SUPPLEMENTAL FIGURE LEGENDS

Figure S1. VACV infection of the RMA-HLA-A*0201 cell line in presence of different protease inhibitors.

RMA-HLA-A*0201 target cells infected for 16 hr with VACV at a multiplicity of infection of 40 plaque-forming units/cell were treated with the indicated inhibitors. A mock infected control was included as negative control. The cells were stained with the Omnitope antiserum-FITC that recognizes VACV purified virions. Samples were analyzed by FACS. The results, calculated as fluorescence index ± SD, are the mean of 4 independent experiments. The fluorescence index was calculated as the ratio of mean channel fluorescence of the sample to that of the control incubated without VACV. All VACV-infected conditions (with and without inhibitors) show significant P values ($P < 0.01$) versus mock infected controls. In contrast, all inhibitor conditions show non significant P values versus VACV-infected control without an inhibitor.

Figure S2. Identification of three HLA-A*0201 ligands in infected cell extracts by mass spectrometry.

MS/MS fragmentation spectra obtained from quadrupole ion trap mass spectrometry of the ion peaks at *m/z* 926.4 (upper left panel), *m/z* 974.6 (medium left panel), and *m/z* 514.8 (lower left panel) from the VACV-infected cell extract and the corresponding synthetic peptide (right panels). The vertical axis represents the relative abundance of the parental ion and each fragmentation ion detected. The horizontal axis corresponds to the m/z region in which significant daughter ions were detected. Ions generated by the fragmentation are detailed, and the sequence deduced from the indicated fragments is shown in the upper left box of each panel.

Figure S3. Identification of three HLA-B27 ligands in infected cell extracts by mass spectrometry.

MS/MS fragmentation spectra obtained from quadrupole ion trap mass spectrometry of the ion peaks at *m/z* 428.2 (upper left panel), *m/z* 567.6 (medium left panel), and *m/z* 472.1 (lower left panel) from the VACV-infected cell extract and the corresponding synthetic peptide (right panels). The axes are as described in Figure S1.

Figure S4. Identification of three HLA ligands in infected cell extracts by mass spectrometry (I).

MS/MS fragmentation spectra obtained from quadrupole ion trap mass spectrometry of the ion peaks at *m/z* 594.4 (upper left panel), *m/z* 803.5 (medium left panel), and *m/z* 926.5 (lower left panel) from the VACV-infected cell extract and the corresponding synthetic peptide (right panels). The axes are as described in Figure S1.

Figure S5. Identification of three HLA ligands in infected cell extracts by mass spectrometry (II).

MS/MS fragmentation spectra obtained from quadrupole ion trap mass spectrometry of the ion peaks at *m/z* 843.5 (upper left panel), *m/z* 833.9 (medium left panel), and *m/z* 851.0 (lower left panel) from the VACV-infected cell extract and the corresponding synthetic peptide (right panels). The axes are as described in Figure S1.