	0.000	-



**Lampiran 13. Gambaran Letak Residu TLR 3**



**Lampiran 14. Gambaran Letak Residu Desain Vaksin**

