Reading the Antibody Repertoires

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Previous work has shown that peptide libraries in microarray format can efficiently probe the antibody repertoire dynamics as a source of information about the internal environment of the organism [1-2]. The rationale for using the immune system as a natural biosensor is based on the weak autoreactivity of the repertoires (mostly of the IgM), the integration of specific and non-specific signals of danger and the huge information capacity of the immunoglobulin variable region diversity. We probed the serum IgM reactivities of 22 patients with glioblastoma multiforme, lung cancer brain metastases or non-tumor bearing individuals using peptide arrays. Unlike previous reports with random peptides, we used rationally designed library scanning the sequences of 20 tumor antigens and including in addition 209 tumor related B cell epitopes. The analysis of the high binders shows intriguing differences between the support vector machine based predictor build on the basis of the high binders and the published ones (lbtope[3] and BepiPred[4]) .

References

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