Immunoinformatics Approach for Designing Multiple Epitope-Based Vaccine against Human Metapneumovirus Utilizing its Fusion Protein.

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Abstract

Background

Human Metapneumovirus is a major cause of acute respiratory infections especially in children besides it's responsible for substantial hospitalizations associated with significant morbidity and treatment cost. Hence vaccination is required. Consequently, we aim to predict effective, safe, and universal epitope-based peptides vaccine against the HMPV using its Fusion Protein via the Immunoinformatics approach since there are no licensed vaccines or antiviral treatments yet.

To achieve this goal, various Immunoinformatics databases and web servers, including, the Immune Epitope Database used the Allergen FP v.1.0, and ToxinPred web servers as well as Phyre2 web portal for the modeling of peptide 3D structure and molecular docking study on Cresset Flare software.

Result

According to the results, the peptide GSTVYYPN was the best predicted B-cells epitopes. Moreover, the peptide VIYMQQLPI with population coverage 48.27% in class(C) I, 35.12% in (C)II, and the peptides LIGVYGSSV with 44.03% in C II, YTNVFTLEV with 61.92% in class I were the best-predicted T-cells epitopes that will interact effectively with the MHC I and MHC II molecules respectively.

Conclusions

We recommend the use of them, the highest coverage, and the best -combined allele's bindings of immunogenic multiple peptide vaccines. Also, experimental studies recommend validating the results.

Background

Human metapneumovirus is one of the leading causes of upper and lower respiratory tract infections in human [1–8]. It is a single negative-stranded RNA virus that belongs to the paramyxoviridae family, pneumovirinae subfamily, metapneumovirus genus [1, 7, 9–12]. It is composed of 13000 nucleotides [12], eight genes and, nine proteins, namely: matrix protein, fusion protein, nucleoprotein, phosphoprotein, small hydrophobic protein, attachment protein, transcription elongation factor, RNA synthesis regulatory factor, and RNA dependent RNA polymerase [1, 11–14]. Minor hydrophobic protein, attachment protein, and fusion proteins are glycoproteins that are present on the virion surface [1, 15–18]. Both attachment and fusion glycoproteins are required for the human metapneumovirus to enter the host cell as these proteins enable the attachment and fusion of the virus to the host cells, respectively, and subsequently causing the infection [15–18]. There are four clades of human metapneumovirus genes: A1, A2, B1, B2 [1, 19–23]. Fusion proteins are immunogenic and highly conserved among these different subtypes of human metapneumovirus [24]. The infection caused by human metapneumovirus affects all ages, but it could be severe and fatal in infants, elderly and immunocompromised individuals [5, 7, 12, 25, 31–33]. It also can worsen the condition of asthmatic patients [12, 31–34] and patients with chronic obstructive

pulmonary disease, and it may lead to bronchitis or pneumonia [1, 29, 35, 36, 37] in elderly patients and children. It is responsible for 5 to 15% hospitalization of children with acute respiratory tract infection [10, 26] and 20% of deaths in 2000, with the majority of deaths occurring in sub-Saharan Africa and south of Asia [1, 27]. The infection was transmitted by direct or close contact with infected patients [30, 35]. Although many vaccines and treatments are under investigation, there are no licensed vaccines or antiviral cures against human metapneumovirus yet [9]. The study aims to use in silico approach to determine antigenic peptides from all strains of human metapneumovirus glycoprotein that could be used for peptide-based vaccine design against human metapneumovirus using immunoinformatic tools that are available online. This study is unique because B cells and T cells epitopes are predicted from human metapneumovirus fusion glycoprotein only, which is highly conserved among different subtypes of human metapneumovirus [24], immunogenic [28] and needed for the first step of virus-cell binding interaction [15–18].

Results

The predicted B-cells epitopes and their Emini and antigenicity in Table 1 showed the peptide GSTVYYPN was the best peptide, Moreover, the peptide VIYMVQLPI with population coverage 48.27% in class(C) I, 35.12% in (C)II, and the peptides LIGVYGSSV with 44.03% in C II, YTNVFTLEV with 61.92% in class I were the best-predicted T-cells epitopes that will interact effectively with the MHC I and MHC II molecules respectively see table (4)

Table1: Predicated B cell epitope with their eimini and antigenicity score

Peptide	Start	End	Length	Emini Score	Antigenicity Score
YLEESCSTITE	23	33	11	0.868	1.034
GDVENLTC	53	60	8	0.391	1.04
DGPSLIK	62	68	7	0.878	1.021
QLAREEQIENPRQS	88	101	14	9.75	0.976
AAVT	116	119	4	0.455	1.105
TNEAVSTLGN	144	153	10	0.883	0.98
KCDI	181	184	4	0.523	1.09
QFSDNAGITPA	206	216	11	0.785	0.99
AAPSCS	288	293	6	0.414	1.105
QGWYC	307	311	5	0.688	1.071
GSTVYYPN	315	322	8	1.557	1.042
KDCETRGDHVF	324	334	11	1.166	1.015
AAGINVAEQS	338	347	10	0.396	1.026
ECNIN	349	353	5	0.564	0.993
TNYPCKV	357	363	7	0.992	1.091
TGRHP	365	369	6	1.974	0.965
SYITNQDADTVTIDN	408	422	15	1.925	0.988
SKVEGEQHVI	428	437	10	0.836	1.056
SFDP	445	448	4	1.248	1.008
FPEDQFNV	451	458	8	1.245	1.017
IENSQALV	467	474	8	0.503	1.063
SAEKG	483	488	6	2.031	0.918

Table 2: The predicted T-cell epitopes that interact with MHCI alleles with their percentile rank and IC50

Percentile	Ic50	Allele	End	Start	Peptide
0.6	285.95	HLA-B*40:02	28	20	KESYLEESC
0.17	93.0	HLA-C*14:20	30	22	SYLEESCST
0.48	44.36	HLA-A*02:01	31	23	YLEESCSTI
0.78	79.74	HLA-A*02:06			
0.68	421.61	HLA-C*03:03			
0.2	428.87	HLA-C*05:01			
0.1	40.13	HLA-C*12:30			
0.37	262.58	HLA-C*14:02			
1.9	226.09	HLA-A*02:01	45	37	SVLRTGWYT
1.6	415.33	HLA-B*27:05	47	39	LRTGWYTNV
0.11	365.35	HLA-C*07:01			
0.36	203.72	HLA-A*24:02	48	40	RTGWYTNVF
0.9	243.06	HLA-A*30:02			
0.02	6.61	HLA-A*32:01			
0.78	171.06	HLA-B*15:01			
0.22	47.72	HLA-B*58:01			
0.23	436.9	HLA-C*15:02			
0.17	46.75	HLA-A*23:01	50	42	GWYTNVFTL
0.3	171.89	HLA-A*24:02			
0.05	209.73	HLA-C*07:02			
0.23	138.87	HLA-C*14:02			
0.17	63.41	HLA-A*01:01	52	44	YTNVFTLEV
0.43	39.42	HLA-A*02:01			
0.55	49.99	HLA-A*02:06			
0.15	14.51	HLA-A*68:02			
0.2	111.42	HLA-C*12:03			
0.01	16.47	HLA-C*15:02			

0.09	25.8	HLA-B*40:01	58	50	LEVGDVENL
0.85	431.91	HLA-B*40:02			
0.28	27.18	HLA-B*07:02	71	63	GPSLIKTEL
0.75	364.35	HLA-A*30:01	81	73	LTKSALREL
0.15	102.67	HLA-B*44:02	103	95	IENPRQSRF
0.01	4.42	HLA-B*07:02	105	97	NPRQSRFVL
0.19	72.33	HLA-B*07:02			
0.68	68.53	HLA-A*02:06	107	99	RQSRFVLGA
0.87	478.32	HLA-A*30:01			
1.7	479.78	HLA-B*27:05			
0.14	77.11	HLA-C*14:02	110	102	RFVLGAIAL
1.9	279.92	HLA-A*02:06	111	103	FVLGAIALG
0.58	54.08	HLA-A*02:01	112	104	VLGAIALGV
1.8	261.15	HLA-A*02:06			
1.9	302.3	HLA-A*02:06	134	126	KTIRLESEV
0.04	58.71	HLA-C*15:02			
1.2	128.79	HLA-A*02:06	155	147	AVSTLGNGV
0.99	219.15	HLA-A*68:02			
2.4	439.34	HLA-A*02:06	157	149	STLGNGVRV
0.84	156.59	HLA-A*68:02			
0.58	241.0	HLA-A*30:01	162	154	GVRVLATAV
1.9	226.09	HLA-A*02:01	165	157	VLATAVREL
1.6	216.61	HLA-A*02:06	196	188	KMAVSFSQF
0.78	371.42	HLA-A*23:01			
0.69	458.54	HLA-A*24:02			
0.26	237.52	HLA-A*32:01			
0.05	11.33	HLA-B*15:01			
0.34	81.96	HLA-B*58:01			
0.55	263.06	HLA-B*35:01	197	189	MAVSFSQFN
1.5	370.18	HLA-A*03:01	198	190	AVSFSQFNR

0.13	22.16	HLA-A*11:01			
0.17	14.32	HLA-A*31:01			
0.11	15.98	HLA-A*68:01			
0.69	102.27	HLA-A*11:01	199	191	VSFSQFNRR
0.16	13.62	HLA-A*31:01			
0.72	95.2	HLA-A*68:01			
0.61	393.3	HLA-A*24:02	200	192	SFSQFNRRF
0.06	137.33	HLA-C*06:02	201	193	FSQFNRRFL
0.13	60.38	HLA-C*12:03			
0.08	34.12	HLA-C*12:03	204	196	FNRRFLNVV
0.27	72.0	HLA-B*27:05	206	198	RRFLNVVRQ
0.15	38.7	HLA-A*23:01	207	199	RFLNVVRQF
0.16	106.71	HLA-A*24:02			
0.25	215.15	HLA-A*32:01			
0.56	490.25	HLA-C*14:02			
0.59	253.25	HLA-A*30:01	211	203	VVRQFSDNA
0.58	54.22	HLA-A*02:06	214	206	RQFSDNAGI
1.3	301.73	HLA-B*15:01			
1.5	407.1	HLA-B*27:05			
0.35	111.38	HLA-C*05:01	215	207	FSDNAGITP
1.6	416.65	HLA-A*68:02	217	209	DNAGITPAI
0.35	127.59	HLA-C*03:03	219	211	AGITPAISL
0.52	450.44	HLA-C*14:02	221	213	ITPAISLDL
0.27	85.95	HLA-B*35:01	222	214	TPAISLDLM
1.7	166.24	HLA-A*31:01	248	240	QIKLMLENR
1.7	311.74	HLA-A*68:01			
1.3	465.82	HLA-B*07:02	250	242	KLMLENRAM
0.99	251.82	HLA-B*15:01			
0.07	40.02	HLA-C*14:02			
0.38	33.58	HLA-A*02:01	251	243	LMLLENRAMV

0.23	17.43	HLA-A*02:06			
0.49	414.98	HLA-C*12:03			
1.8	192.75	HLA-A*31:01	252	244	MLENRAMVR
1.2	167.51	HLA-A*68:01			
0.93	326.77	HLA-B*07:02	256	248	RAMVRRKGF
0.11	41.4	HLA-B*08:01			
0.58	185.15	HLA-B*57:01			
0.14	28.29	HLA-A*30:01	258	250	MVRRKGFGI
0.31	129.72	HLA-B*08:01			
0.6	268.16	HLA-A*30:01	260	252	RRKGFGILI
0.08	25.05	HLA-B*27:05			
0.74	74.41	HLA-A*02:06	262	254	KGFGILIGV
1.2	307.12	HLA-A*29:02	263	255	GFGILIGVY
0.82	261.58	HLA-A*30:02			
0.44	105.26	HLA-A*03:01	269	261	GVYGSSVIY
0.7	102.81	HLA-A*11:01			
0.17	22.0	HLA-A*29:02			
0.31	87.83	HLA-A*30:02			
0.78	167.62	HLA-B*15:01			
0.65	350.49	HLA-B*35:01			
0.08	44.78	HLA-C*14:02	270	262	VYGSSVIYM
2.7	427.15	HLA-A*02:01	271	263	YGSSVIYMV
2.1	359.13	HLA-A*02:06			
0.38	46.96	HLA-A*68:02			
0.2	115.96	HLA-C*12:03			
1.3	137.15	HLA-A*02:01	275	267	VIYMVQLPI
1.7	231.88	HLA-A*02:06			
0.11	79.87	HLA-A*32:01			
0.28	182.9	HLA-C*14:02			
0.23	456.3	HLA-C*15:02			

0.05	15.34	HL:0A-A*23:01	276	268	IYMVQLPIF
0.02	15.62	HLA-A*24:02			
0.16	88.99	HLA-C*14:02			
1.3	133.11	HLA-A*02:01	278	270	MVQLPIFGV
0.25	20.62	HLA-A*02:06			
0.07	7.67	HLA-A*68:02			
0.21	16.39	HLA-A*02:06	279	271	VQLPIFGVI
1.7	472.81	HLA-B*15:01			
0.75	296.91	HLA-B*58:01	309	301	CLLREDQGW
1.4	360.17	HLA-A*30:02	310	302	LLREDQGWY
1.3	314.49	HLA-B*15:01			
0.49	278.92	HLA-B*18:01	334	326	CETRGDHVF
0.26	80.04	HLA-B*35:01	340	332	HVFCDTAAG
0.4	51.76	HLA-A*68:02	344	336	DTAAGINVA
1.8	264.17	HLA-A*02:06	370	362	KVSTGRHPI
0.3	84.76	HLA-A*30:01			
0.21	156.17	HLA-A*32:01			
0.59	171.75	HLA-B*07:02			
0.32	483.17	HLA-B*39:01	375	367	RHPISMVAL
0.04	385.56	HLA-B*48:01			
0.23	146.04	HLA-C*14:02			
0.49	216.61	HLA-B*35:01	376	368	HPISMVALS
0.58	53.87	HLA-A*02:06	378	370	ISMVALSPL
0.91	220.25	HLA-B*15:01			
0.62	209.97	HLA-B*58:01			
0.09	165.86	HLA-C*15:02			
0.14	54.37	HLA-A*68:02	380	372	MVALSPLGA
2.2	374.62	HLA-A*02:06	381	373	VALSPLGAL
1.2	394.88	HLA-B*07:02			
0.06	9.92	HLA-C*03:03			

0.39	34.86	HLA-A*02:01	382	374	ALSPLGALV
0.53	48.2	HLA-A*02:06			
1.3	468.47	HLA-B*07:02	384	376	SPLGALVAC
0.64	64.16	HLA-A*02:06	388	380	ALVACYKGV
0.13	235.57	HLA-C*15:02	418	410	ITNQDADTV
0.69	69.02	HLA-A*02:06	420	412	NQDADTVTI
0.06	37.05	HLA-B*39:01			
0.07	7.73	HLA-A*68:02	424	416	DTVTIDNTV
1.4	388.21	HLA-A*30:02	425	417	TVTIDNTVY
0.3	103.47	HLA-B*35:01			
2.7	422.96	HLA-A*02:01	427	419	TIDNTVYQL
2.5	458.02	HLA-A*02:06			
0.18	363.75	HLA-B*05:01			
0.17	17.37	HLA-A*68:02	430	422	NTVYQLSKV
2.2	362.99	HLA-A*02:06	433	425	YQLSKVEGE
0.23	66.27	HLA-B*35:01	459	451	FPEDQFNVA
0.14	52.47	HLA-B*40:01	460	452	PEDQFNVAL
1.4	345.58	HLA-B*15:01	464	456	FNVALDQVF
0.35	133.51	HLA-B*35:01			

Table 4: the predicted MHC1, MHC11, and the MHC combined peptide are having the highest percent in population coverage

MHC I Peptides	The coverage	MHC II peptides	The coverage	MHC combined	The coverage
YTNVFTLEV	61.92%	IKLMLENRA	48.63%	YTNVFTLEV	61.92%
YLEESCSTI	57.06%	LIGVYGSSV	44.03%	YLEESCSTI	57.06%
VIYMVQLPI	48.27%	VIYMVQLPI	35.12%	IKLMLENRA	48.63%
Epitope set	99.52%		81.94%		99.91%

Table 5: The predicted Allergicity, toxicity, and the molecular docking scores of the predicted peptides with MHC IA, MHC IB, and MHC II molecules.

The Peptides	MHC IA Docking score (6AM5)	MHC IB Docking score (5TXS)	MHC II Docking score (5NI9)	The Allergenicity	The Toxicity
YTNVFTLEV	Not docked	Not docked	—	Non-allergen	Non-Toxin
YLEESCSTI	Not docked	Not docked	—	Probable allergen	Non-Toxin
VIYMVQLPI	-4.893	-4.235	—	Probable allergen	Non-Toxin
IKLMLENRA	—	—	Not docked	Probable allergen	Non-Toxin
LIGVYGSSV	—	—	-6.244	Non-allergen	Non-Toxin
VIYMVQLPI	—	—	-6.556	Probable allergen	Non-Toxin
YTNVFTLEV	Not docked	Not docked	Not docked	Non-allergen	Non-Toxin
YLEESCSTI	Not docked	Not docked	Not docked	Probable allergen	Non-Toxin
IKLMLENRA	Not docked	Not docked	Not docked	Probable allergen	Non-Toxin

Discussion

We highlighted our most promising antigenic peptide of the B-cells epitopes **GSTVYYPN** (Table 1). And for the T-cells epitopes the best MHC I Peptides are **YTNVFTLEV**, **YLEESCSTI** and **VIYMVQLPI** (Table 2).

Moreover, the best MHC II peptides are **IKLMLENRA**, **LIGVYGSSV** and **VIYMVQLPI** (Table 3) the epitope-based peptide vaccines that include the B-cells and T-cells epitopes are well antigenic [38] and could be produced simply [39]. comparing our study with other studies predicted immunogenic epitope for the Design of Epitope-Based HMPV Vaccines (Rock et al., 2011) in terms of agreement MHC class 1 binding with 3 conventional alleles HLA-A*01:01, HLA-A*02:01, and with HLA-B*07:02 alleles using (BIMAS) bioinformatics analysis tool [40] Our finding for MHC 1 Peptides binds 17 alleles HLA-A*01:01, HLA-A*02:01, HLA-A*02:06, HLA-A*68:02, HLA-C*12:03, and HLAC*15:02,HLA-A*02:01, HLA-A*02:06, HLAC*03:03, HLA-C*05:01, HLA-C*12:30 and HLA-C*14:02, HLA-A*02:01, HLA-A*02:06, HLA-A*32:01, HLA-C*14:02, and HLA-C*15:02 (Table 2).

Moreover, the best MHC II peptides binds 8 with the alleles

HLADRB1*01:01, HLA-DRB4*01:01, HLA-DRB1*04:01, HLA-DRB1*11:01, HLADRB1*15:01, HLA-DRB1*04:05, HLA-DRB5*01:01 and HLA-DRB1*09:01,

(Table 3).

The predicted peptides for MHC I and MHC II have a highest population coverage. For MHC I, MHC II peptides the percentage were 99.52% , 81.94% , respectively and for MHC combined was 99.91% (Table 4).

Conclusion

The study led to the prediction of effective and safe epitope-based peptides vaccine against the HMPV using its Fusion Protein via the Immunoinformatics approach. The peptide **GSTVYYPN** was the best predicted B-cells epitopes. Moreover, the peptide **VIYMVQLPI** and the peptides **LIGVYGSSV, YTNVFTLEV** were the best-predicted T-cells epitopes that will interact effectively with the MHC I and MHC II molecules, respectively. Consequently, we recommend the use of them as combined multiple peptide vaccines. Also, experimental studies recommended to validate the results.

Methods

Retrieval of the targeted sequences

A total of 182 Human Metapneumovirus Fusion Protein sequences were obtained from the NCBI database [41] as the FASTA format in August 2018. The accession numbers of the obtained sequences with the area and date of the collection were listed in Table 6.

Table 6
*the retrieved Human Metapneumovirus Fusion Protein
sequences with their Accession number, Date and area of
Collection*

Accession number	Date of collection	country
YP_012608	2004	USA
BBB35016	2015	japan
BBB35015	2015	Japan
BBB35014	20/3/2015	Japan
BBB35013	2015-03-16"	Japan
BBB35012	2015-03-16"	Japan
BBB35011	2015-02-27	Japan
BBB35010	2015-02-21	Japan
BBB35009	2015-02-21	Japan
BBB35008	2015-02-21"	Japan
BBB35007.1	2014-04-12	Japan
BBB35006.1	2014-04-13"	Japan
BBB35005.1	2014-04-05	Japan
BBB35004.1	2013-07-08"	Japan
BBB35003.1	2013-06-22"	Japan
BBB35002.1	2013-06-24	Japan
BBB35001.1	2013-06-24	Japan
BBB35000.1	2013-04-30	Japan
BBB34999.1	2013-04-16	Japan
BBB34998.1	2013-04-08"	Japan
BBB34997.1	2013-03-25	Japan
BBB34996.1	2013-01-21	Japan
BBB34995.1	2015-03-02	Japan
BBB34994.1	2014-08-04	Japan

Accession number	Date of collection	country
BBB34992.1	2013-06-25	Japan
BBB34991.1	2013-06-24	Japan
BBB34990.1	2013-06-22	Japan
ANW38002.1	2011	Croatia
ANW38000.1	2013	Croatia
ANW37997.1	2012	Croatia
ANW37998.1	2012	Croatia"
ANW37996.1	2012	Croatia
ANW37993.1	2011	Croatia"
ANW37992.1	2011	Croatia"
ANW37991.1	2011	Croatia"
ANW37990.1	2011	Croatia
ANW37989.1	2011	Croatia
All17595.1	10-Aug-2011	South Korea

Determinant of the conserved regions

The obtained Sequences subjected to the multiple alignment tests via the CLUSTALW algorithm [42] on BioEdit software [43] version 7.0.9.1 to identify the conserved regions.

B-Cells Epitopes Prediction

The linear Epitope Prediction tool BepiPred-test on the Immune Epitope Database (IEDB) [44] (figure).

The epitopes were predicted at a default threshold value of (0.4) from the conserved region in the Human Metapneumovirus Fusion Protein sequences that obtained from the multiple sequences, alignment. The prediction performed using the Markov model [45]. The results listed in Table 1.

The Surface Accessibility Prediction

The Emini surface accessibility prediction tool [43] on the IEDB [46] used to predict the surface accessibility with a default threshold value for each conserved region (Fig. 9). The results are listed in Table 1.

The Antigenic Sites Prediction

The Kolaskar and Tongaonker antigenicity tool on IEDB [47] used for the prediction of the antigenic sites within the Human Metapneumovirus Fusion Protein sequences at a default threshold value of 1.04. The results listed in Table 1, (Fig. 10). For the whole first alignment, sequences see (Fig. 11).

T-Cell Epitopes Prediction

The prediction of the cytotoxic T-cell epitopes performed by using the Major Histocompatibility Complex class I (MHC I) binding prediction tool on IEDB [48]. The epitopes' length adjusted at 9. The conserved epitopes that bind with various HLA alleles at score equal or less than 1.0 percentile rank and 500 IC50 selected for further analysis. Moreover, the prediction of T-cell helper epitopes performed by using the Major Histocompatibility Complex class II (MHC II) binding prediction tool of IEDB [49]. The results listed in Table 3.

The Population Coverage Prediction

The prediction of epitopes binding with various MHC I and MHC II alleles that cover the world population was performed by using the population coverage tool on the IEDB [50]. The results are listed in Table 4.

The Peptides Allergicity and Toxicity Prediction

The AllergenFP v.1.0 [47] web servers used to predict the Allergenicity. Furthermore,

ToxinPred web server [48] used to predict the Toxicity. The results listed in Table 5.

The 3D Structure Modeling and Visualization

The 3D structure of the Human Metapneumovirus Fusion Protein modeled by using the Phyre2 web portal [49] and 3D structure the predicted peptides we modeled by using PEP-FOLD 3.5 web server [50]. The modeled 3D structures visualized by Chimera 1.8 software [51]. The results presented in Figs. 1, 2, and .

5 The Molecular Docking Study

The predicted epitopes were docked with MHC I and MHC II molecules. The Protein Databank [52] was used to obtain the 3D structures of MHC I and MHC II. The 3D structures (PDBIDs:

6AM5, 5TXS, and 5NI9 for MHC IA, MHC IB, and MHC II respectively) were downloaded in PDB format. The. The structures were prepared, minimized for the docking process, and the molecular docking calculation performed by using Cresset Flare software [53]. The results listed in Table 5 and showed in Figs. 4,5,6, and 7.

Declarations

Ethics approval and consent to participate

Not applicable

Consent for publication

Not applicable

Availability of data and materials

The datasets generated during and/or analyzed during the current study are available from the corresponding author on reasonable request.

Competing interests

The authors declare that having no conflict of interest.

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Authors' contributions

All authors contributed in this work as follows:

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Tables

Due to technical limitations, table 3 is only available as a download in the Supplemental Files section.

Figures

Figure 1

The position of predicted B -cells peptide GSTVYYPN (purple) on the 3D structure of human Metapneumovirus Fusion Protein

Figure 2

The position of predicted MHC I peptides (purple) on the 3D structure of human

Figure 3

The position of predicted MHC II peptides (purple) on the 3D structure of human Metapneumovirus Fusion Protein

Figure 4

The 3D interaction between the predicted peptide (violet) VIYMOVQLPI with MHC IA molecule

Figure 5

The 3D interaction between the predicted peptide VIYMOVQLPI (violet) with the MHC IB molecule

Figure 6

The 3D interaction between the predicted peptide LIGVYGSSV (violet) with the MHC II molecule

Figure 7

The 3D interaction between the predicted peptide VIYMVQLPI (violet) with MHC II molecule

Average: 0.553 Minimum: 0.259 Maximum: 0.653

Figure 8

Biperid linear prediction diagram, where green color referred to predicted peptides

Figure 9

Emini Surface Accessibility Prediction Results, where green color referred to predicted peptides.