

# European Journal of Immunology

**Supporting Information**

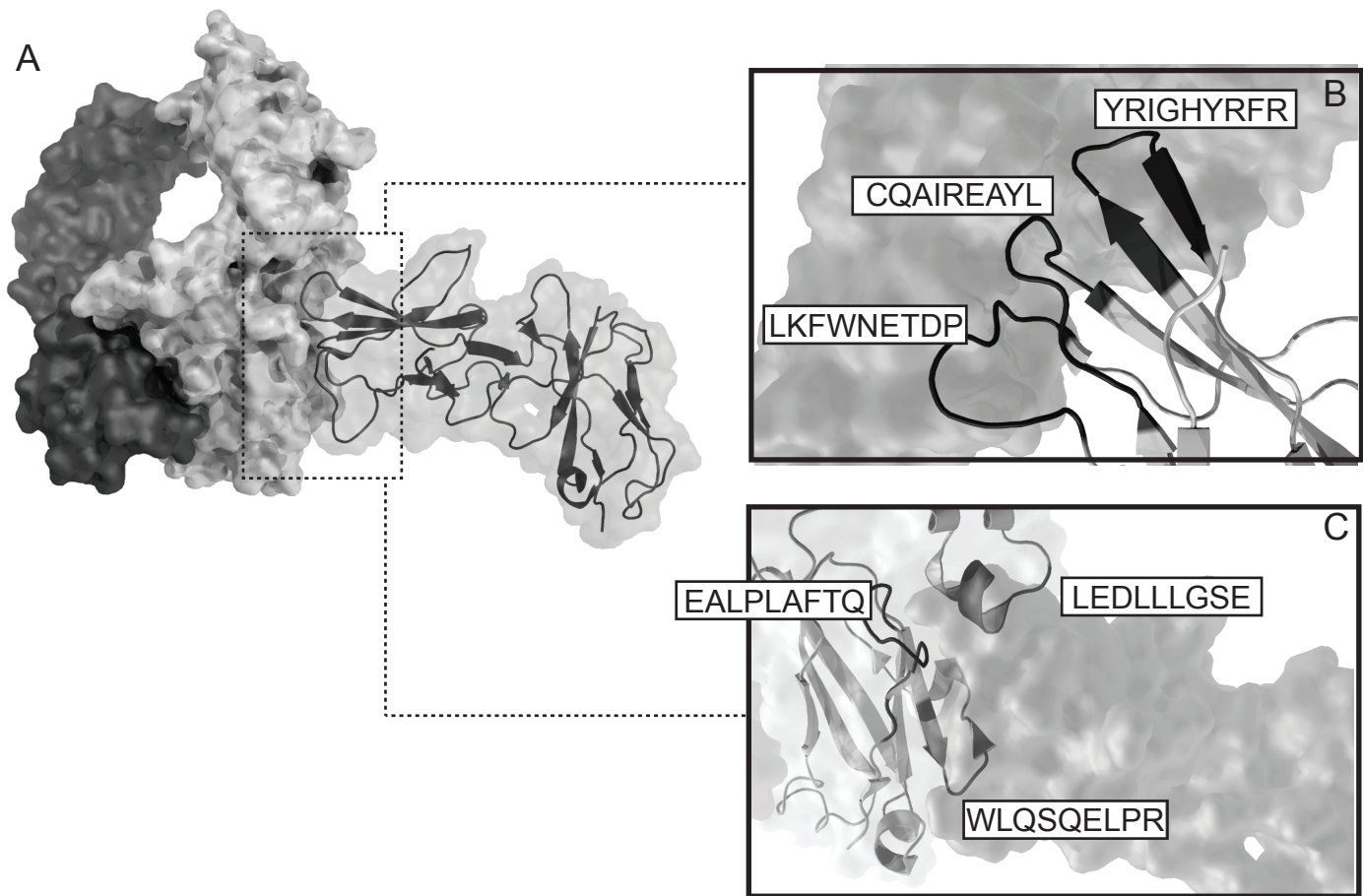
**for**

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**Peptide mimetics of immunoglobulin A (IgA) and Fc $\alpha$ RI block IgA-induced  
human neutrophil activation and migration**

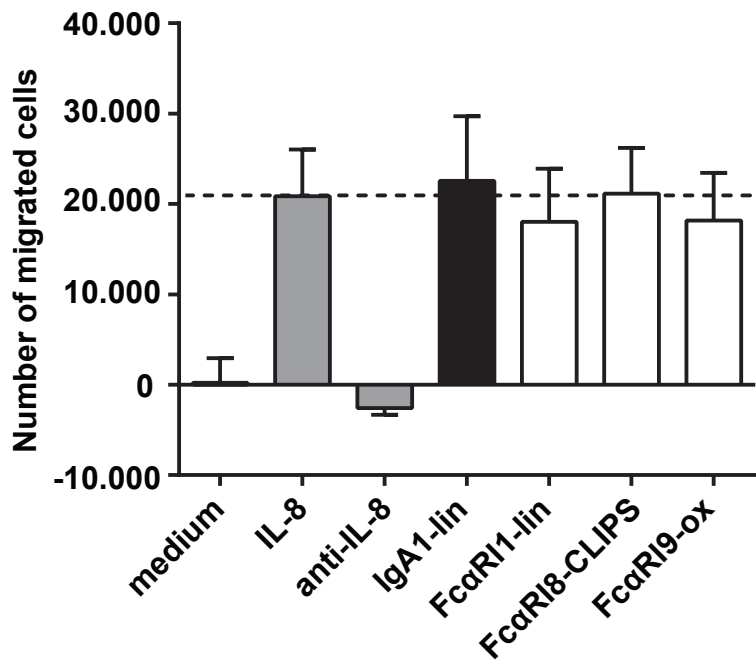
# Supporting Information Figure 1



## Supporting Figure 1. Model of interaction sites of IgA and FcαRI

(A) Model of the structure of the complex of two IgA Fc heavy chains, interacting with two extracellular domains of FcαRI. (Two molecules of FcαRI form a complex with one IgA molecule).  
(B and C) Magnification of position of FcαRI sequences (B) and IgA sequences (C) involved in binding.

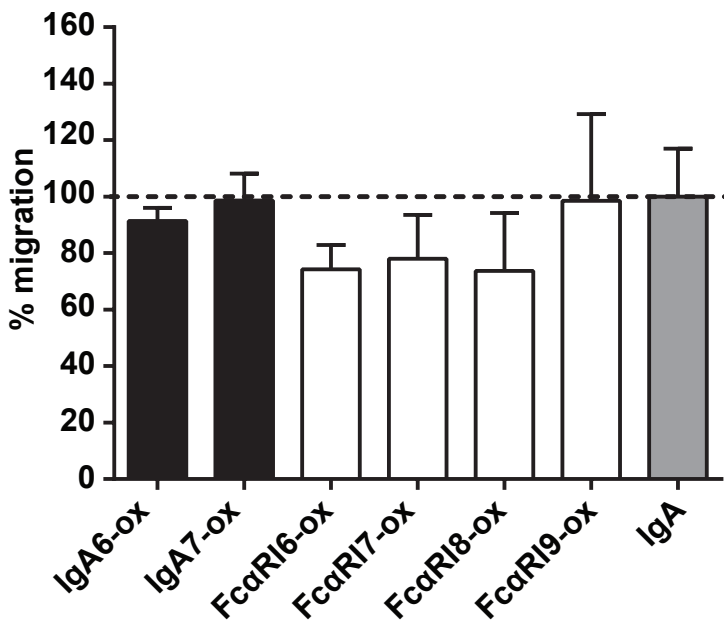
### Supporting Information Figure 3



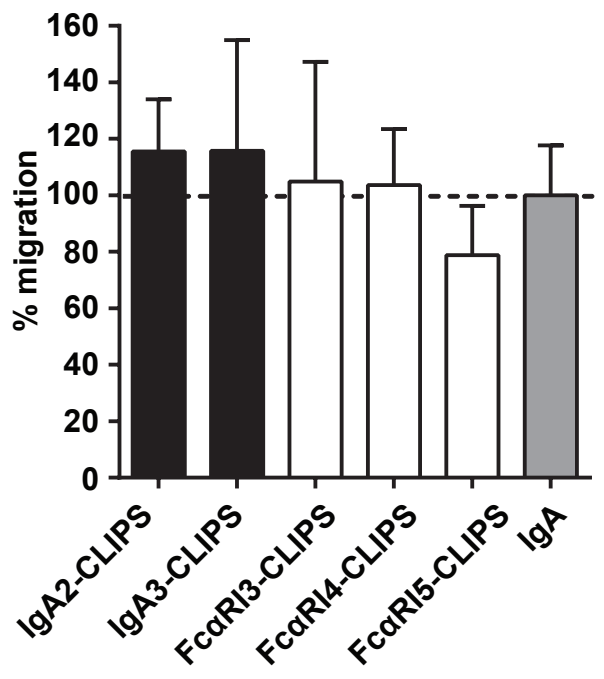
#### Supporting Figure 3. Peptide mimetics do not block IL-8 induced chemotaxis

Number of fluorescently labelled neutrophils which migrated to IL-8 in a chemotaxis chamber, either in the presence or absence of peptide mimetics. The number of migrated neutrophils was determined with a fluorimeter. Neutrophil migration to IL-8 is indicated with a dotted line. Medium and blocking IL-8 antibody (anti-IL-8) were used as controls. Experiments were performed three times in triplo. Mean  $\pm$  SD of one representative experiments in triplo is shown. Statistical analysis: ANOVA

A



B



**Supporting Figure 2. Oxidated or small peptide mimetics do not block IgA-induced migration *in vitro***

Percentage of migration of fluorescently labelled neutrophil to IgA-coated beads, either in the presence or absence of peptide mimetics. The number of migrated neutrophils was determined with a fluorimeter. Neutrophil migration to IgA was normalized to 100% (dotted line). Neutrophils or beads were pre-incubated with (A) oxidated or (B) small cyclic peptides mimicking FcαRI-sequences (white bars) or IgA-sequences (black bars). Data are representative of 3 independent experiments, performed in triplicates. Mean ± SD of one representative experiment is shown. Statistical analysis: ANOVA