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## Biography

Alon Savidor completed his PhD at 2008 from the University of Tennessee and The Oak Ridge National Laboratory at Tennessee, USA. He completed his post-doctorate fellowship at the Tel Aviv University, Israel, at 2013, and since then he is a staff scientist at the Nancy and Stephen Grand Israel National Center for Personalized Medicine, Weizmann Institute of Science, Israel.

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# DATABASE INDEPENDENT PROTEIN SEQUENCING (DIPS) ENABLES FULL-LENGTH DE-NOVO PROTEIN AND ANTIBODY SEQUENCE DETERMINATION

*De-novo*, full-length sequencing of unknown proteins such as antibodies or constituents of metaproteomes remains a challenging problem. Traditional 'bottom-up' proteomics approaches use proteolytic digestion, LC-MS/MS and database searching to elucidate peptide identities and their parent proteins. Protein sequences absent from the database cannot be identified, and even if present in the database, complete sequence coverage is rarely achieved even for the most abundant proteins in the sample. To this aim we have developed Database Independent Protein Sequencing (DiPS), a novel method for unambiguous, rapid, database independent, full-length protein sequencing. The method is based on non-enzymatic, semi-random cleavage of the protein by microwave assisted acid hydrolysis (MAAH), LC-MS/MS analysis, peptide de novo sequencing, extraction of peptide tags, and their assembly into a consensus sequence using a novel algorithm named Peptide Tag Assembler (pTA). The method, which was recently published, now also allows for differentiation between the isobaric leucine and isoleucine residues, and was successfully applied to a variety of proteins and clinically relevant antibodies.

Note: