

Supplementary Material

Table S1. B cell epitopes identified with the IMED server of PE_PGRS49 and PE_PGRS56 proteins

Protein	Ubication	Sequence
PE_PGRS49	14-20	HGGPATN
	58-73	GSFGATSGPASIGVTG
	109-120	GSIGANSGIVGG
	132-138	GNGSLSS
	154-162	VGGNSSVTQ
	175-182	GGSGFFGG
	197-206	GGGTVGTVAG
	209-215	GNGGVGG
	217-225	GGDGVFAGA
	227-233	GQGGLGG
	276-284	GGGTQSATG
	301-307	SGAKAGG
PE_PGRS56	12-18	GDGGVGG
	26-34	NTTTAAAGT
	37-43	GAGGAGG
	81-91	GDGALAGSSGG
	101-113	DAGKAGTGSAPGT
	126-144	GGIGAAGTTGPVGTGASGG
	161-169	ANGGTAGAG
	181-190	GGAGVTSSTA
	204-219	GDAGAGGAGATPGANG
	228-242	GDGAAGAVGISGATG
	262-273	GAGGSGIDGVGG
	284-294	NGAIGGAGGDA
	314-320	GAGGAAG
	322-328	NGGTVGA
	339-346	GAAGAATA
	376-382	GIGGVGG
	389-401	ADGEVGGAGGAGG
	419-432	GSGGAGGAAGAGGA
	452-461	GGAGAASSAT
	488-495	GTGGAAGD
	500-516	GQGGAGGGAGGQGGAGG
	531-537	TAGTAGA
	576-589	GDRTVGGGTVPAGS
	600-609	GAGGQGGADG
	751-757	GDGGLTG
	783-789	NMTAQAG
	800-815	FGGGAGAGGGGLTAGA
	829-841	GNGAIGGHGPLTD
	859-868	GGAGIGSLGG
	885-891	EGGEVGG
	925-936	GTGGLGDPRVGG
	984-998	DAEPGVPPGAGGAGG
	1052-1060	DGGKAPAGG

Table S2. T cell epitopes identified with the Rankpep and Propred I servers of PE_PGRS49 and PE_PGRS56 proteins

Alleles	Epitopes sequence	
	PE_PGRS49	PE_PGRS56
<i>HLA-A0101</i>	(18-26) ATNPGSGSR (320-328) GTEPGFGGD (63-71) TSGPASIGV	
<i>HLA_A0201</i>	(110-118) SIGANSIV	(832-839) AIGGHGPL.
<i>HLA_A0301</i>	(135-143) SLSSGEGGK	
<i>HLA_A2402</i>	(178-186) GFFGGKGGF (128-136) GGAGGNGSL (223-231) AGAGGQGGL (240-248) GSTGGNGGL	
<i>HLA*B0702</i>		
<i>HLA_B0801</i>		
<i>HLA_B1501</i>		
<i>HLA*B3901</i>	(128-136) GGAGGNGSL (223-231) AGAGGQGGL (240-248) GSTGGNGGL (277-285) GGTQSATGL	
<i>HLA_B5801</i>	(63-71) TSGPASIGV (52-60) GGNGGDGSF (109-117) GSIGANSI (171-179) AGGAGGSGF	
<i>DRB1*0101</i>		(781-789) TANMTAQAG (1037-1045) WNGGKGDTG (694-702) IAGMGNGG (811-819) LTAGANGTG (527-535) ITGGTAGTA
<i>DRB1*0301</i>		(29-37) TAAAGTTGG (208-216) AGGAGATPG (579-587) TVGGGTVPA (159-167) GAANGGTAG (339-347) GAAGAATAG (780-788) NTANMTAGA (433-441) GGGANGTAG (996-1004) AGGAGTTGG (102-110) AGKAGTGSA (325-333) TVGANGTGG (104-112) KAGTGSAPG (22-30) NGADNTTTA (128-136) IGAAGTTGP (51-59) GGAAGTGTG (537-545) AAGNGGAAG (812-820) TAGANGTGG
<i>DRB1*0401</i>	(222-230) FAGAGGQGG (302-310) GAKAGGAGG (274-282) GIGGGTQSA (262-270) GFGGNGGKG (278-286) GTQSATGLG (225-233) AGGQGGGLG (179-187) FFGGKGGFG	

<i>DRB1*0701</i>		(333-GGAAGAATA
<i>DRB1*0801</i>		
<i>DRB1*1101</i>	(263-271) FGGNGGKGG (111-119) IGANSGIVG	(1036-1044) GWNGGKGD (645-653) GGANGGAGG (585-593) VPAGSGGQG (1034-1042) GTAWNGGKG
<i>DRB1*1301</i>		
<i>DRB1*1501</i>	(177-185) SGFFGGKGG	

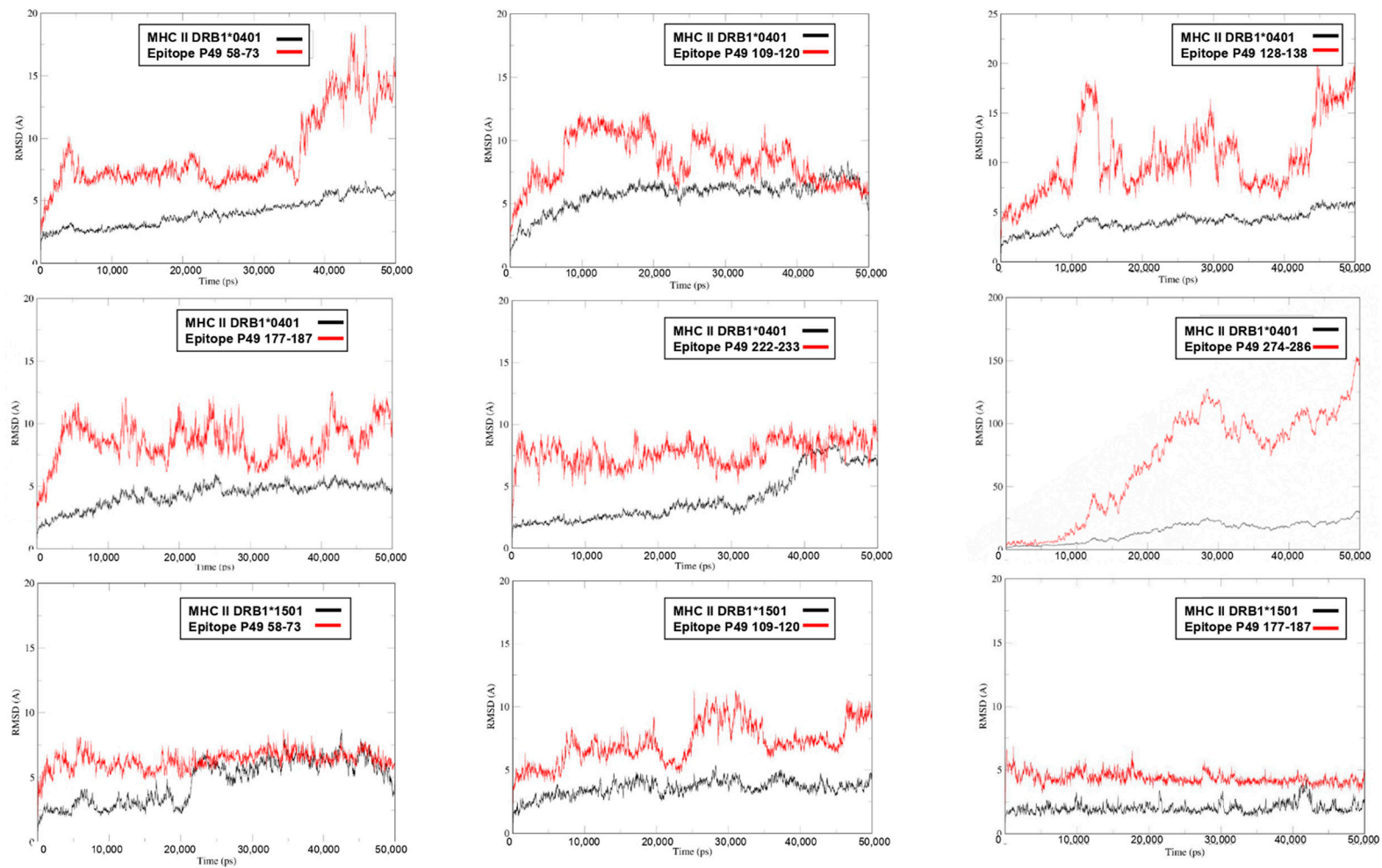


Figure S1. Molecular dynamics simulation of the epitope-receptor complex. The plots are showing the RMSD (X-axis = time in Frame and Y-axis = RMSD) of the epitopes PE_PGRS49 (red) and DRB1*0401 or DRB1*1501 (black). The most stable interaction is shown between the 222-233 and 177-187 epitope complex with DRB1*0401, The most stable interaction is shown between the 177-187 epitope complex with DRB1*1501.

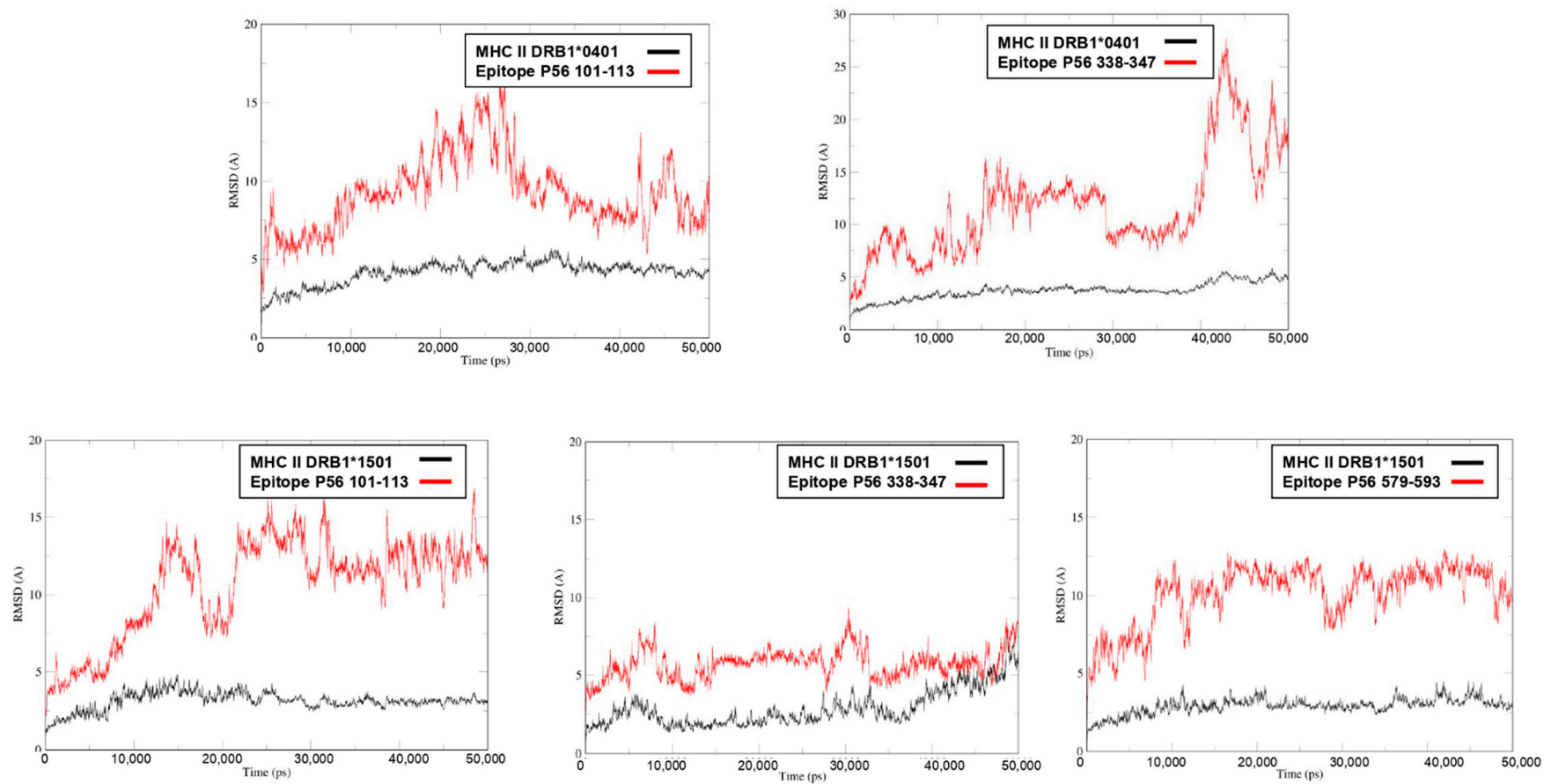
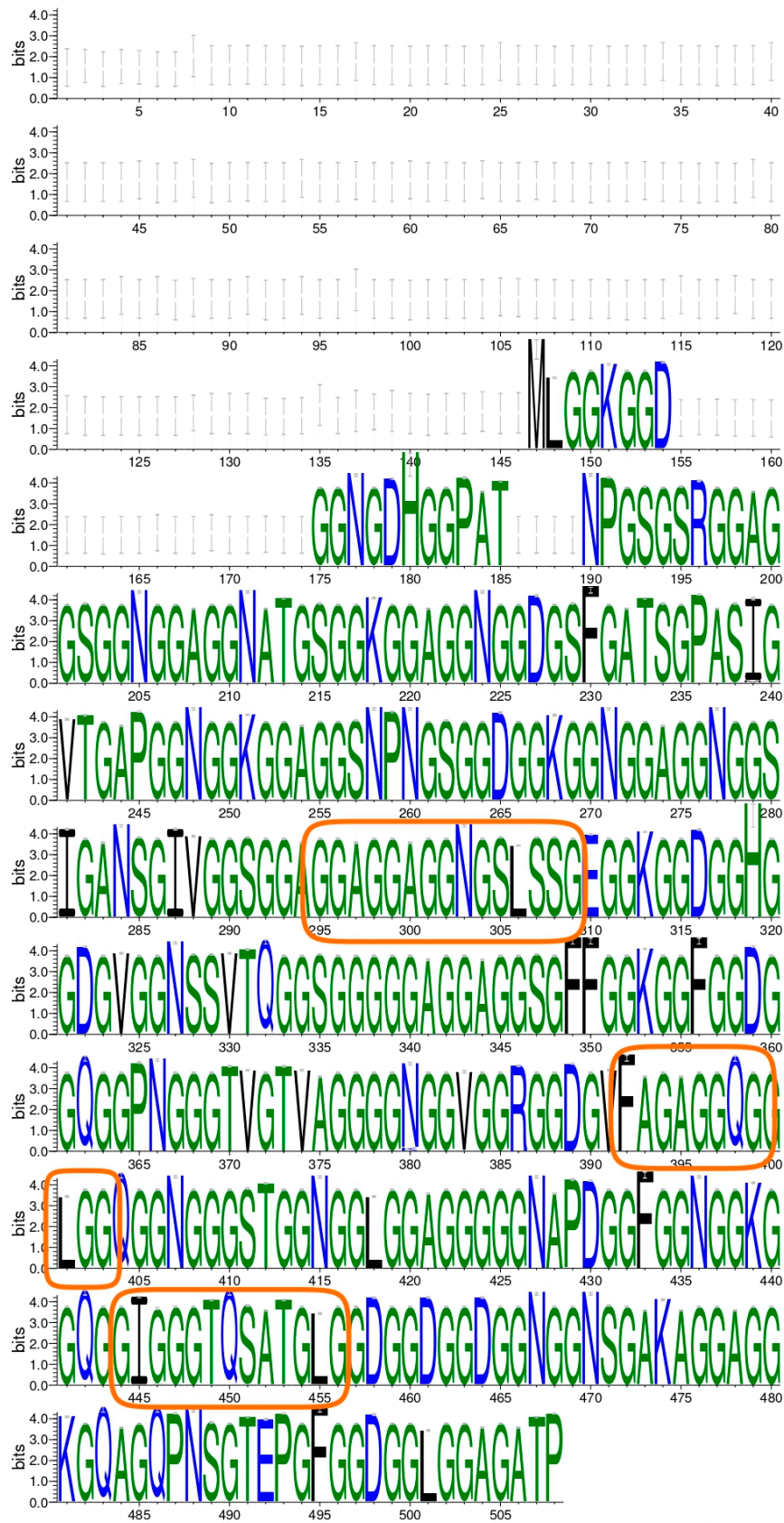


Figure S2. Molecular dynamics simulation of the epitope-receptor complex. The plots are showing the RMSD (X-axis = time in Frame and Y-axis = RMSD) of the epitopes (red) PE:PGRS56 and DRB1*1501 or DRB1*1501 (black). The most stable interaction is shown between the 338-347 epitope complex with DRB1*1501 and 579-593 epitope-DRB1*1501 showed an unstable interaction.



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Figure S3. Graphic representation of the sequence alignment of the PE-PGRS49 protein. The red boxes indicate the location of the selected epitopes, all of which are in conserved regions.

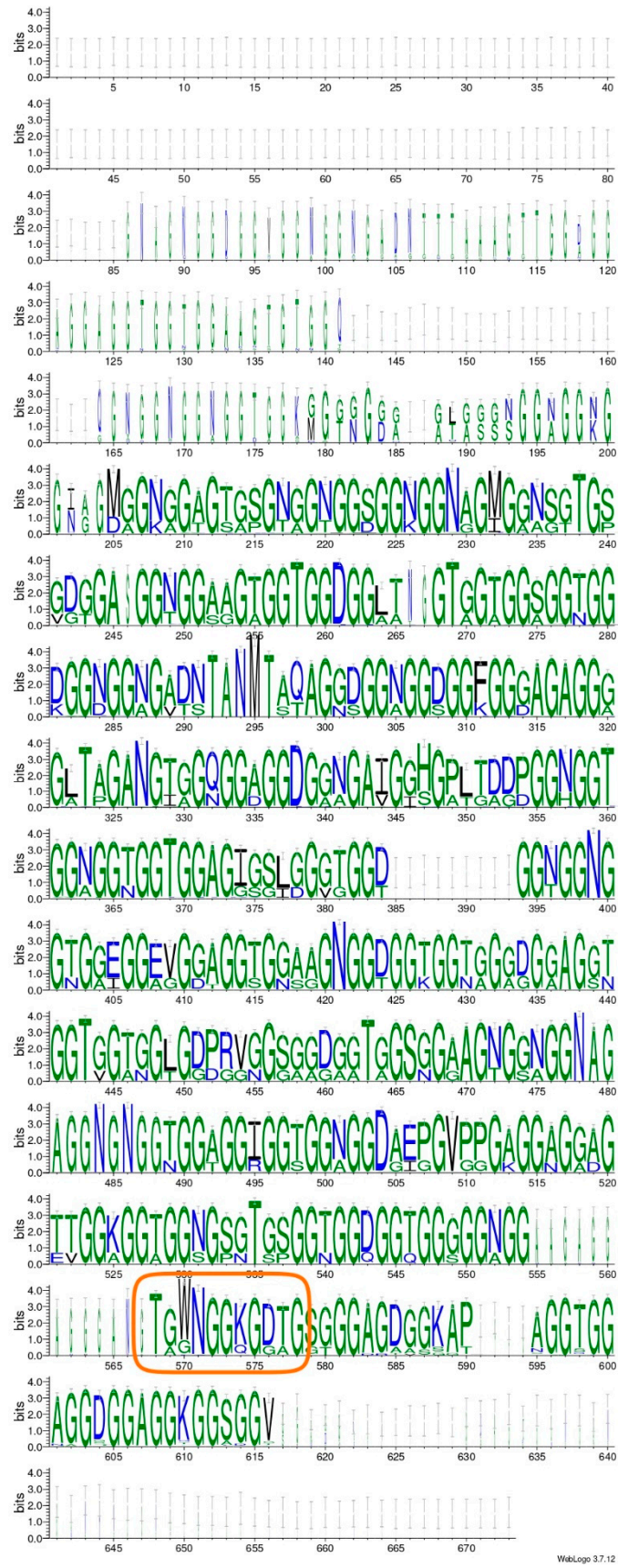


Figure S4. Graphic representation of the sequence alignment of the PE-PGRS56 protein. The red boxes indicate the location of the selected epitope, which is found in a conserved region.