# C-IMMSIM simulation results

## April 20, 2023

#### 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://kraken.iac.rm.cnr.it/C-IMMSIM

CITATIONS: For publication of results, please cite:

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. doi:10.1371/journal.pone.0009862, 2010.

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

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

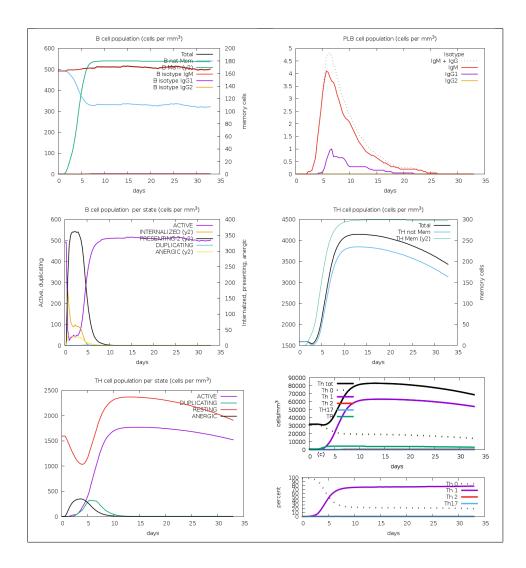


Figure 1: Cell counts shown. Legend: Act=active, Intern=internalized the Ag, Pres II = presenting on MHC II, Dup = in the mitotic cycle, Anergic = anergic, Resting = not active.

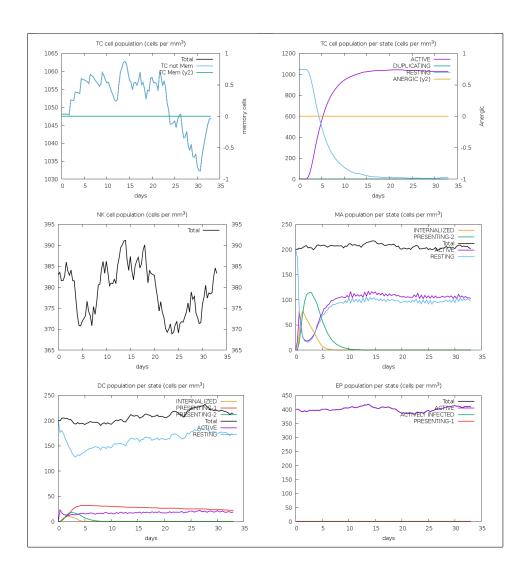


Figure 2: Legend: symbols as figure above.

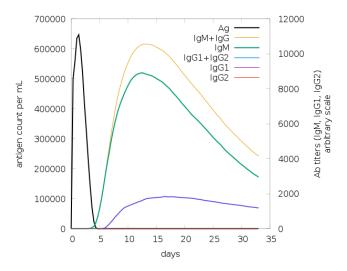


Figure 3: The virus, the immunoglobulins and the immunocomplexes.

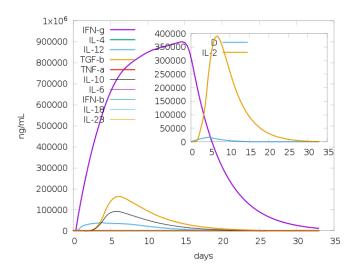


Figure 4: Concentration of cytokines and interleukins. Inset plot shows danger signal together with leukocyte growth factor IL-2.

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.

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Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/12364\_20230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001

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ILIFALILVAAYLYFDLIYSIAAYNYDNVRVEFAAYMMPAPGDKFAAYDVFGANYYYAAYKYRSITVRVGPGPGKNLLSF DVQTNKKKVGPGPGYLLIYNDNKTVESKSGPGPGTVQVTIDNRQSLGFTGPGPGQFLYFDLIYSIKDTKGPGPGVFHNIN YANSQPDPKGPGPGFVPYKFLNIYGDNKGPGPGQSLGFTITTNKNMVTGPGPGSEINIKAQEKFLQHDGPGPGNMRYLY DDKHVSEINGPGPGSAINVKSIDQFLYFDGPGPGKDKYVDVFGANYYYQGPGPGGFTITTNKNMVTIQEKKDINSHQTDK RKKKNQIDKNNSTDNHHHHHH

Epitopes of protein 0 -----

1]	pos=83 len=6	TNKKKV
2]	pos=100 len=12	DNKTVESKSGPG
3]	pos=146 len=5	DTKGP
4]	pos=162 len=10	NSQPDPKGPG
5]	pos=187 len=6	NKGPGP
6]	pos=271 len=4	GPGK

7] pos=310 len=27 KDINSHQTDKRKKKNQIDKNNSTDNHH

#### DoPeptideList\_I:

Given the antigen injected creates the list of peptides for all the  ${\tt NumAgProts}$  proteins and for all i.e., 4 MHCI molecules

Read class I peptide list from file? NO

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Allele: A0101

Pseudo sequence: KAVHAEQRNKAQTRA

Threshold: 9.456400 Max score: 29.236000

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 $\textbf{Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/12364\_20230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143-135143-135143-135143-135143-135143-135143-135143-135143-135143-135143-135143-135143-1351443-135144-135144-135144-135144-135144-135144-135144-1351$ 

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ILIFALILVAAYLYFDLIYSIAAYNYDNVRVEFAAYMMPAPGDKFAAYDVFGANYYYAAYKYRSITVRVGPGPGKNLLSF DVQTNKKKVGPGPGYLLIYNDNKTVESKSGPGPGTVQVTIDNRQSLGFTGPGPGQFLYFDLIYSIKDTKGPGPGVFHNIN YANSQPDPKGPGPGPFVPYKFLNIYGDNKGPGPGQSLGFTITTNKNMVTGPGPGSEINIKAQEKFLQHDGPGPGNMRYLY DDKHVSEINGPGPGSAINVKSIDQFLYFDGPGPGKDKYVDVFGANYYYQGPGPGGFTITTNKNMVTIQEKKDINSHQTDK RKKKNQIDKNNSTDNHHHHHH

Epitopes of protein 0 -----

0] pos= 277 score=0.057606 unnormalised=6.4086000000 YVDVFGANY

pos= -1 score=0.942394 unnormalised=104.8410000000 non-binding event

Allele: A0202 Pseudo sequence: KAAHVEQRKKAQTRV Threshold: 9.589400 Max score: 27.292000 Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/12364\_20230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001 ILIFALILVAAYLYFDLIYSIAAYNYDNVRVEFAAYMMPAPGDKFAAYDVFGANYYYAAYKYRSITVRVGPGPGKNLLSF  ${\tt DVQTNKKKVGPGPGYLLIYNDNKTVESKSGPGPGTVQVTIDNRQSLGFTGPGPGQFLYFDLIYSIKDTKGPGPGVFHNIN}$  ${\tt YANSQPDPKGPGPGPFVPYKFLNIYGDNKGPGPGQSLGFTITTNKNMVTGPGPGSEINIKAQEKFLQHDGPGPGNMRYLY}$ DDKHVSEINGPGPGSAINVKSIDQFLYFDGPGPGKDKYVDVFGANYYYQGPGPGGFTITTNKNMVTIQEKKDINSHQTDK RKKKNQIDKNNSTDNHHHHHH Epitopes of protein 0 -----ALILVAAYL pos= 4 score=0.011639 unnormalised=1.2346000000 pos= -1 score=0.988361 unnormalised=104.8410000000 1] non-binding event Allele: B0702 Pseudo sequence: KAAREEQQIKAQTRE Threshold: 8.702800 Max score: 28.406000 Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/12364\_20230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001 ILIFALILVAAYLYFDLIYSIAAYNYDNVRVEFAAYMMPAPGDKFAAYDVFGANYYYAAYKYRSITVRVGPGPGKNLLSF  ${\tt DVQTNKKKVGPGPGYLLIYNDNKTVESKSGPGPGTVQVTIDNRQSLGFTGPGPGQFLYFDLIYSIKDTKGPGPGVFHNIN}$ YANSQPDPKGPGPGFVPYKFLNIYGDNKGPGPGQSLGFTITTNKNMVTGPGPGSEINIKAQEKFLQHDGPGPGNMRYLY DDKHVSEINGPGPGSAINVKSIDQFLYFDGPGPGKDKYVDVFGANYYYQGPGPGGFTITTNKNMVTIQEKKDINSHQTDK RKKKNQIDKNNSTDNHHHHHH Epitopes of protein 0 ----pos= 37 score=0.002446 unnormalised=0.2572000000 MPAPGDKFA 0]

pos= 109 score=0.000677 unnormalised=0.0712000000 1]

pos= -1 score=0.996877 unnormalised=104.8410000000 21 non-binding event

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Allele: B5801

Pseudo sequence: KAAREEQRNKAQTRE

Threshold: -11.757400 Max score: 26.104000

Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/12364\_20230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001

 ${\tt ILIFALILVAAYLYFDLIYSIAAYNYDNVRVEFAAYMMPAPGDKFAAYDVFGANYYYAAYKYRSITVRVGPGPGKNLLSF}$  ${\tt DVQTNKKKVGPGPGYLLIYNDNKTVESKSGPGPGTVQVTIDNRQSLGFTGPGPGQFLYFDLIYSIKDTKGPGPGVFHNIN}$ YANSQPDPKGPGPGFVPYKFLNIYGDNKGPGPGQSLGFTITTNKNMVTGPGPGSEINIKAQEKFLQHDGPGPGNMRYLY  ${\tt DDKHVSEINGPGPGSAINVKSIDQFLYFDGPGPGKDKYVDVFGANYYYQGPGPGGFTITTNKNMVTIQEKKDINSHQTDK}$ RKKKNQIDKNNSTDNHHHHHH

Epitopes of protein 0 -----

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4]	pos=	4 score=0.008968 unnormalised=11.7454000000	ALILVAAYL
5]	pos=	5 score=0.012562 unnormalised=16.4524000000	LILVAAYLY
6]	pos=	6 score=0.017025 unnormalised=22.2974000000	ILVAAYLYF
7]	pos=	7 score=0.006317 unnormalised=8.2734000000	LVAAYLYFD
8]	pos=	8 score=0.011308 unnormalised=14.8094000000	VAAYLYFDL
9]	pos=	9 score=0.010525 unnormalised=13.7844000000	AAYLYFDLI
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11] 12]	pos=	11 score=0.003006 unnormalised=3.9364000000 12 score=0.005977 unnormalised=7.8284000000	YLYFDLIYS LYFDLIYSI
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24]	pos=	30 score=0.001501 unnormalised=1.9664000000	VEFAAYMMP
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741
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781
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801
                                                                      IDNRQSLGF
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           pos= 122 score=0.002360 unnormalised=3.0904000000
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931
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            pos= 201 score=0.005597 unnormalised=7.3304000000
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1297
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130]
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131]			unnormalised=9.0394000000	VTGPGPGSE
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133]	•		unnormalised=1.0264000000	PGPGSEINI
134]	-		unnormalised=15.2004000000	INIKAQEKF
135]	pos= 217 so	core=0.002044	unnormalised=2.6774000000	NIKAQEKFL
136]	pos= 218 s	core=0.000377	unnormalised=0.4934000000	IKAQEKFLQ
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148]	-		unnormalised=2.3244000000	HVSEINGPG
149]	•		unnormalised=3.770400000	VSEINGPGP
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154]	1		unnormalised=6.3274000000	SAINVKSID
155]	•		unnormalised=13.689400000	INVKSIDQF
156]	-		unnormalised=13.0634000000	NVKSIDQF
157]	-			
	•		unnormalised=11.9654000000	VKSIDQFLY
158]	•		unnormalised=27.3334000000	KSIDQFLYF
159]	•		unnormalised=1.5944000000	FLYFDGPGP
160]	-		unnormalised=5.4474000000	GPGPGKDKY
161]	-		unnormalised=3.6914000000	GKDKYVDVF
162]	-		unnormalised=13.0474000000	YVDVFGANY
163]	-		unnormalised=10.6524000000	VDVFGANYY
164]	-		unnormalised=11.7884000000	DVFGANYYY
165]	-		unnormalised=2.8784000000	VFGANYYYQ
166]	-		unnormalised=1.4614000000	FGANYYYQG
167]	•		unnormalised=5.3144000000	GANYYYQGP
168]	-		unnormalised=13.7194000000	YQGPGPGGF
169]	pos= 289 s	core=0.007156	unnormalised=9.3724000000	GPGPGGFTI
170]	pos= 293 s	core=0.001215	unnormalised=1.5914000000	GGFTITTNK
171]	pos= 295 s	core=0.010476	unnormalised=13.7194000000	FTITTNKNM
172]	pos= 296 s	core=0.000402	unnormalised=0.5264000000	TITTNKNMV
173]	pos= 297 sc	core=0.005183	unnormalised=6.7884000000	ITTNKNMVT
174]	pos= 298 so	core=0.011511	unnormalised=15.0754000000	TTNKNMVTI
175]	pos= 301 sc	core=0.003572	unnormalised=4.6784000000	KNMVTIQEK
176]	pos= 302 so	core=0.001554	unnormalised=2.0354000000	NMVTIQEKK
177]	pos= 303 so	core=0.001028	unnormalised=1.3464000000	MVTIQEKKD
178]	pos= 304 sc	core=0.006660	unnormalised=8.7224000000	VTIQEKKDI
179]	pos= 309 so	core=0.001369	unnormalised=1.7924000000	KKDINSHQT
180]	•		unnormalised=4.7074000000	KDINSHQTD
181]	-		unnormalised=0.2954000000	INSHQTDKR
182]	•		unnormalised=1.523400000	NSHQTDKRK
183]	•		unnormalised=7.095400000	KNNSTDNHH
184]	•		unnormalised=1.0684000000	NNSTDNHHH
185]			unnormalised=7.309400000	NSTDNHHHH
186]	-		unnormalised=7.2104000000	STDNHHHHH
187]	•		unnormalised=104.841000000	non-binding event
	r 1 50	0.000002		

### DoPeptideList\_II:

Given the antigen injected creates the list of peptides for all the

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

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 $\textbf{Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/12364\_20230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001230420-135143-135144-135144-135144-135144-135144-13514$ 

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 $ILIFALILVAAYLYFDLIYSIAAYNYDNVRVEFAAYMMPAPGDKFAAYDVFGANYYYAAYKYRSITVRVGPGPGKNLLSF\\ DVQTNKKKVGPGPGYLLIYNDNKTVESKSGPGPGTVQVTIDNRQSLGFTGPGPGQFLYFDLIYSIKDTKGPGPGVFHNIN\\ YANSQPDPKGPGPGFVPYKFLNIYGDNKGPGPGQSLGFTITTNKNMVTGPGPGSEINIKAQEKFLQHDGPGPGNMRYLY\\ DDKHVSEINGPGPGSAINVKSIDQFLYFDGPGPGKDKYVDVFGANYYYQGPGPGGFTITTNKNMVTIQEKKDINSHQTDK\\ RKKKNQIDKNNSTDNHHHHHH$ 

Epitopes of protein 0 -----

0]	pos= 5	score=0.024928	unnormalised=2.5395600000	LILVAAYLY
1]	pos= 14	score=0.066271	unnormalised=6.7515600000	FDLIYSIAA
2]	pos= 17	score=0.021914	unnormalised=2.2325600000	IYSIAAYNY
3]	pos= 50	score=0.000329	unnormalised=0.0335600000	FGANYYYAA
4]	pos= 55	score=0.016172	unnormalised=1.6475600000	YYAAYKYRS
5]	pos= 88	score=0.004256	unnormalised=0.4335600000	VGPGPGYLL
6]	pos= 155	score=0.012157	unnormalised=1.2385600000	FHNINYANS
7]	pos= 198	score=0.018204	unnormalised=1.8545600000	FTITTNKNM
8]	pos= 200	score=0.014484	unnormalised=1.4755600000	ITTNKNMVT
9]	pos= 206	score=0.028736	unnormalised=2.9275600000	MVTGPGPGS
10]	pos= 28	35 score=0.049820	0 unnormalised=5.0755600000	YYYQGPGPG
11]	pos= 28	86 score=0.060558	8 unnormalised=6.1695600000	YYQGPGPGG
12]	pos= 29	5 score=0.01820	4 unnormalised=1.8545600000	FTITTNKNM
13]	pos= 29	7 score=0.01448	4 unnormalised=1.4755600000	ITTNKNMVT
14]	pos= -	1 score=0.64948	4 unnormalised=66.1680000000	non-binding event

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Allele: DRB1\_1501

Pseudo sequence: RVTLGRDASW

Threshold: 3.125180 Max score: 28.118000

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Antigen sequence file: /opt/lampp/htdocs/C-IMMSIM/Jobs/input/12364\_20230420-135143\_5\_3WBpIhMm0EHq.FSA\_1\_001

ILIFALILVAAYLYFDLIYSIAAYNYDNVRVEFAAYMMPAPGDKFAAYDVFGANYYYAAYKYRSITVRVGPGPGKNLLSF DVQTNKKKVGPGPGYLLIYNDNKTVESKSGPGPGTVQVTIDNRQSLGFTGPGPGQFLYFDLIYSIKDTKGPGPGVFHNIN YANSQPDPKGPGPGPFVPYKFLNIYGDNKGPGPGQSLGFTITTNKNMVTGPGPGSEINIKAQEKFLQHDGPGPGNMRYLY DDKHVSEINGPGPGSAINVKSIDQFLYFDGPGPGKDKYVDVFGANYYYQGPGPGGFTITTNKNMVTIQEKKDINSHQTDK RKKKNQIDKNNSTDNHHHHHH

Epitopes of protein 0 ------

0]	pos=	0	score=0.069176	unnormalised=6.7358200000	ILIFALILV
1]	pos=	5	score=0.022489	unnormalised=2.1898200000	LILVAAYLY
2]	pos=	14	score=0.063938	unnormalised=6.2258200000	FDLIYSIAA
3]	pos=	17	score=0.029996	unnormalised=2.9208200000	IYSIAAYNY
4]	pos=	58	score=0.077607	unnormalised=7.5568200000	AYKYRSITV
5]	pos=	200	score=0.028630	unnormalised=2.7878200000	ITTNKNMVT
6]	pos=	297	score=0.028630	unnormalised=2.7878200000	ITTNKNMVT