

HLA-B*27:05	<sup>1</sup> GSHSMRYF <b>H</b> TSVSRPGRGEPRFIT <b>T</b> VG YVDDT <b>L</b> FVRFDSDA <b>A</b> SPRE <b>E</b> PRAPW <b>I</b> EQEGPEYW	
Mamu-B*008:01	----- <b>S</b> ----- <b>S</b> ----- <b>Q</b> ----- <b>E</b> ----- <b>M</b> -----	
HLA-B*27:05	<sup>61</sup> <b>D</b> RE <b>T</b> <b>Q</b> <b>I</b> <b>C</b> <b>K</b> <b>A</b> <b>K</b> AQT <b>D</b> RE <b>D</b> L <b>R</b> <b>T</b> <b>L</b> <b>L</b> <b>R</b> <b>Y</b> YNQSEAGSHT <b>L</b> <b>Q</b> <b>N</b> <b>M</b> <b>Y</b> GCD <b>V</b> GPDGRLLRGY <b>H</b> <b>Q</b> <b>D</b> AYDG	
Mamu-B*008:01	<b>E</b> <b>E</b> ----- <b>R</b> <b>R</b> <b>A</b> ----- <b>G</b> <b>H</b> ----- <b>A</b> ----- <b>G</b> ----- <b>R</b> <b>G</b> ----- <b>T</b> ----- <b>L</b> ----- <b>Y</b> -----	
HLA-B*27:05	<sup>121</sup> K <b>D</b> <b>Y</b> <b>I</b> ALNEDL <b>S</b> <b>S</b> <b>W</b> TAAD <b>T</b> AAQIT <b>T</b> QR <b>K</b> <b>W</b> EAAR <b>V</b> AE <b>Q</b> L <b>R</b> AYLE <b>G</b> <b>E</b> CV <b>E</b> WLRRLRYLENGKETLQ	
Mamu-B*008:01	----- <b>F</b> ----- <b>R</b> ----- <b>V</b> ----- <b>T</b> ----- <b>E</b> ----- <b>V</b> ----- <b>T</b> -----	
HLA-B*27:05	<sup>181</sup> RADPPKTHVTHHP <b>I</b> SDHEATLRCWALGFYPAEITLTWQ <b>R</b> DGEDQTQDTEL <b>V</b> ETRP <b>A</b> GD <b>R</b> <b>T</b>	
Mamu-B*008:01	----- <b>V</b> ----- <b>G</b> ----- <b>G</b> -----	
HLA-B*27:05	<sup>241</sup> F <b>Q</b> <b>K</b> <b>W</b> <b>A</b> AVVVPSGEEQRYTCHVQHEGLP <b>K</b> PLTLRWEPS <b>S</b> QST <b>V</b> PIVGIVAGLAVL <b>A</b> <b>V</b> <b>V</b> <b>V</b> IG	
Mamu-B*008:01	----- <b>G</b> ----- <b>E</b> ----- <b>I</b> ----- <b>G</b> <b>A</b> ----- <b>F</b> -----	
HLA-B*27:05	<sup>301</sup> AVVAAVM <b>C</b> RRKSSGGKGGSYSQA <b>A</b> <b>C</b> <b>S</b> DSAQGS <b>D</b> VSLTA	
Mamu-B*008:01	----- <b>W</b> ----- <b>S</b> <b>N</b> -----	
		 <b>B pocket</b>  <b>F pocket</b>

**Supplemental data S1: Alignment of the mature protein sequences of HLA-B\*27:05 and Mamu-B\*008:01.** Conserved residues are represented by dashes in the Mamu-B\*008:01 sequence. Polymorphic positions are indicated in bold type. The  $\alpha_1$  and  $\alpha_2$  domains that form the peptide binding groove encompass residues 1-180. Residues that belong to the B or the F pocket are highlighted in blue or red, respectively.