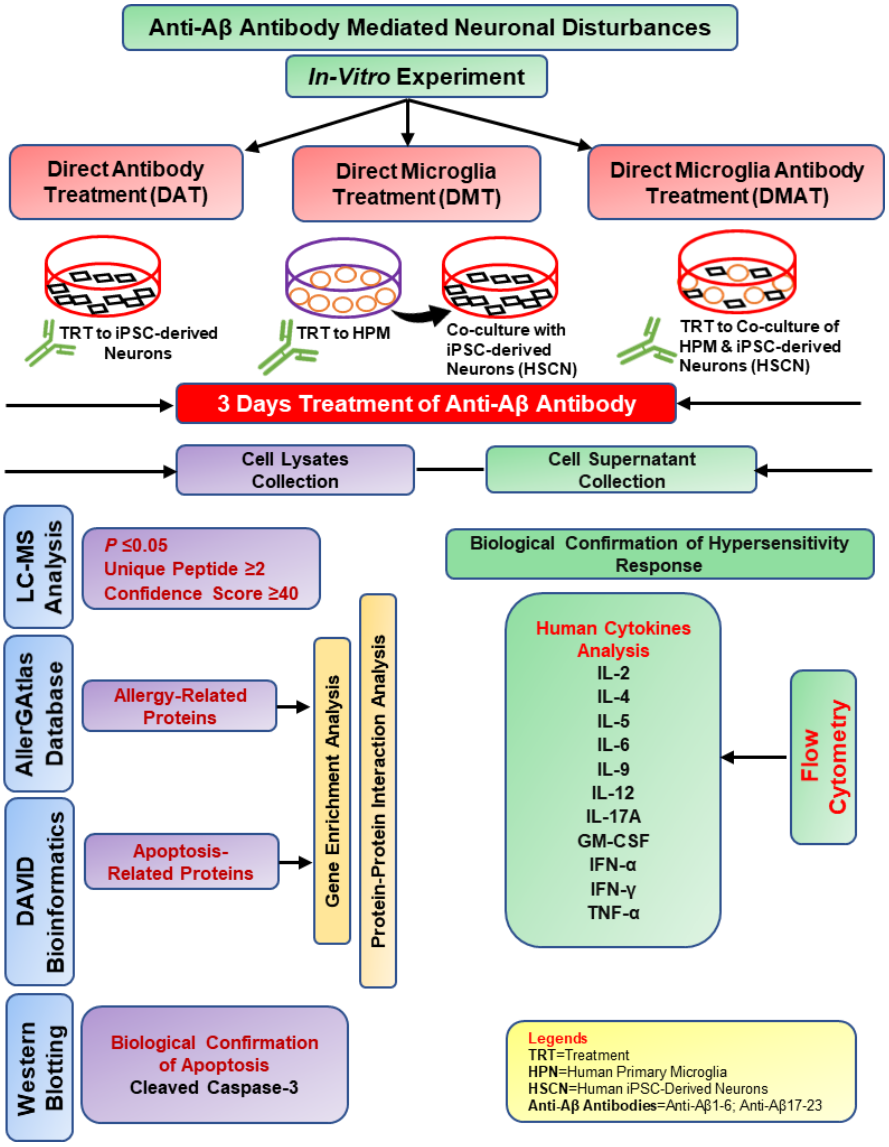

Figure 1: Overall workflow of the *in-vitro* study for the identification of allergenic and apoptosis-related proteins following anti-Aβ antibody treatment and LC-MS analysis.

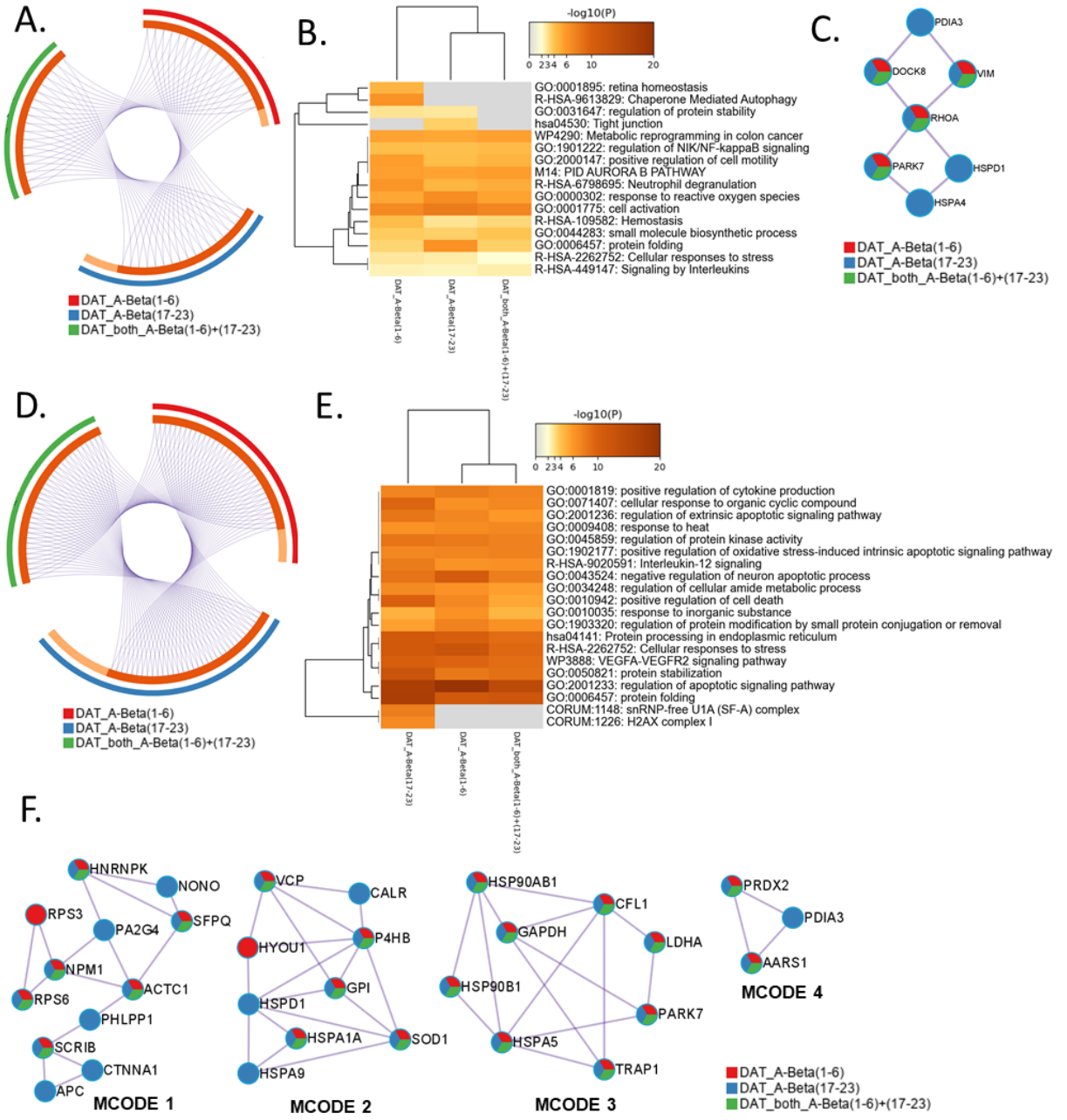

Figure 2. Gene enrichment analysis of the identified allergy- and apoptosis-related proteins following DAT. A) Gene overlap analysis for the identified allergy-related genes following $_{allg}DAT_{A\beta 1\text{-}6}$ and $_{Allg}DAT_{A\beta 17\text{-}23}$ predicted by Metascape. On the outside, each arc represents the identity of each gene list, using the same color code. On the inside, each arc represents a gene list, where each gene member of that list is assigned a spot on the arc. Dark orange color represents the genes that are shared by multiple lists and light orange color represents genes that are unique to that gene list. **B**) Heat map of the gene enriched term for the identified allergy-related genes following $_{Allg}DAT_{A\beta 1\text{-}6}$ and $_{Allg}DAT_{A\beta 17\text{-}23}$. Herein, Log10(P)" is the *p*-value in log base 10. The heatmap cells are colored by their *p*-values, white cells indicate the lack of enrichment for that term in the corresponding gene list. **C**) Protein-protein interaction MCODE components for the identified allergy-related gene sets following $_{Allg}DAT_{A\beta 1\text{-}6}$ and $_{Allg}DAT_{A\beta 17\text{-}23}$. MCODE

components were identified from the merged network. Herein, network nodes are displayed as pies. Color code for pie sector represents a gene list and is consistent with the colors. All the protein-protein interaction network was edited using the Cytoscape software v3.9.0. **D**) Gene overlap analysis for the identified apoptosis-related genes following $_{Apop}DAT_{A\beta 1\text{-}6}$ and $_{Apop}DAT_{A\beta 17\text{-}23}$ predicted by Metascape. **E**) Heat map of the gene enriched term for the identified apoptosis-related following $_{Apop}DAT_{A\beta 1\text{-}6}$ and $_{Apop}DAT_{A\beta 17\text{-}23}$. **F**) Protein-protein interaction MCODE components for the identified apoptosis-related gene sets following $_{Apop}DAT_{A\beta 1\text{-}6}$ and $_{Apop}DAT_{A\beta 17\text{-}23}$.

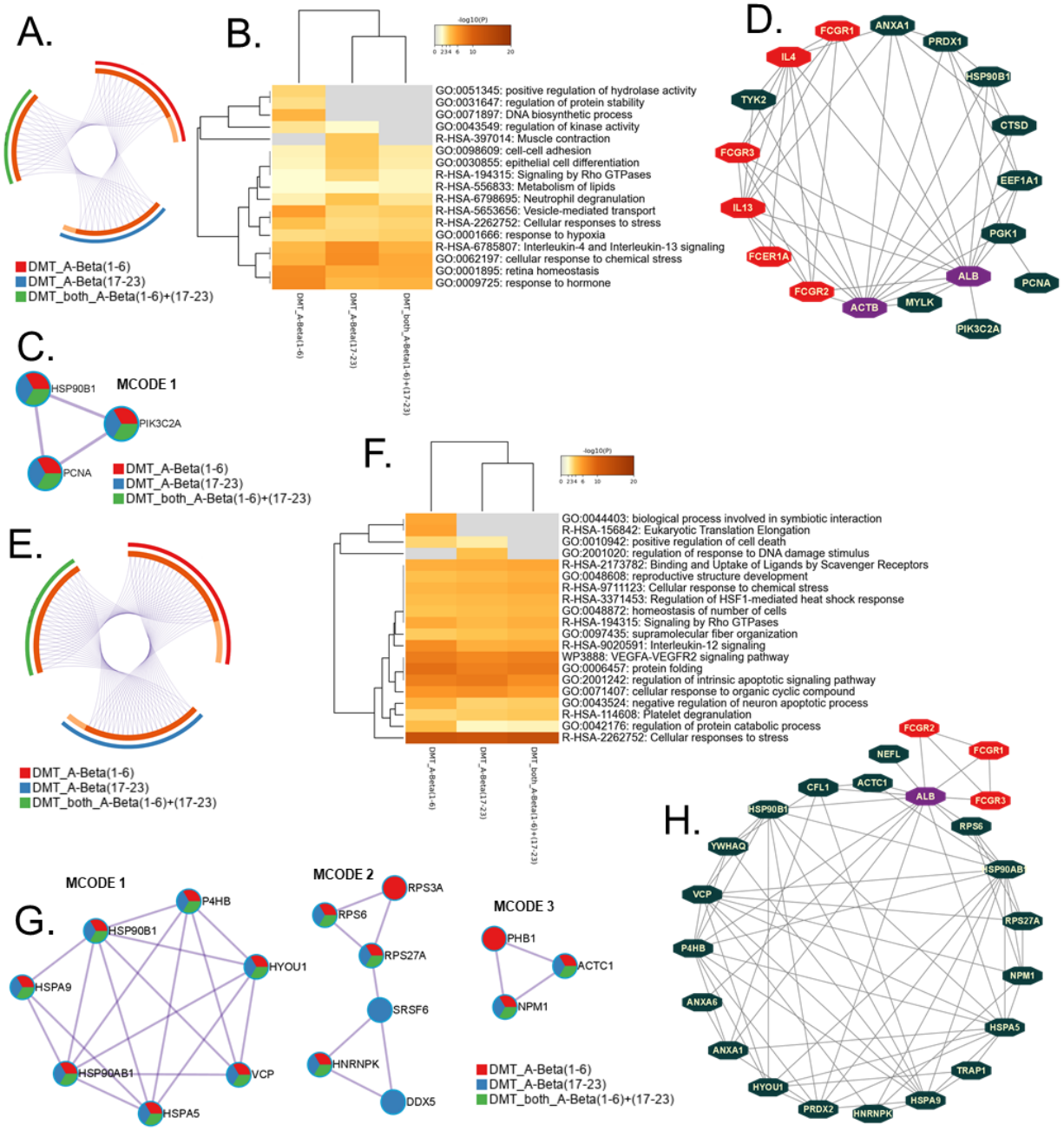

Figure 3: Gene enrichment analysis of the identified allergy- and apoptosis-related proteins following DMT. A) Gene overlap analysis for the identified allergy-related genes following $_{allg}DMT_{A\beta1\text{-}6}$ and $_{Allg}DMT_{A\beta17\text{-}23}$ predicted by Metascape. On the outside, each arc represents the identity of each gene list, using the same color code. On the inside, each arc represents a gene list, where each gene member of that list is assigned a spot on the arc. Dark orange color represents the genes that are shared by multiple lists and light orange color represents genes that are unique to that gene list. **B**) Heat map of the gene enriched term for the identified allergy-related genes following $_{Allg}DMT_{A\beta1\text{-}6}$ and $_{Allg}DMT_{A\beta17\text{-}23}$. Herein, Log10(P)" is the *p*-value in log base 10. The heatmap cells are colored by their *p*-values, white cells indicate the lack of enrichment for that term in the corresponding gene list. **C**) Protein-protein interaction MCODE components for the identified allergy-related gene sets following $_{Allg}DMT_{A\beta1\text{-}6}$ and $_{Allg}DMT_{A\beta17\text{-}23}$. MCODE

components were identified from the merged network. Herein, network nodes are displayed as pies. Color code for pie sector represents a gene list and is consistent with the colors. All the protein-protein interaction network was edited using the Cytoscape software v3.9.0. **D**) Protein-protein interaction analysis of the identified allergy-related genes with FcγR1, FcγR2, FcγR3, FcεR1A, IL-4, and IL-13 (red color). Purple color indicates the high interaction with other proteins. Protein-protein interaction was performed using the STRING v11.5 database and the data was edited using the Cytoscape v3.9.0 software. **E**) Gene overlap analysis for the identified apoptosis-related genes following $_{apop}DMT_{A\beta 1\text{-}6}$ and $_{Apop}DMT_{A\beta 17\text{-}23}$ predicted by Metascape. **F)** Heat map of the gene enriched term for the identified apoptosis-related genes following $_{Apop}DMT_{A\beta 1\text{-}6}$ and $_{Apop}DMT_{A\beta 17\text{-}23}$. **G**) Protein-protein interaction MCODE components for the identified apoptosis-related gene sets following $_{Apop}DMT_{A\beta 1\text{-}6}$ and $_{Apop}DMT_{A\beta 17\text{-}23.}$ **H**) Protein-protein interaction analysis of the identified apoptosis-related genes with FcγR1, FcγR2, FcγR3, FcεR1A (red color). Purple color indicates the high interaction with other proteins.

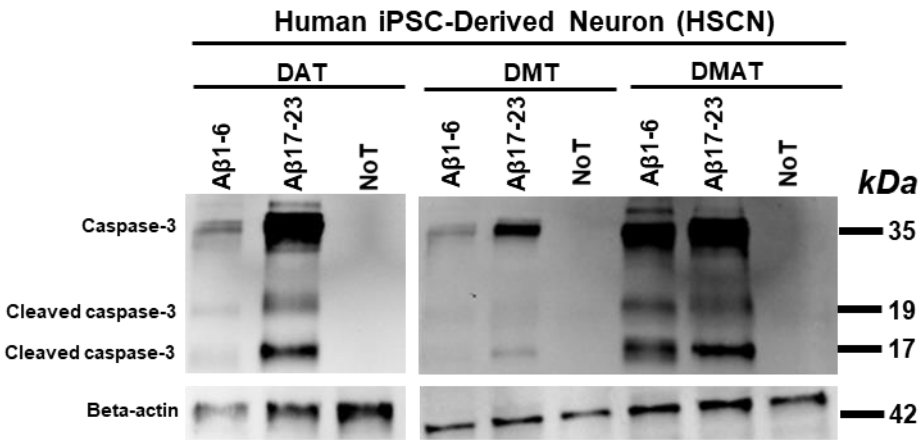

Figure 4: Differential expression of cleaved caspase-3 confirms apoptosis following DAT, DMT, and DMAT. Herein**,** Western blotting of samples derived from cell lysates following DAT, DMT, and DMAT for the confirmation of apoptosis.

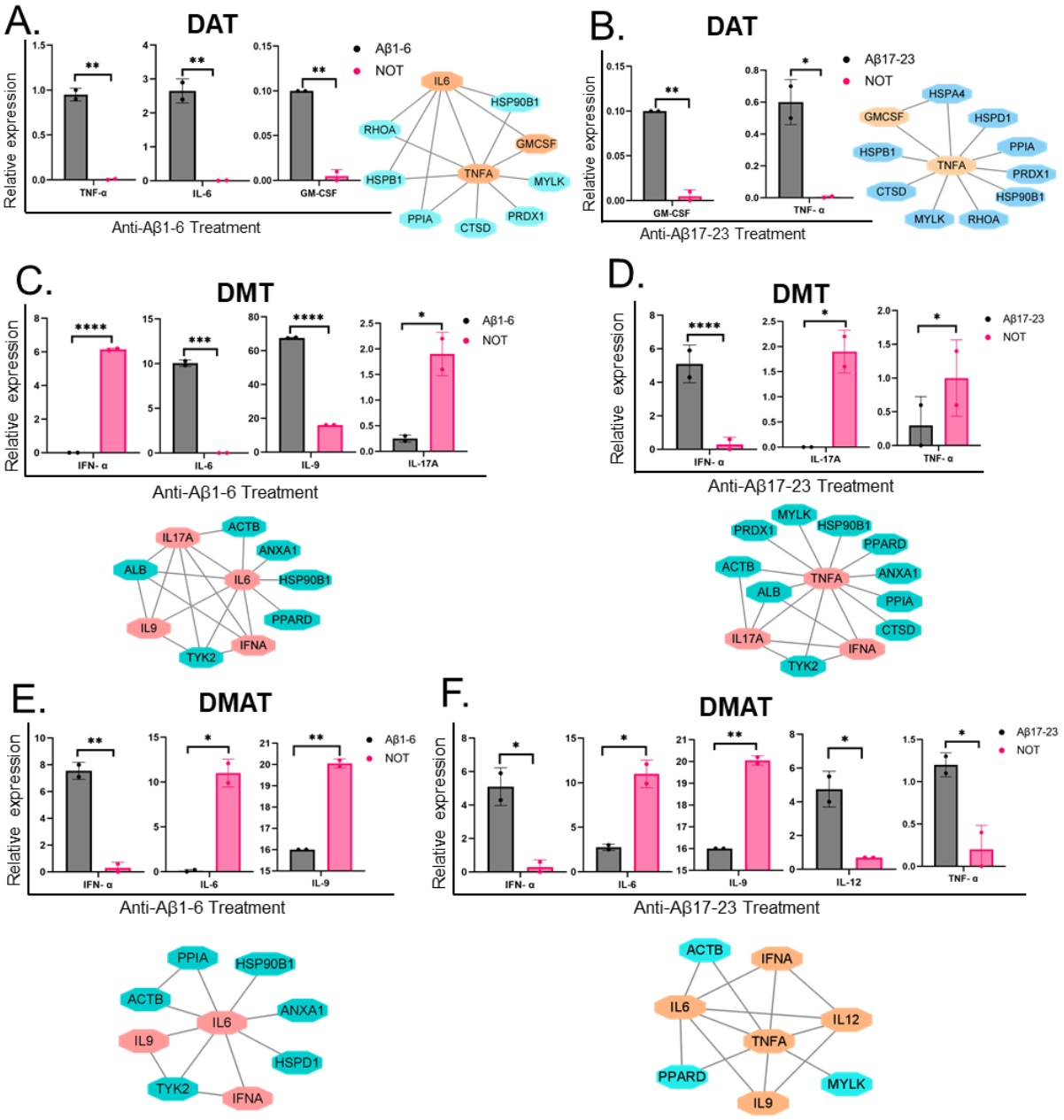

Figure 5: Production of proinflammatory cytokines following treatment with anti-Aβ antibodies. A) expression of TNF-α, IL-6, and GM-CSF following $DAT_{Aβ1-6}$ **B**) expression of TNF-α and GM-CSF following $DAT_{Aβ17-23}$ **c**) production of IFN-α, IL-6, IL-9, and IL-17A following $DMT_{Aβ1-6}$ **D**) production of IFN-α, TNF-α, and IL-17A following $DMT_{Aβ17-23}$ **E**) production of IFN-α, IL-6, and IL-9 following $DMAT_{Aβ1-6}$ **F**) production of IFN-α, IL-6, IL-9, IL-12, and TNF-α following $DMAT_{Aβ17-23}$. The protein-protein interaction was performed using the STRING v11.5 database and the data was edited using the Cytoscape v3.9.0 software. Herein, only direct interactions of the released cytokines and the identified allergy related proteins have been shown. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, ****$p < 0.0001$.