

Supplementary materials for the manuscript:

Antigenic Peptide Molecular Recognition by DRB1 - DQB1 Haplotype modulates
Multiple Sclerosis Susceptibility

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Table S1. In (A) is shown, non conserved binding site residue positions in the two DQB1 alleles. In (B) is shown the non conserved binding site residue positions in the two DRB1 alleles. In (C) is shown the amino acid sequence of the two peptides under investigation. Single letter code is used for the amino acid description.

(A)

| DQB1 | 9 | 14 | 26 | 30 | 38 | 57 | 71 | 74 | 75 | 77 | 87 |
|--------|---|----|----|----|----|----|----|----|----|----|----|
| *06:02 | F | M | L | Y | A | D | T | E | L | T | F |
| *05:02 | Y | L | G | H | V | S | A | S | V | R | Y |

(B)

| DRB1 | 47 | 67 | 70 | 71 | 86 |
|--------|----|----|----|----|----|
| *15:01 | F | I | Q | A | V |
| *16:01 | Y | F | D | R | G |

(C)

| | | | | | | | | | | | | | | |
|---------------|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| MBP-85-98 | E | N | P | V | V | H | F | F | K | N | I | V | T | P |
| EBNA1-400-413 | P | G | R | R | P | F | F | H | P | V | G | E | A | D |

Table S2. RMSD of C-alpha atoms in binding cleft. The table reports root mean square deviation (RMSD) average value obtained from 100 ns of MD simulation for the both DQB1 in wild type (WT) and mutant alleles (V38A/A38V) for free and bound peptide complexes. The error represents standard deviation error from the mean value of RMSD obtained from MD simulation.

| RMSD (in Å) | DQB1*05:02 | | DQB1*06:02 | |
|----------------|------------|---------|------------|---------|
| | WT | V38A | WT | A38V |
| MBP | 1.6 ±0.2 | 1.3±0.2 | 1.5 ±0.3 | 1.4±0.2 |
| EBNA-1 | 1.7±0.4 | 1.8±0.3 | 1.5 ±0.2 | 1.7±0.3 |
| FREE | 2.2 ±0.3 | - | 1.9 ±0.3 | - |

Fig. S1. Binding cleft width distribution for region D2 and D3 of DQB1 protective allele (DQB1*05:02) in free and bound peptide complexes.

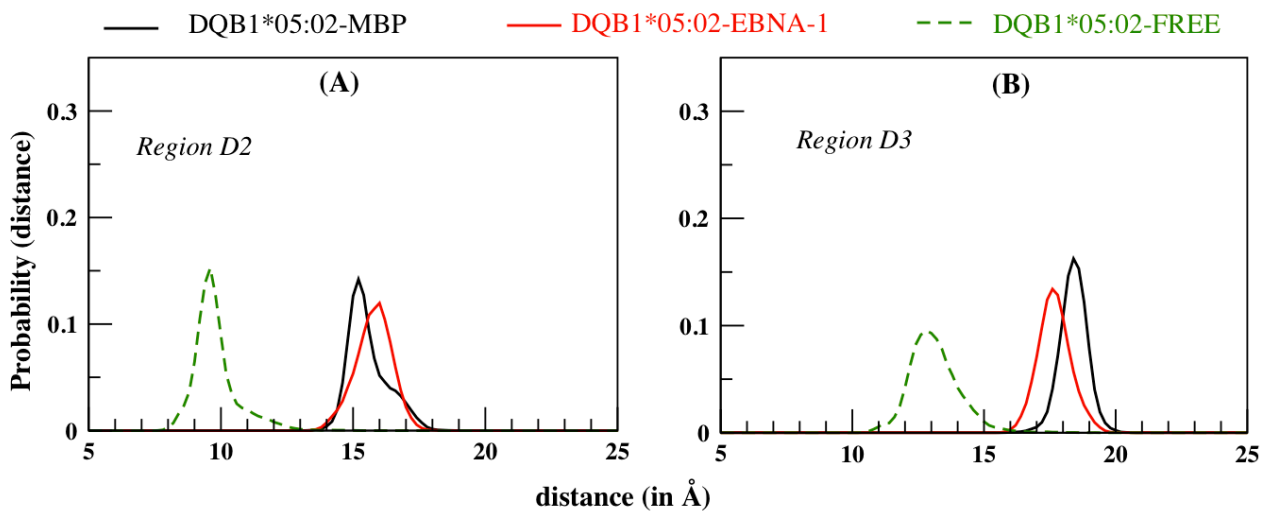


Fig. S2. Binding cleft width distribution for region D2 and D3 of DQB1 predisposing allele (DQB1*06:02) in free and bound peptide complexes.

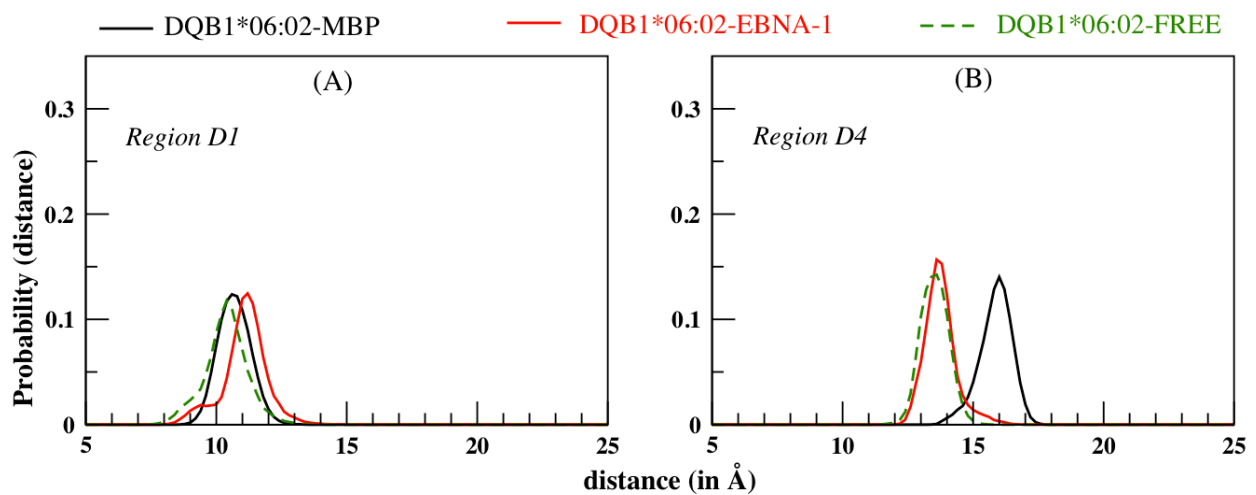


Fig. S3. Binding cleft width distribution for region D4 of DQB1 predisposing and mutant A38V allele complexed to MBP and EBNA-1 peptide.

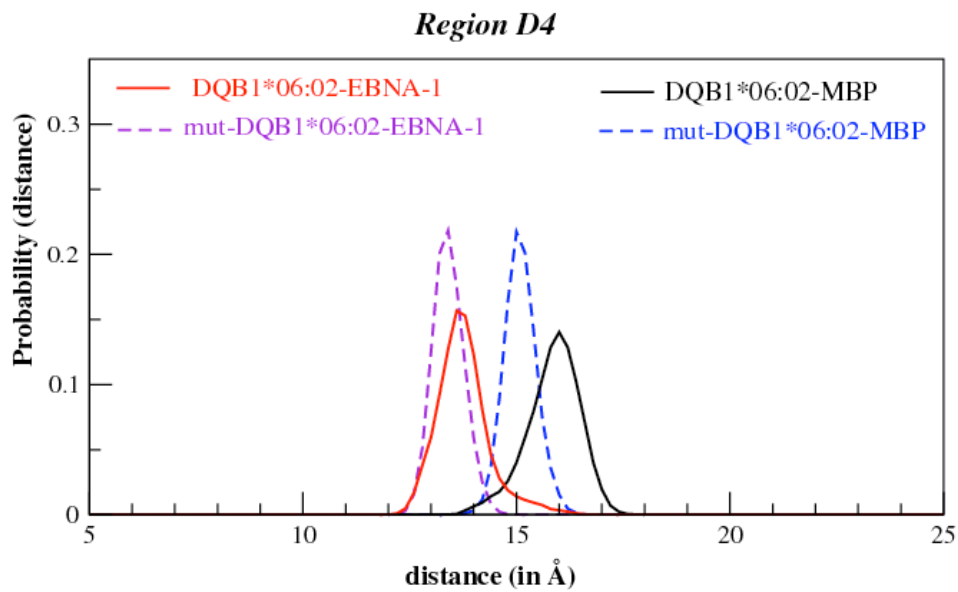


Fig. S4. Binding cleft width distribution of DR2 protective and mutant G86V allele complexed to MBP.

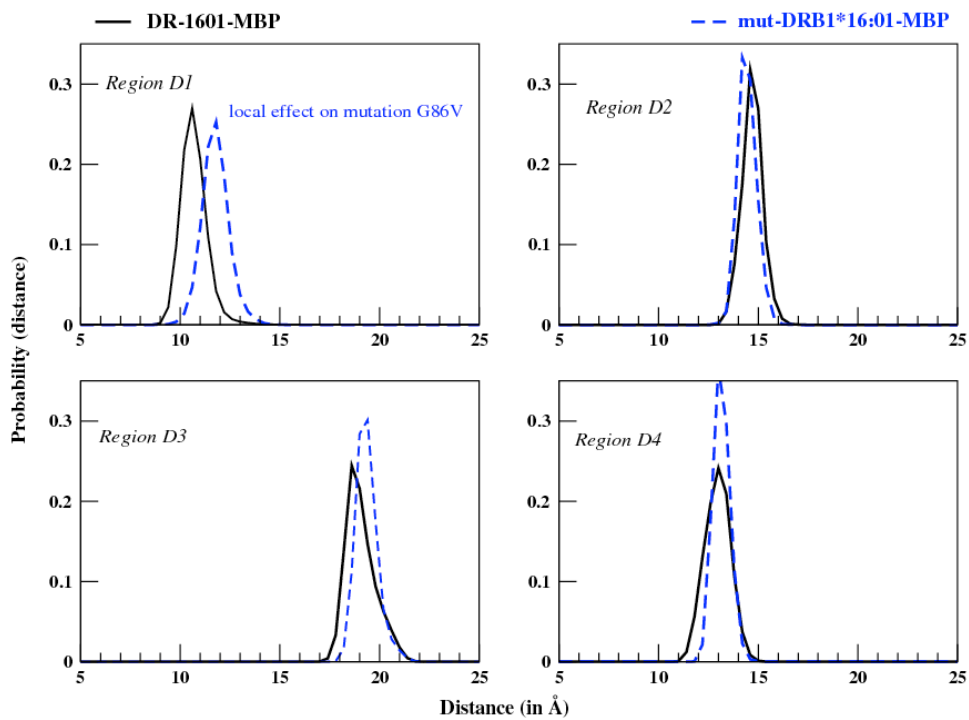


Fig. S5 RMSD plot of C-alpha atoms in peptide binding cleft for (A) DQB1*05:02 allele in wild type and mutant pMHC complexes. In (B) DQB1*06:02 allele in wild type and mutant pMHC complexes.

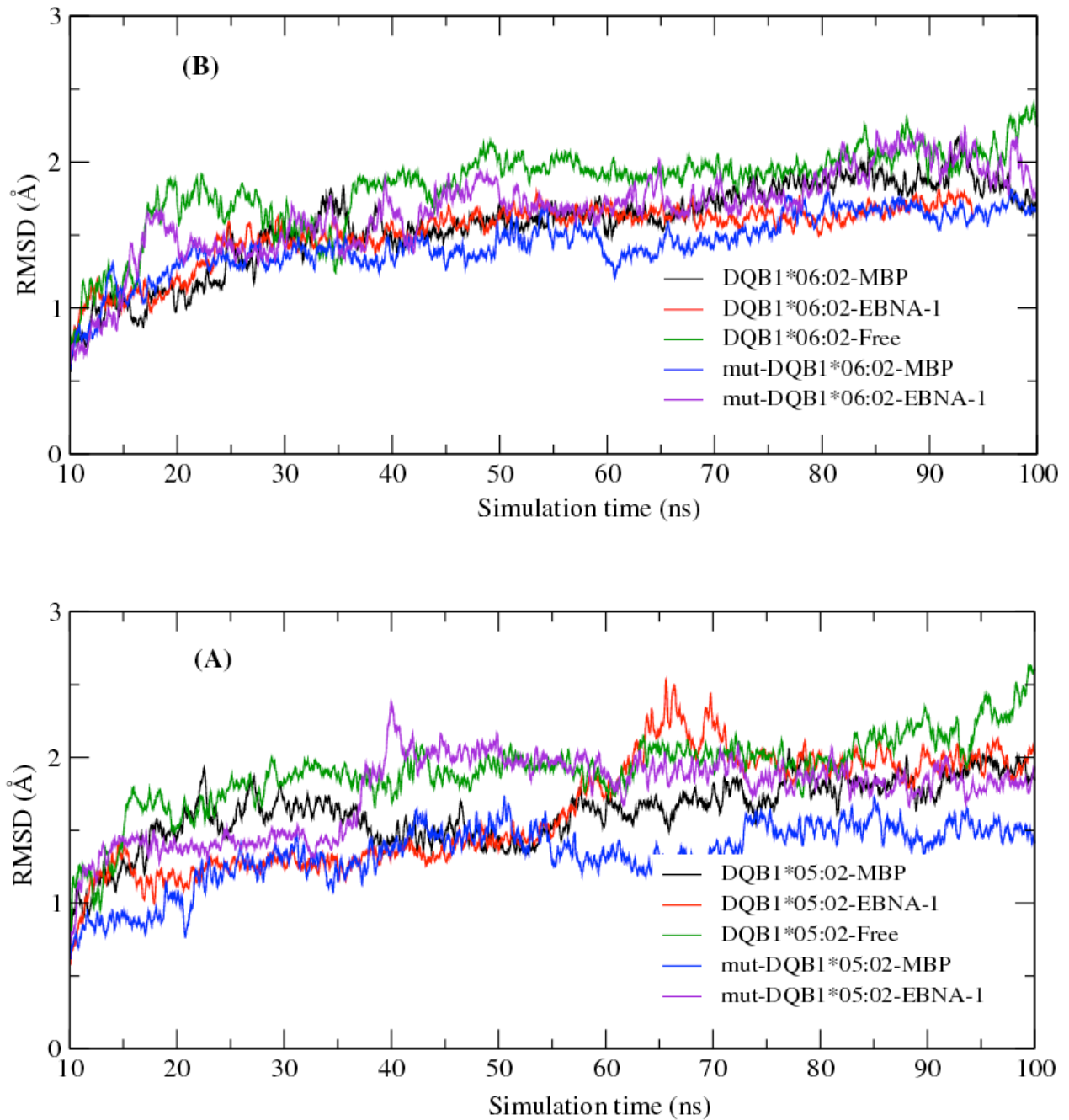


Fig. S6. Root mean square fluctuations (RMSF) of C-alpha atoms of $\beta 1$ chain binding site residues of DQB1 protective allele and mutant (V38A) in free and peptide bound complexes.

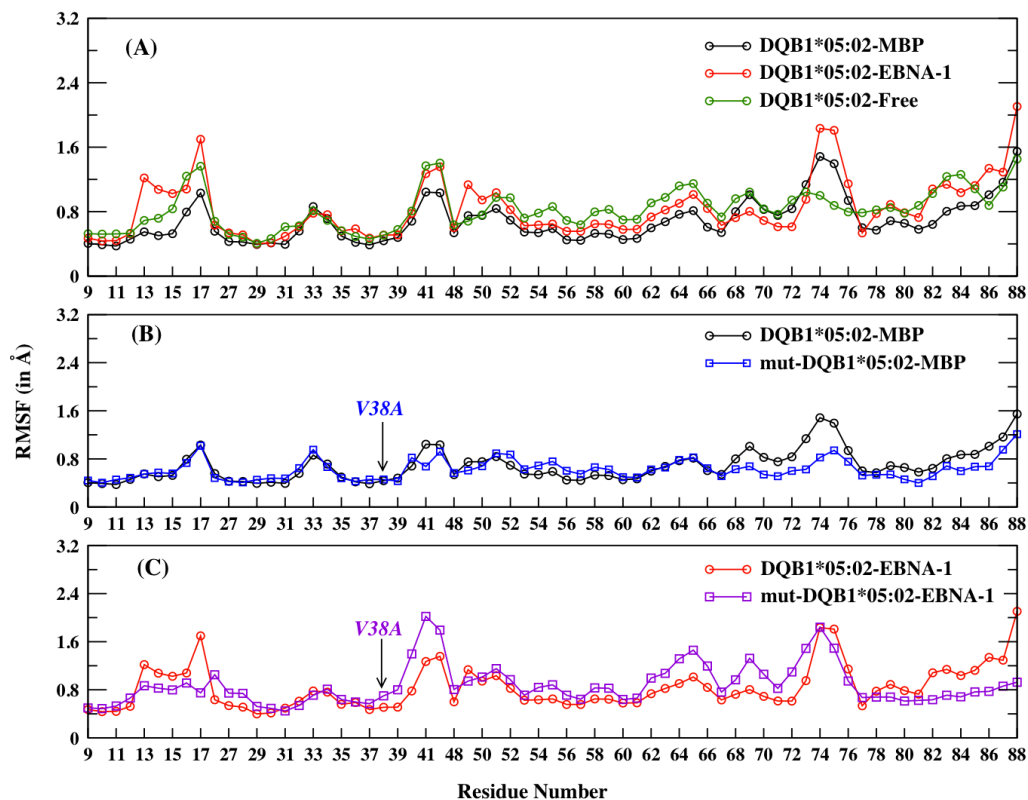


Fig. S7. RMSF of C-alpha atoms of $\beta 1$ chain binding site residues of DQB1 predisposing and mutant (A38V) allele in free and peptide bound complexes.

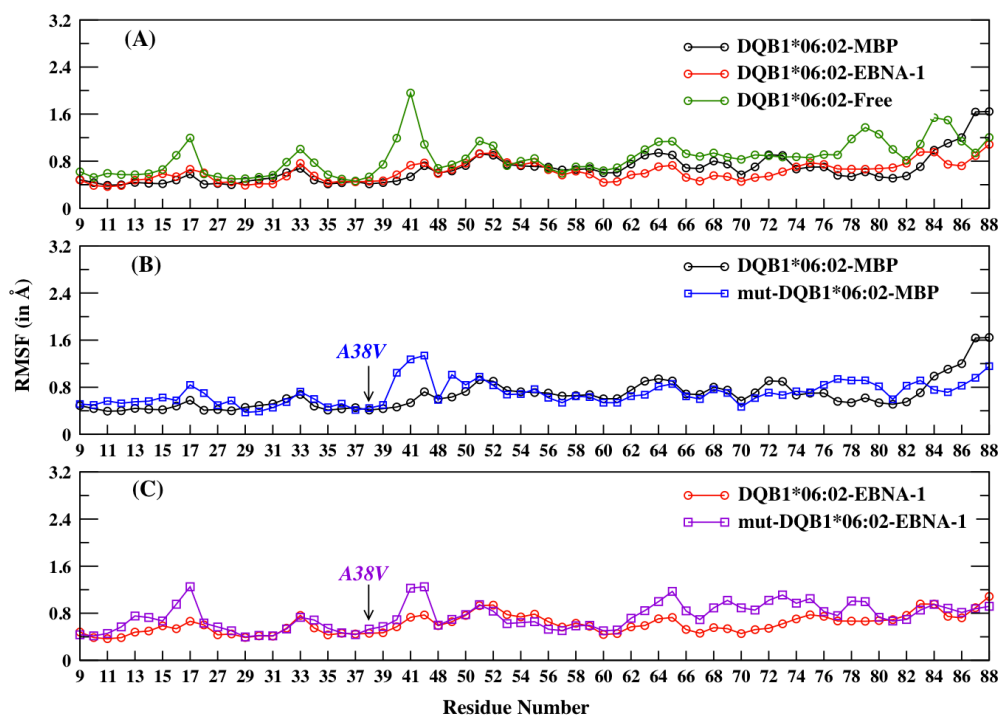


Fig. S8. RMSF of C-alpha atoms of $\beta 1$ chain binding site residues of DRB1 protective and mutant (G86V) allele in free and peptide bound complexes.

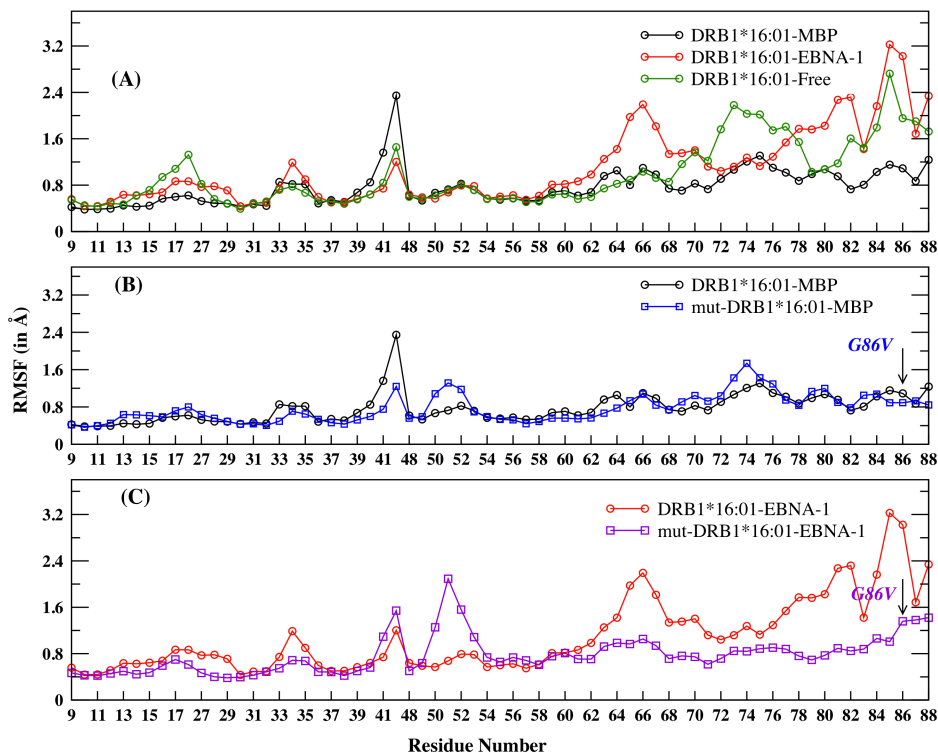


Fig. S9. RMSF of C-alpha atoms of $\beta 1$ chain binding site residues of DRB1 predisposing and mutant (V86G) allele in free and peptide bound complexes.

