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Commentary to article entitled: Chemo Proteomics, a Valuable Tool for Biomarker and Drug Discovery

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Commentary

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The article completely focuses on Novel drug discovery and use of small molecules as drug target, which is mostly a protein molecule. During current molecular research period, we have seen many small molecules as drug target but still these are very few while comparing to total druggable target in human proteome [1]. This kind of researches are not limited to a fixed demography, rather it is trending in almost all countries involved in molecular researches.

These recent progress is a result of inclusion of various techniques in biological research. These tools and techniques mainly belongs to a group of chemo proteomics [1], such as mass spectrometry, computational data analysis and other chemistry evaluation techniques with biological research and combined together as chemo proteomic analysis. Main goal of author is to highlight the increasing reliability on these techniques in research biology [2-8].

Marjeta Urh has tried very efficiently to cover on these topics in an understandable manner in order to reach and convey his message to maximum scientific community audience. He also explained elaborately about mass spectrometry and different types of chromatography. Discussion about affinity-based protein profiling [9] also was a great point to mention. Use of tools like this has been drastically increased in this current decade and are very effective also for actual calculation and estimation of properties of molecules [10-14]. We can see implementation of new techniques by taking research observation by eminent scientists all over the world in consideration.

However, if I would say my opinion about this editorial article, importance of bioinformatics tools in minimizing time limits of analysis of chemo proteomic factor was an important thing to discuss [15]. There are bioinformatics tool such as Mascot and smileMS, which are very helpful while analyzing data with mass spectrometry results and small molecules identification is a need. There are many other

proteomic analysis tools available on ExPASy bioinformatics resource portal, which can be a great help to researchers in field of biology [16-17].

In current research scenario, proteomic analysis strategy played a vital role to understand complete phenomenon of drug discovery. There are many researches going on in field such as cervical cancer and amyloidotic diseases [18-22]. These techniques are also found helpful in research related to antibody expression and various researches related to development of anticancer drugs [23-28].

Over all, article is a superb example and a clear message to upcoming researchers like me to follow these techniques, and how we can implement these chemo proteomics tools in our researches related to biomarker and drug discovery researches.

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