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Computational identification of non-synonymous polymorphisms within regions corresponding to protein interaction sites

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Keywords: *In silico,* PiSITE database, protein-protein interactions (PPIs), non-synonymous SNPs (nsSNPs)

Abstract

Background

Protein-protein interactions (PPI) play an important role in function of all organisms and enable understanding of underlying metabolic processes. Computational predictions of PPIs are an important aspect in proteomics, as experimental methods may result in high degree of false positive results and are more expensive. Although there are many databases collecting predicted PPIs, exploration of genetics information underlying PPI interactions has not been investigated thoroughly. The aim of the present study was to identify genomic locations corresponding to regions involved in predicted PPIs and to collect non-synonymous polymorphisms (nsSNPs) located within those regions; which we termed PPI-SNPs. **Methods**: Predicted PPIs were obtained from PiSITE database (http://pisite.hgc.jp). Non-synonymous

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