Roald Nezlin, J Mol Biomark Diagn 2013, 4:3
http://dx.doi.org/10.4172/2155-9929.S1.019

OMICS Group Conferences
Accelerating Scientific Discovery

4th International Conference on
Biomarkers & Clinical Research
July 15-17, 2013 Courtyard by Marriott Philadelphia Downtown, USA

Non-immune complexes of IgG molecules and biomarkers

Roald Nezlin
Weizmann Institute of Science, Israel

Constant (C) parts of immunoglobulin peptide chains are composed from Ig folds or domains which belong to C1 structural variant. They have an enormous capacity to interact with various peptides and proteins through their "hot regions". Last decades it was found that IgG, the most abundant immunoglobulin molecules readily form complexes in a non-immune manner with a great number of protein molecules of animal, bacterial and viral origin. A variety of non-immune IgG complexes were detected in the sera of the healthy people as well in pathological sera. Among them are complexes with the participation of several disease biomarkers (for example, prostate specific protein, PSA). About half of the serum proteins have a molecular mass below 45 kDa, i.e. the kidney size cutoff. Such protein molecules cannot exist in bloodstream for long, and they are removed from the circulation more or less rapidly by glomerular filtration or proteolytic degradation. The fast elimination of many serum proteins from the circulation is an obvious obstacle for finding potential clinical biomarkers. The association of small proteins with large molecules, such as IgG, which have long half-time, could prolong their presence in the circulation as compared with their free form. Therefore the chances to discover new specific clinical biomarkers in the circulation would be significantly higher if searches encompass not only molecules that are in a free state in the bloodstream but also large abundant protein molecules with associated proteins.

roald.nezlin@weizmann.ac.il