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# An Excel Macro Code to Retrieve and Analyze the Homologous microRNA-Binding Sites from the *TargetScan* Database

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**ABSTRACT**

We present the Excel macro code for the facilitated identification of the homologous miR-binding sites and their corresponding miRs, as well as some related data retrieval for the following analysis: the site and miR densities within the 3'UTR mRNA fragment, the structural characteristics of the homologous miR-binding sites, and the number of the homologous sites per miR.

**Keywords:** microRNA; mRNA; Seed; Repetitive; Homologous

**Abbreviations:** miR: microRNA; mRNA: Messenger RNA; UTR: Untranslated Region

## Mini Review

MicroRNAs are small non-coding RNAs that regulate the expression of virtually all genes in nearly all biological species. They exert their function by binding to the complementary site on the targeted mRNA. The 5'-end of miR exhibits the so-called seed sequence that is complementary to 6-8 nucleotides at the 3'-UTR of mRNA [1,2]. Canonical miR target sites are classified upon the extent and location of matching miR nucleotides: 6mers perfectly pair to nucleotides 2-7 on the 5'-end of microRNA, 7-merA1 and 7mer8 – additional pairing with miR nucleotide 1 or 8 respectively, and 8mer sites match miR nucleotides 1-8 [3]. The reported multiple (homologous) seed-matching sites for the same miR on the mRNA target sequence are suggested to act synergistically [4] to enhance microRNA-mediated effects. These sites are abundant, present in all human genes, and characterized by various structural types [5]. Here we present an Excel Macro code (Supplementary Data 1) that allows the user to quickly process the downloaded from the *TargetScan* Database row data spreadsheet to retrieve the records related to the miRs targeting more than 2 sites within the mRNA 3'-UTR. The information includes the list of miRs targeting the homologous sites, the position of the sites within the 3'UTR, structural characteristics of the sites (7-merA1, 7mer8, and 8mer sites), presence (percentage) of each structural type, information about how many homologous sites are targeted by miRs (from 2 to 50 homologous sites can be targeted by one miR within the same 3'-UTR), length of the 3'UTR fragment, and the density of the homologous sites as well as the density of miRs with homologous sites within 3'UTR (per base). The proposed macro

code is useful in Data Mining of the *TargetScan* Database for the analysis and characterization of the homologous miR-binding sites in various biological species.

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