

**Fig** 1: Formation of PMN (CD16<sup>+</sup>)-platelet (CD42a<sup>+</sup>) complexes in whole blood after activation (Act) with 33.5  $\mu$ M TRAP-6, as assessed by flow cytometry (A). Anti-CD11b and anti-C3a inhibited conjugate formation (B).



**Fig. 2** Del-1 attenuated thrombin-antithrombin (TAT) complex generation and platelet-monocyte aggregation in human whole blood incubated onto porcine islets of Langerhans.







**Fig. 4** Results from the TAT (a), C3a (b.) and TCC (c.) ELISAs after the blood chamber experiments using the nanostructures prepared in Task 3b.



**Fig 5** a. Image of the clot formation at the surfaces S1-S5 after incubation in whole blood. b. Result of the TAT ELISA. c. Result from the C3a ELISA. d. Result from the TCC ELISA. e. FXII + C1q



## Fig 6 a and b (upper)

## Sensitivity and kinetics of polymer-ligand recognition.

(a) Resonant frequency change as a function of BtOMe concentration. Inset is the calibration plot for BtOMe on the MIP (n = 3, 6 injections per surface) and REF (n = 1, 6 injections) films. (b) Variation of observed  $k_{app}$  calculated from the associative part of the frequency vs time response curves for BtOMe binding to MIP and REF films.

Fig 6 a and b (lower)

Selectivity of polymer-ligand recognition. (a) Frequency response for dextran and biotinylated dextran (B-Dextran) binding to the MIP film. (b) Resonant frequency changes for the binding of different analytes to MIP and REF films. \* p > 0.05, \*\* p < 0.01, n = 3-8, 3-6 injections per surface.





**Fig. 7** Surface modification of cell-surface-binding heparin conjugates. Top: chemical structure of heparinbinding peptide-conjugated PEG-lipid for surface modification of cells, and amino acid sequences of heparinbinding peptides either derived from fibronectin (I); positively charged (II); identified by phage display . Bottom: chematic representation of heparin-conjugate immobilization by a cell-surface modification with heparin-binding peptide-PEG-lipid. Each heparin conjugate consisted of a conjugate of approximately 70 heparin molecules to a polymer chain.



**Fig. 8** (a) Structure of C3b–miniFH-FI. C3b, gray; miniFH, orange; FI colored by domain as shown at the bottom of the figure. (b) Superposition of C3b–miniFH (C3b, cyan; miniFH, black) and the corresponding parts from the C3b–miniFH–FI complex (C3b, gray; miniFH, orange). (c) Top view of superposition showing binding of FI (colored by domain as indicated) to CTC domain of C3b (gray); the CTC domain as found in C3b–miniFH is shown (cyan) for reference. (d) Contact regions for FI domains shown as footprints on C3b–miniFH (left) and contact region of C3b–miniFH domains on FI (right); domain coloring as defined by labels and schematic domain compositions of C3b, FI and miniFH as shown at the bottom.

## Specificity of C3b ELISA





Assay specificity was assessed with 10% C57bl/6 NMS EDTA-, Lepirudinplasma & C-deficient sera.



**Fig. 10** The members of the DIREKT consortium at the Aegean Conference in Chania, Crete, Greece, October 2014.