

Table S1. The identification and evaluation of BCL epitopes.

Protein	Peptide	Position	Score	Antigenicity
HP0197	MKKEEVKTPSVQSNP	494-509	0.85	1.1755
	EEEYNAHLKQDEGKSI	153-168	0.91	1.0451
	PSVQSNPTLSHKGAPS	503-518	0.87	1.0259
	PAPIPDAPTPKVEEET	277-292	0.93	1.0125
	KAEDSAPKTAVPEVAP	392-407	0.86	0.9703
	APDAAPAPAPTPEVDP	231-246	0.89	0.8808
PepO	PGDNTIEEEYNAHLKQ	147-162	0.88	0.8736
	KENYDGTDEFSLKNQK	161-176	0.89	1.288
	SKLEVAPGYVNGEIS	538-553	0.85	0.8605
	LKRKDDQGQDGPIVNY	240-255	0.85	1.4914
	IGTGVSGGEKGALEGP	123-138	0.89	1.3547
	MKKEEVKTPSVQSNP	969-984	0.85	1.1755
6PGD	EEEYNAHLKQDEGKSI	628-643	0.91	1.0451
	PSVQSNPTLSHKGAPS	978-993	0.87	1.0259
	PAPIPDAPTPKVEEET	752-767	0.93	1.0125
	KAEDSAPKTAVPEVAP	867-882	0.86	0.9703
	AQLRVASKENNWNLPF	342-357	0.85	0.9185
	APDAAPAPAPTPEVDP	706-721	0.89	0.8808
	PGDNTIEEEYNAHLKQ	622-637	0.88	0.8736

Table S2. The identification and evaluation of CTL epitopes.

Protein	Peptide	Position	Allele	Antigenicity	Immunogenicity
HP0197	KERKVEEAL	420-428	HLA-B*40:01	0.9149	0.30758
	KAGKKVSVY	452-460	HLA-A*30:02	1.3846	0.30454
	DGKVVATNL	466-474	HLA-B*51:01	1.4692	0.44956
PepO	LVKGSLEMK	487-495	HLA-A*68:01	0.9083	0.30154
	ALVPNLPIA	237-245	HLA-A*02:01	1.5535	0.37921
	KERKVEEAL	895-903	HLA-B*40:01	0.9149	0.30758
6PGD	KAGKKVSVY	927-935	HLA-A*30:02	1.3846	0.30454
	QAGVPVPTF	417-425	HLA-A*32:01	1.0979	0.32054
	ESRGYSVAI	23-31	HLA-B*51:01	1.3704	0.40123

Table S3. The identification and evaluation of HTL epitopes.

Protein	Peptide	Position	Antigenicity	IL4	IL10	IFN γ
HP0197	ANKKFRYSIRKFKVG	4-18	0.8611	inducer	inducer	positive
	NDFKYQIKVENYIRQ	124-138	0.8205	inducer	inducer	positive
	IRKFKVGVGSVLIAT	12-26	0.4895	inducer	inducer	positive
PepO	VQEIKATYAERIKAV	359-373	0.7047	inducer	non-inducer	negative
	EVKALVPNLPIAELV	234-248	0.6247	inducer	inducer	positive
	KMRALKKLDLTVVKI	381-395	0.4739	inducer	non-inducer	negative
	IVNYIMDAAGNKGTG	252-266	1.0812	inducer	non-inducer	negative
6PGD	GVVGMAVMGRNLALN	7-21	0.6756	inducer	non-inducer	positive
	LLDEYFLDVTAKYQQ	392-406	0.6437	inducer	non-inducer	positive
	DSYLIEITADILKRK	229-243	0.5099	inducer	inducer	positive
	WRAGCIIRARFLQKI	364-378	0.4151	inducer	inducer	positive

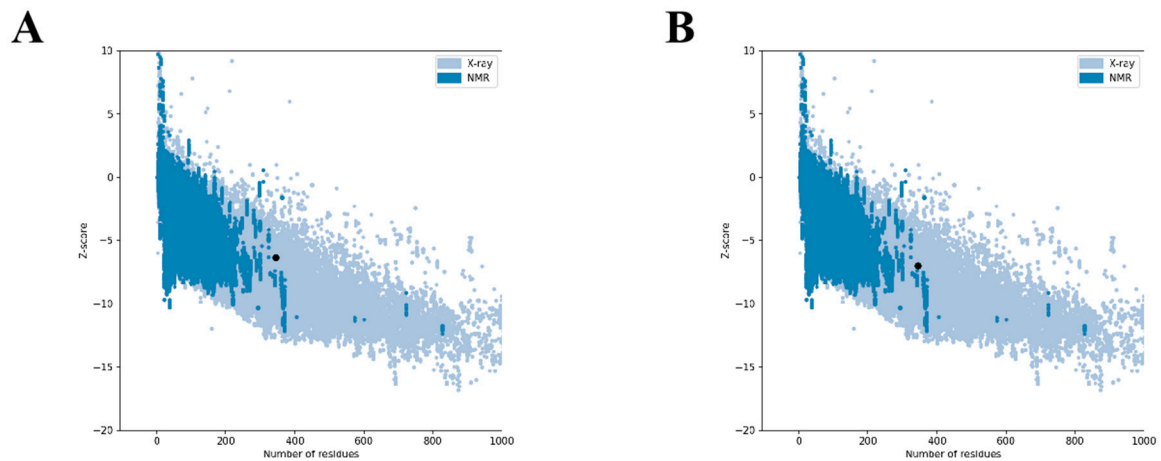


Figure S1. ProSA-web evaluation of the vaccine structure. ProSA-web results of the vaccine 3D structure before(A) and after (B) refined by GalaxyRefine. The value of Z-score was -6.36 and -7.01, respectively.

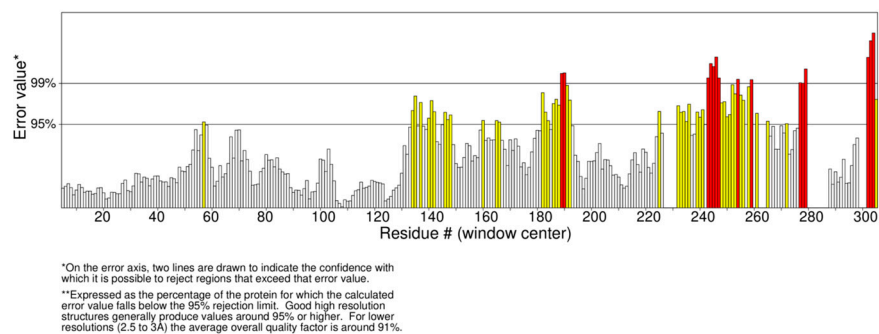


Figure S2. ERRAT error prediction. The quality of 3D model MVHP6 is 79.114.

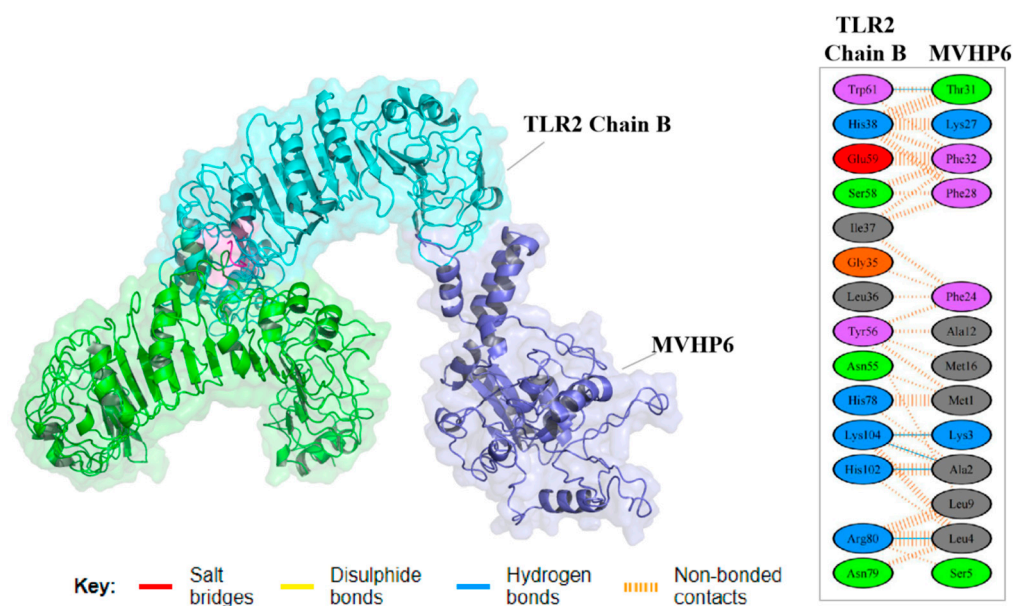


Figure S3. Residues of the interaction between docked MVHP6 and TLR2.

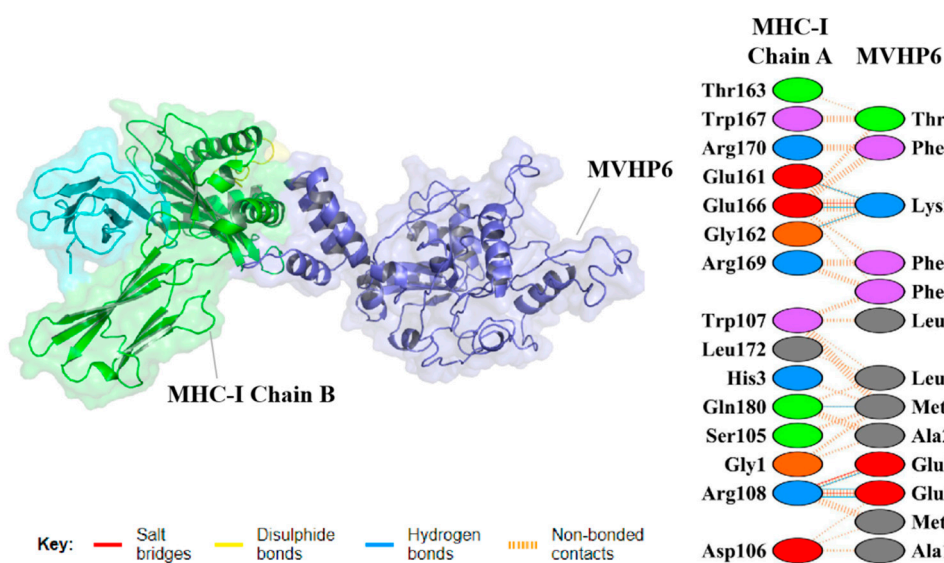


Figure S4. Residues of the interaction between docked MVHP6 and MHC I.

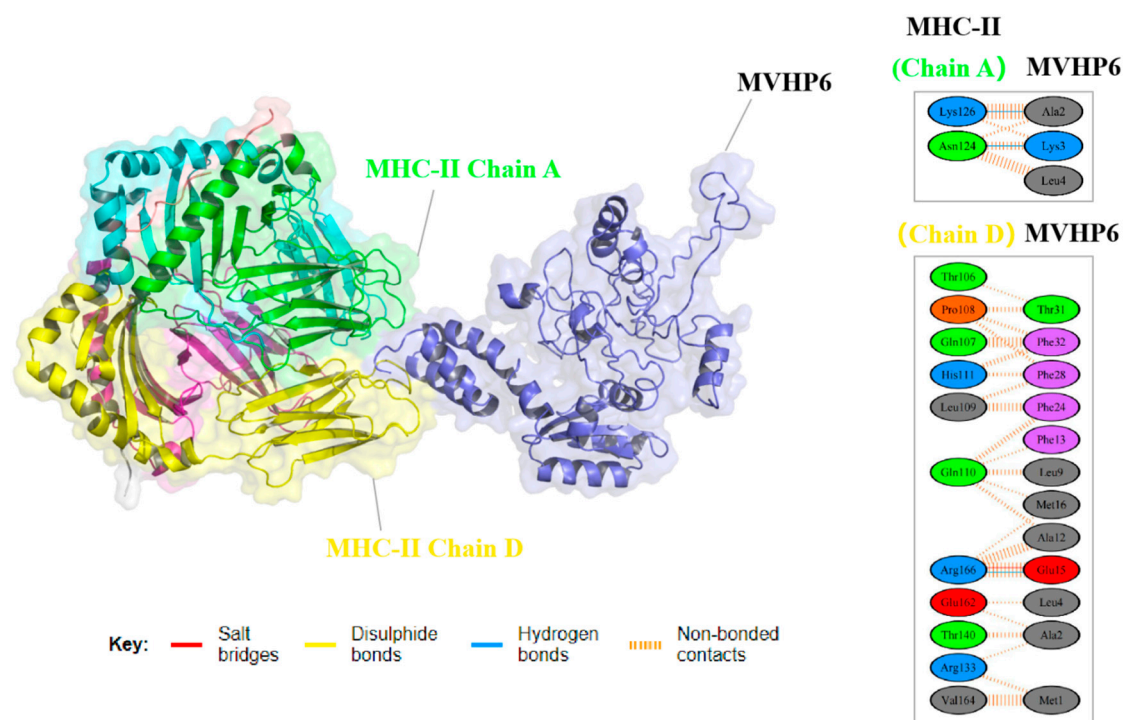


Figure S5. Residues of the interaction between docked MVHP6 and MHC II.