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Corrigendum

Identification of SOX2 as a novel glioma-associated antigen and potential target for T cell-based immunotherapy

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In the abstract of the above paper, a peptide with correct sequence (TLMKKDKYTL) is mentioned. This sequence should also appear in Table 1 as the sequence of peptide 60031. Unfortunately, an incorrect sequence (ALSPASSRSV) was included in Table 1 (all other data in the respective line of the table are correct and refer to peptide TLMKKDKYTL).

The corrected Table 1 is shown below.

Table 1 Prediction of HLA-A*0201-restricted SOX2-derived peptides and determination of binding affinities by a competition assay

Peptide	Position[a]	Sequence	MW	Length[b]	Score	rBA (%)[c]
60029	275–283	SMYLPGAEV	965.5	9	26	97.2
60030	131–139	LLAPGGNSM	858.4	9	25	80.0
60031	118–127	TLMKKDKYTL	1239.7	10	24	43.3

MW = molecular weight; rBA = relative binding affinity. [a]The given numbers indicate the position of the peptide in the amino-acid sequence of SOX2. [b]Number of amino acids. [c]The relative binding affinities were determined by comparing the inhibition of the reporter peptide binding by the analysed peptides in relation to the inhibition obtained with a positive control peptide, which was set as 100%. The positive control peptide was YLLPAIVHI from RNA helicase p72 and the reporter peptide was ILK(FITC)EPVHGV from HIV-1 reverse transcriptase. All peptides were used at a concentration of 10 μM.