The seminar will be held in Hebrew

The growing dependency on depleting fossil fuels and their ecological drawbacks requires the development of alternative energy sources. One way to alleviate the demand for fossil fuels, is by using renewable bio-fuels, such as naturally plentiful lingocellulosic biomass. For the economic conversion of biomass to biofuels, highly active cellulose degrading enzymes (i.e. cellulases) are required. This research used nature’s genetic diversity, i.e. metagenomics, in order to identify novel genes involved in the degradation of cellulose and hemicellulose. Using an algorithm developed in our lab, thermal spring metagenomes were screened, and then further characterized based on their genomic context and bioinformatic analysis. Out of approximately six million open reading frames, two novel glycoside hydrolases were selected for further examination. The target genes were made synthetically, cloned, overexpressed in E. coli and purified. The proteins were biochemically characterized using synthetic and natural substrates. Protein GH5_156, exhibited low activity on several substrates. The protein was crystalized and its three dimensional structure was solved. Protein HP_107 was identified as a glycoside hydrolase family 5, with endo-mannanase activity. The protein showed little similarity to known GH5 subfamilies suggesting HP_107 represents a new subfamily.