Table 3. Synthetic Peptides Tested for Recognition by T Cells against DT Melanoma Antigens

RANK	ANTIGENS							
	gp100/B7$^{(a)}$	Tyr/A26$^{(a)}$	Tyr/B38$^{(b)}$	GPNMB$^{\text{mut.}}$/A3$^{(a)}$	SNRP116$^{\text{mut.}}$/A3$^{(a)}$	RBAF600$^{\text{mut.}}$/B7$^{(a)}$	SIRT2$^{\text{mut.}}$/A3$^{(a)}$	SNRPD1$^{\text{mut.}}$/B38$^{(b)}$
1	LPSPACQLV	DRESWPSVF	HHAFVDSIF	TL**D**WLLQTPK	ILDAVVAQ**K**	**R**PHVPESAF	KIFSEVT**L**K	SHETV**I**IEL
2	AQRLCQPVL	RTCQCSGNF	LHHAFVDSI	TLGWLLQTPK	KILDAVVAQ**K**	GPHVPESAF	KIFSEVTPK	SHETVTIEL
3	QPVLPSPAC	SVFYNRTCQ	LHHAFVDSIF	TL**D**WLLQTP	ILDAVVAQE	**R**PHVPESAFA		
4	GCQPPAQRL	ESWPSVFYN		TLGWLLQTP	KILDAVVAQE	GPHVPESAFA		
5	QPPAQRLCQ	CTERRLLVR		L**D**WLLQTPK				
6	PSPACQLVL	GVDDRESWP		LGWLLQTPK				
7	SPGCQPPAQ	DDRESWPSV		HTL**D**WLLQTP				
8	VLPSPACQL	QCSGNFMGF						
9	SPACQLVLH	CQCSGNFMGF						
10	KGGSGTYCL	GFNCGNCKF						
11	GTYCLNVSL	FTGVDDRES						
12	VSLADTNSL	CQCSGNFMG						
13	SLAVVSTQL	CSGNFMGFN						
14	SSPGCQPPA$^{(c)}$	CSGNFMGFNC						
15	CQLVLHQIL							
16	AVVSTQLIM							
17	ISSPGCQPP							
18	SSPGCQPPAQ							
19	PGCQPPAQR							

Peptides encoded by positive cDNA fragments (for gp100, Tyr/A26 and Tyr/B38) or from the protein regions around mutated residues were ranked according to public peptide prediction algorithms [(a) SYFPEITHI (http://www.syfpeithi.de/), (b) BIMAS (http://thr.cit.nih.gov/molbio/hla_bind/)] and then synthesized and tested for T cell recognition.

white : peptides not recognized at concentrations up to 100 µM;

red : peptides recognized at concentrations below 100 nM; (c) peptide induced half-maximal lysis by independently generated CTL clones against gp100/B7 at concentrations of 0.1 to 1.0 µM only (see **Table 1** and online supplemental **Fig. 8**);

green : overlapping peptides recognized at higher concentrations than optimum peptides;

red characters indicate mutated residues.