Evolutionary adaptation of DHFR via expression of enzyme isoforms with various binding properties and dynamics behavior: a bioinformatics and computational study

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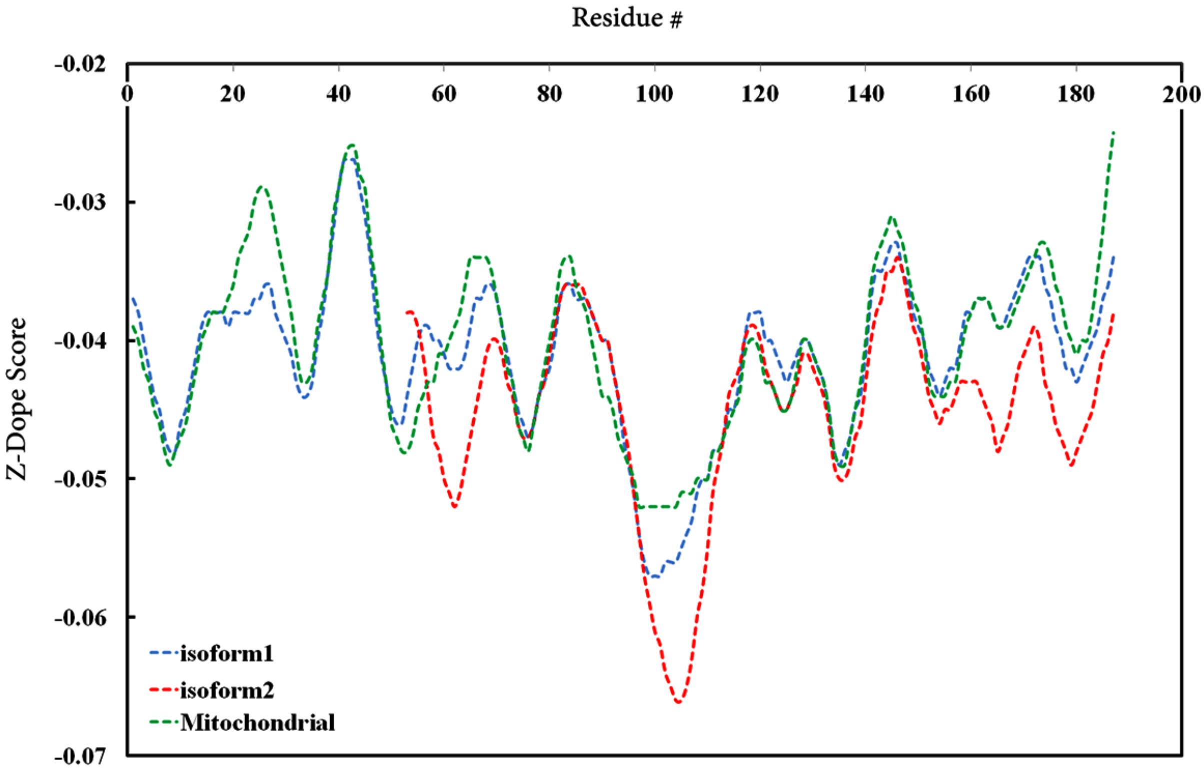
Supplementary material



Supplementary Figure 1. Z-score of all residues in the structure of proteins.

The score was calculated using MODELLER program by running corresponding command for individual structures.