These variants are distributed as follows: two variants were found in 50–UTR, 17 variants were located in introns and 22 variants located in exons.At the time of this sequence analysis of our samples these two variants(D479N and L674L) were novel.From the 22 variants in exons, 11 of which were synonymous, 11 nonsynonymous SNPs, and five were novel (p.W73X, p.D479N, p.E523K, p.L674L, p.I799I; Fig.From the two variants in 50–UTR, one was novel (g.–2 TG; Fig.4 [2–6], respectively).4[1]).