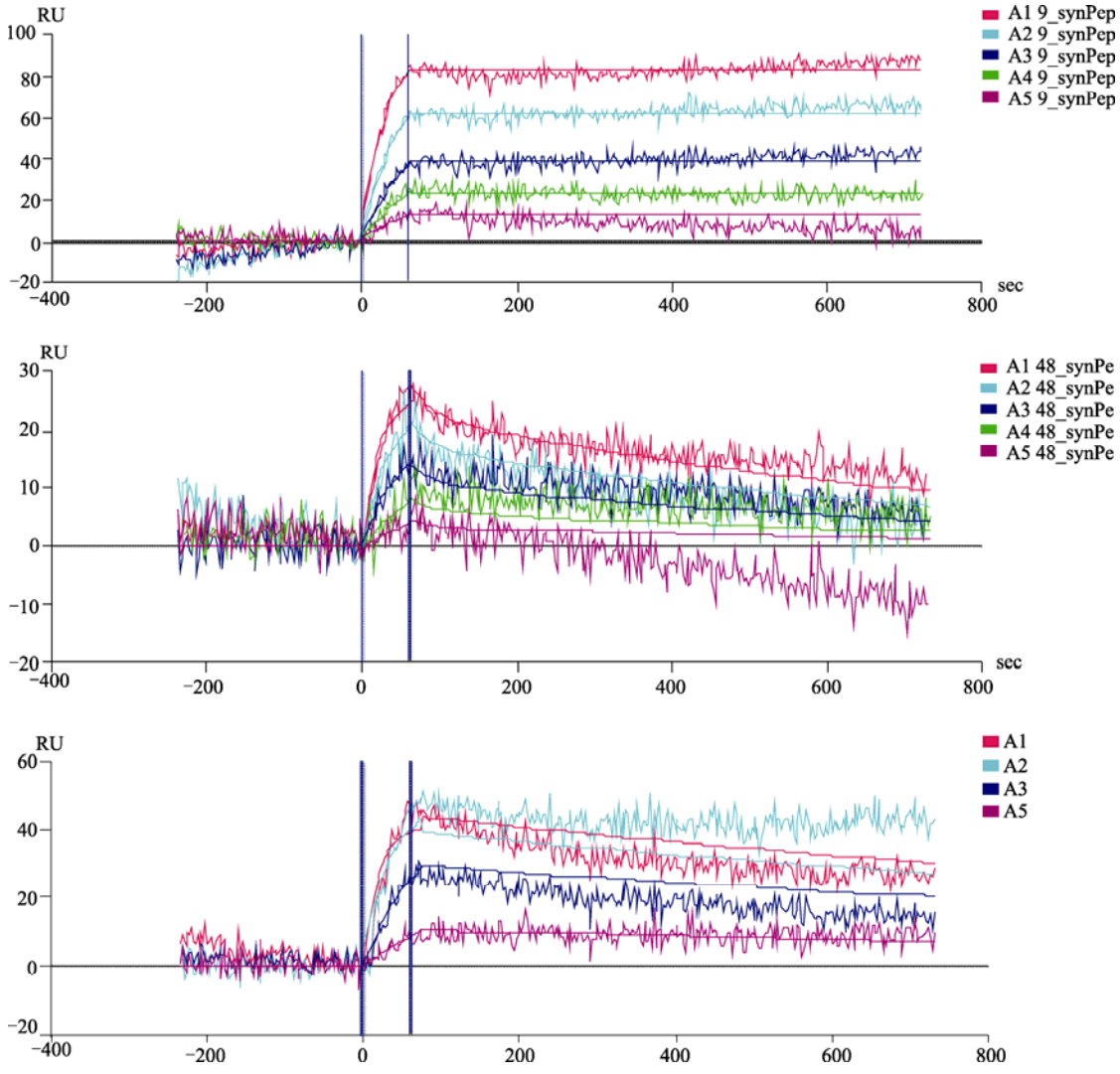
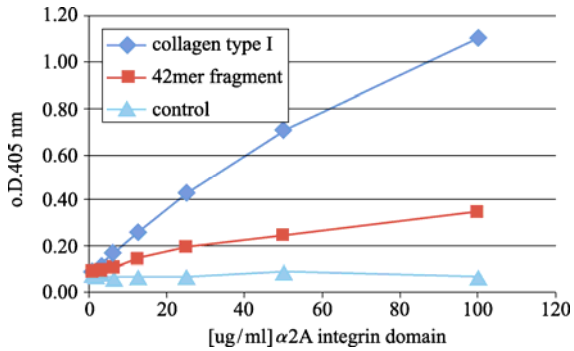
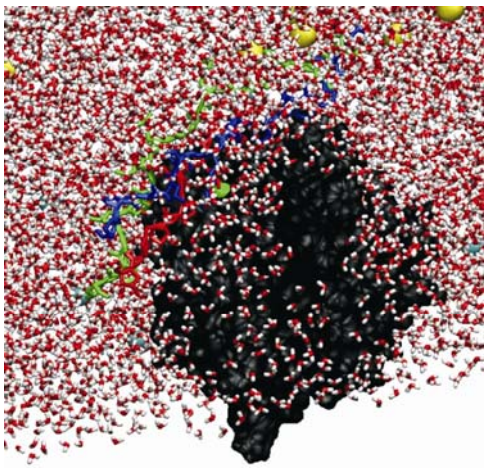
Supplemental data



Supplemental Figure 1. Kinetic results of the 42mer collagen fragment in complex with α2A. Binding curves of the 42mer collagen fragment (at 400, 200, 100, 50 and 25 nM) interacting with (A) ~450 RU of immobilized α2A in the presence of 2mM Mg^{2+} ions, (B) ~200 RU of immobilized α2A in the presence of 2mM Mn^{2+} ions and (C) ~200 RU of immobilized α2A in the presence of 2mM Co^{2+} ions.

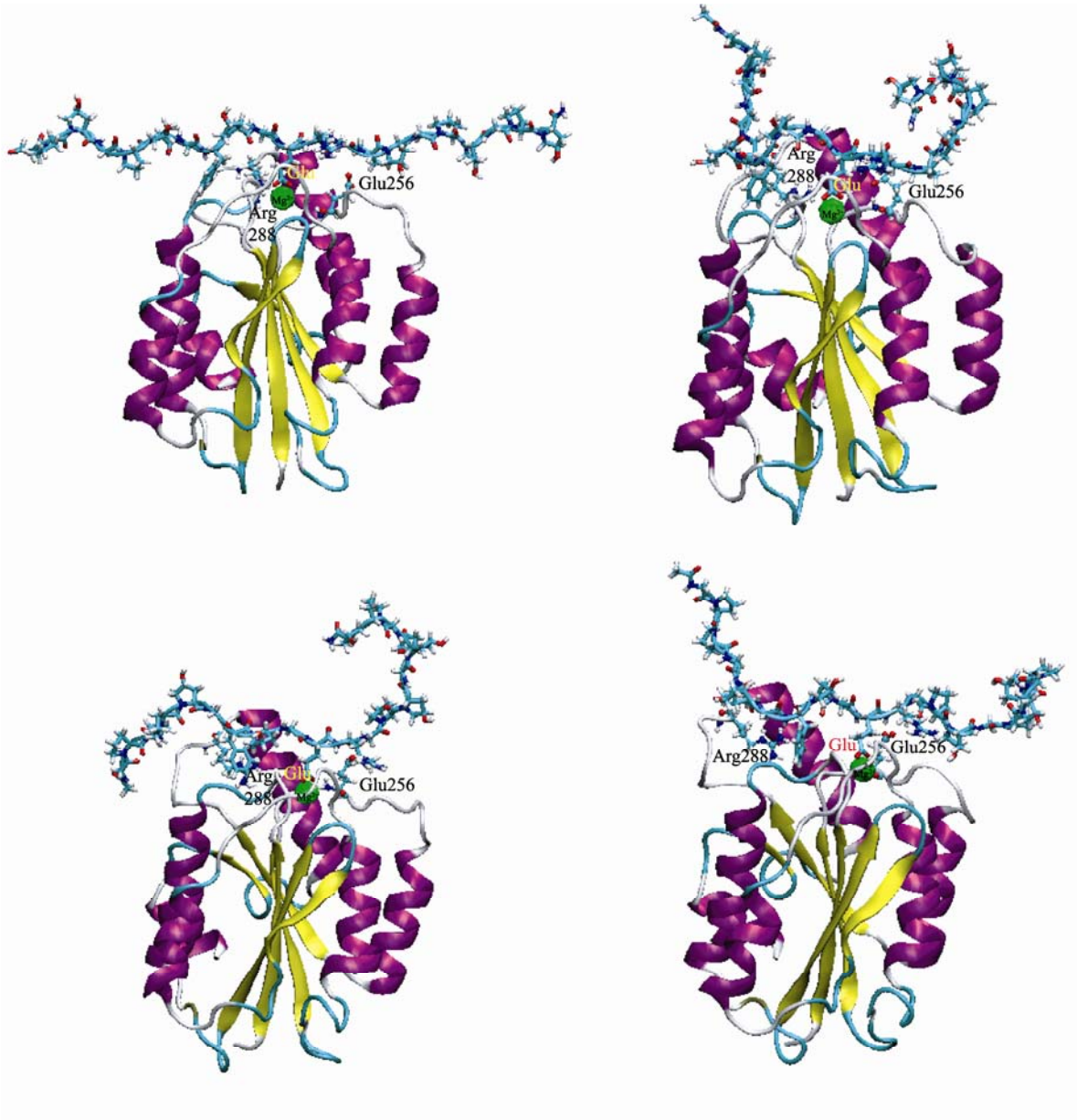


Supplemental Figure 2. Solid phase assay on immobilized collagen type 1, immobilized 42mer collagen fragment and non-coated plate surface.

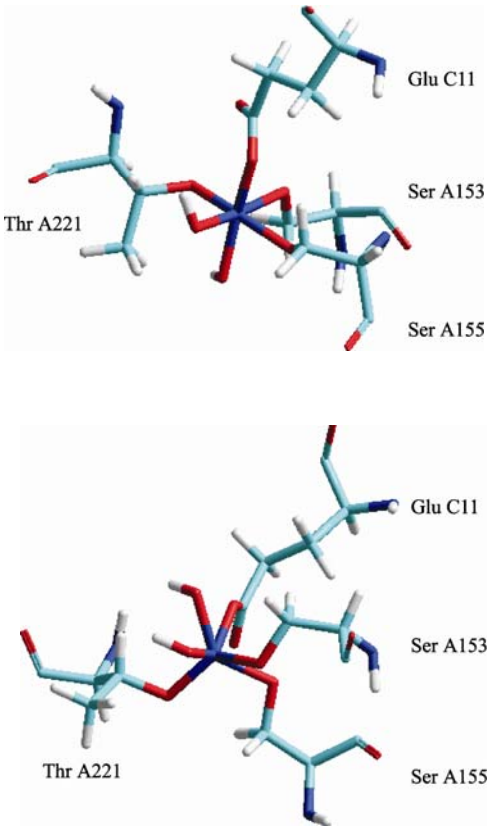


Supplemental Figure 3. Triple-helical collagen fragment (B-, C- and D-chain) in the binding pocket of α2A (A chain). The receptor α2A is shown in black. The sequence of each 21mer strand is GPOGPOGFOGERGPOGPOGPO. Their colour code is as follows: B-chain(blue), C-chain(red), D-chain(green). The NAMD simulations have been performed with Mg^{2+} (light green) in the binding pocket and Na^{+} (cyan) as well as Cl^{-} ions (yellow) in a 100 mM concentration. All surrounding water molecules are explicitly shown.

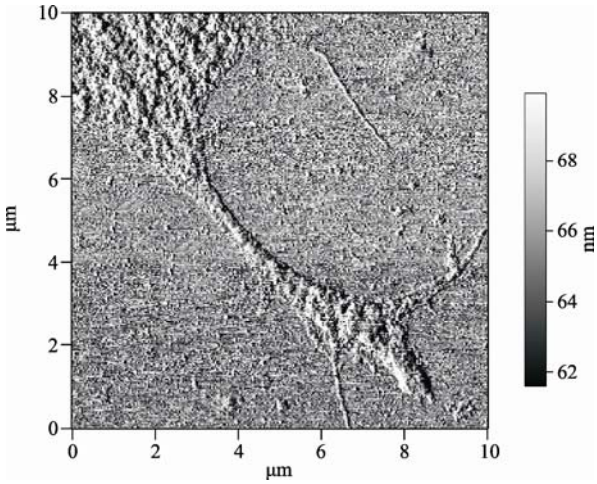
C-chain



Supplemental Figure 4. Single stranded collagen fragment (C-chain) in the binding pocket of α2A (1DZI.pdb). Snapshots are taken at four different states of the NAMD simulation. The sequence of the 21mer single strand is GPOGPOGFOGERGPOGPOGPO.



Supplemental Figure 5. Molecular mechanics calculations of the position of Co^{2+} ion in relation to four crucial amino acid residues in the binding pocket of α2A (1DZI.pdb). Top: MM+ force field, bottom: CHARMM27 force field. The influence of different force field methods in respect to the Co^{2+}-complex between the 21mer collagen fragment and the α2A integrin could be evaluated. The MM+ force field was superior to the CHARMM27 force field. The MM+ force field displayed the environment of the Co^{2+} ion in an octahedric form correctly, while a highly distorted structure was provided by the CHARMM27 force field. Thereby, we have demonstrated that it was necessary to take special care for the surrounding amino acids of the cation during the MD simulations, as we did.



Supplemental Figure 6. AFM picture of filopodia from a chondrocyte obtained in the amplitude mode. Such a morphological presentation of a section from a cell is extremely suited to analyse the impact of various collagen fragments on cell differentiation.