Readme.Sequencing and SPR Data

Sequencing

Full plasmid sequences are for HLA-A2 and TIL 1383I α and TIL 1383I β chains are contained within the SnapGene DNA files. These can be visualized using either SnapGene viewer or the full version of the SnapGene application. Sanger sequencing analysis for each mutation in HLA-A2 and TIL 1383I are provided as both chromatograms (Applied Biosystems Sequence Trace) as well as text files containing the nucleotide sequences only. The Applied Biosystems Sequence Trace files can be viewed with a number of software options including the previously mentioned SnapGene viewer. All oligonucleotide sequences utilized for introducing the aforementioned mutations has been provided in an excel worksheet.

SPR

Raw sensograms for each SPR experiment are provided in the Biacore evaluation (.BME) files. These files require the Biacore Evaluation software in order to visualize the sensograms. Steady state SPR measurement data extracted from the BME files has been input and fit using OriginPro and are contained in the Unicode Origin Graph files.