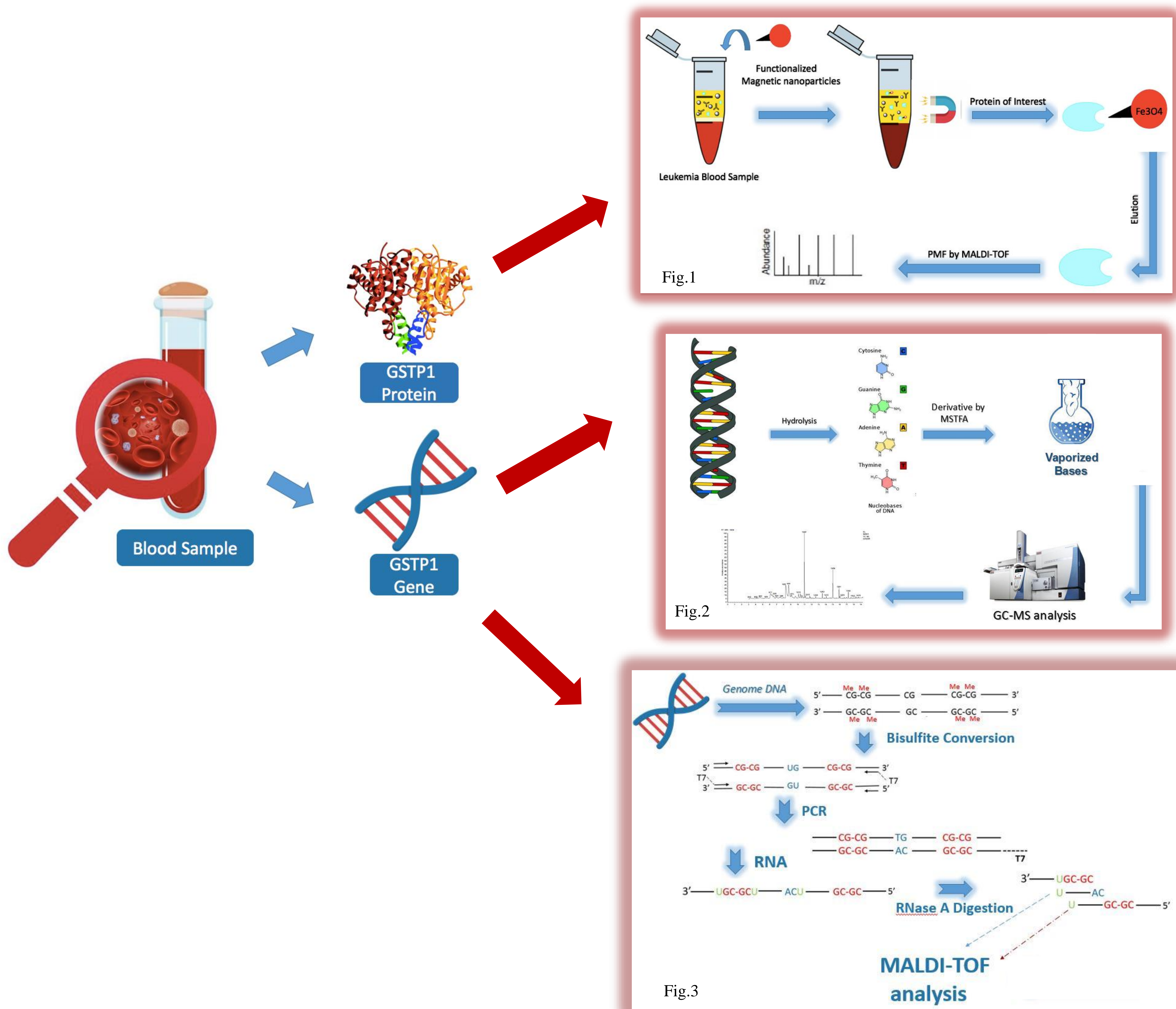


Introduction: Childhood acute lymphoblastic leukemia (ALL) is considered for more than 30% of childhood cancer per a year throughout the world. Some reports confirm the role of Glutathione S Transferase P1 (GST-P1) protein in the childhood ALL risk. In addition, other reports show the role GST-P1 Gene in Leukemia. MS techniques can determine quantitative proteomics, epigenetic levels and gene region involve to methylation in ALL patients.



Results: The extraction of GST-P1 protein by magnetic nanoparticle causes to see low concentration of it in ALL blood patient samples. The proteomics results show the significant variation on GST-P1 protein levels compare to normal blood children (Fig. 1). The Gene hydrolysis and derivatization give to good results of cytosine methylation and its variation in ALL patients (Fig. 2). To discover the exact sites of methylation on Gene sequence, a MALDI-TOF MS method has been developed based on bisulfite conversion, PCR and Rnase A Digestion samples (Fig. 3).