Text-mining in the Biomedical domain aims at supporting life-science researchers in utilizing automatic information extraction in solving their research problems. The purpose of the study was to demonstrate the specific application of using EVEX, a homology-based event extraction database to solve a biological problem in identifying novel regulators of NADP(H) metabolism in a prokaryotic model organism, *Escherichia coli*. The study was divided into four stages: (i) identification of potential regulators using homology-based generalized events, (ii) evaluation of event extraction and gene family assignment, (iii) integration of the event-based NADP(H) regulatory network with microarray data and (iv) interpretation of biological relevance. Given 14 key genes known for their implications in NADP(H) metabolism as a starting point, 41 candidate families were identified. The generalized events was consequently interpreted as a network and integrated with selected microarray data from the conditions known to influence NADP(H) metabolism. The resulting integrated network supports a biological interpretation which leads to identifying an interesting candidate gene, *hexR*. The success of the current study warrants a further research in multiple directions including extending the current network to cover the second degree of interactions and developing tools to aid the future work.

The primary result of this work has been accepted as a peer-reviewed paper (Kaewphan et al., 2012) for oral presentation at the Third Workshop on Building and Evaluating Resources for Biomedical Text Mining in 2012 (BioTxtM2012). (http://www.nactem.ac.uk/biotxtm2012/)

Keywords: homology-based, text-mining, integration, DNA microarray