Supplementary Material for

CriTER-A: a novel temperature-dependent noncoding RNA switch in the telomeric transcriptome of *Chironomus riparius*

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CriTER-A. Secondary Structure Prediction

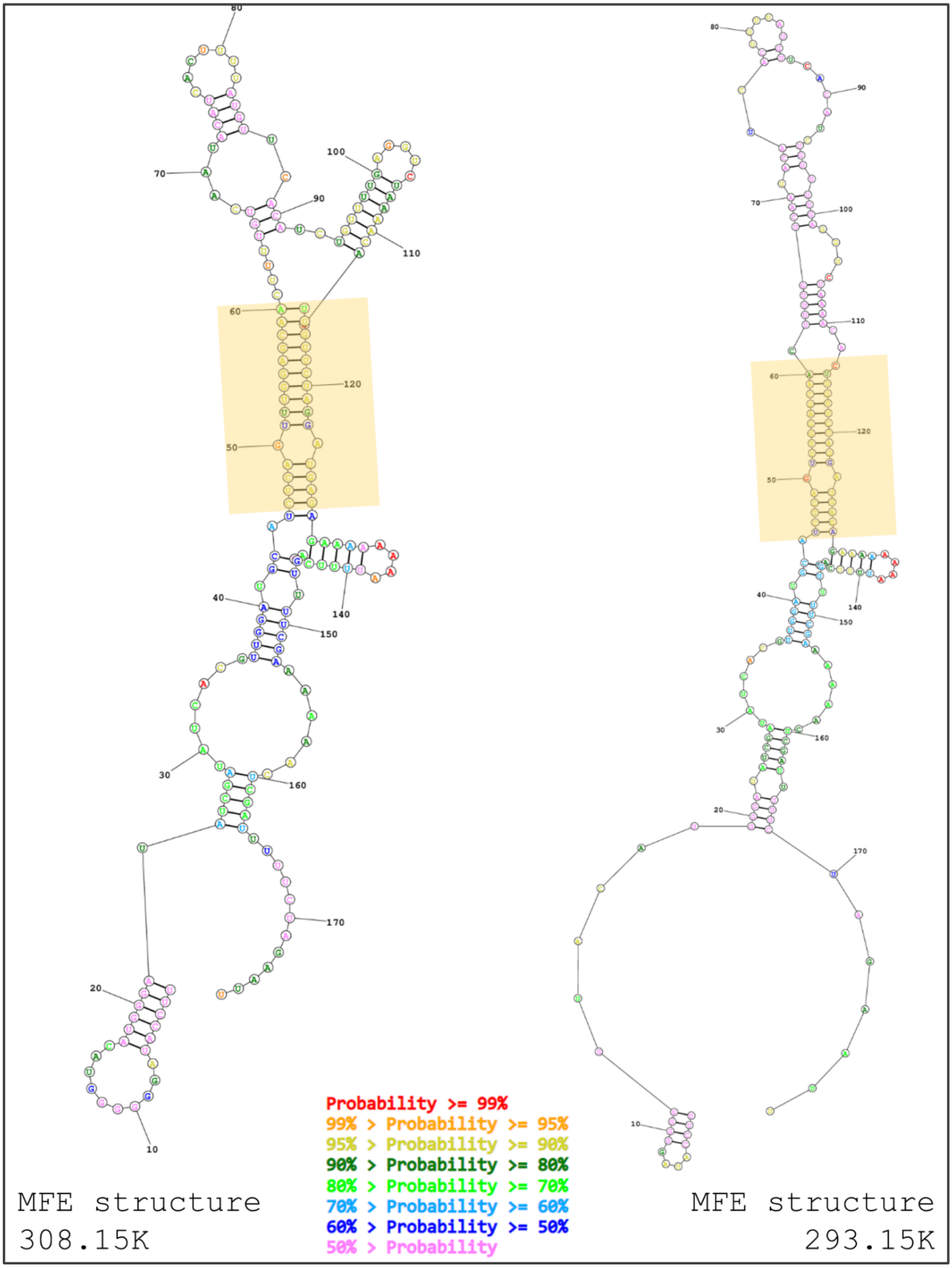

Figure S1. The minimun free energy (MFE) structure predicted for CriTER-A at 308,15 K (35°C) and 293,15 K (20°C). Calculations were performed with RNAStructure 6.3 using default parameters. The region involving high base pairing probabilities is highlighted (shadowed).

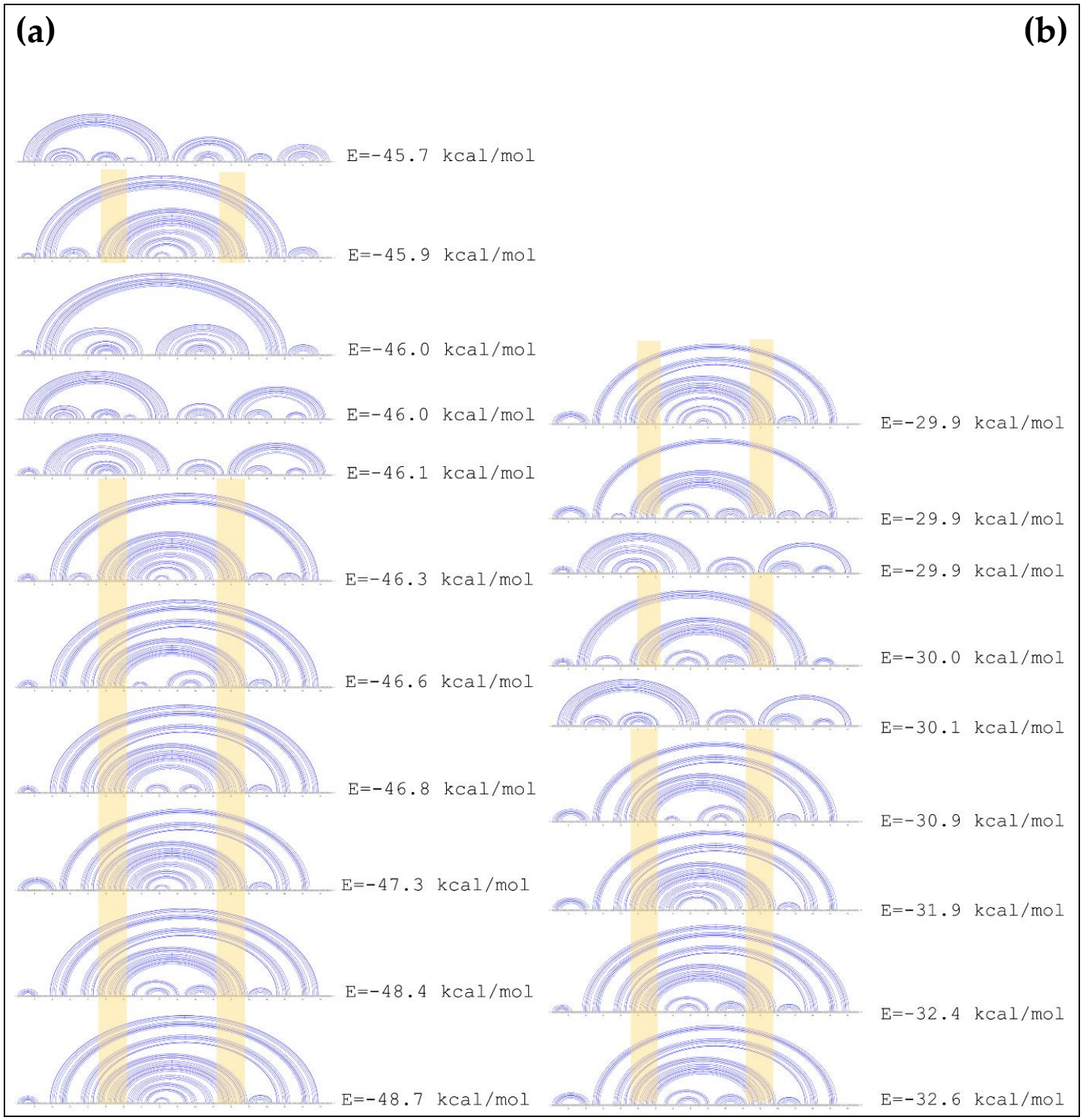

Figure S2. Arc diagram of predicted MFE and suboptimal structures in a energy range of 3 kcal/mol for CriTER-A. Calculations were performed with RNAStructure 6.3 using default parameters at (a) 293,15 K (20°C) and (**b**) 305,15 K (35°C). The region involving high base pairing probabilities is highlighted (shadowed).

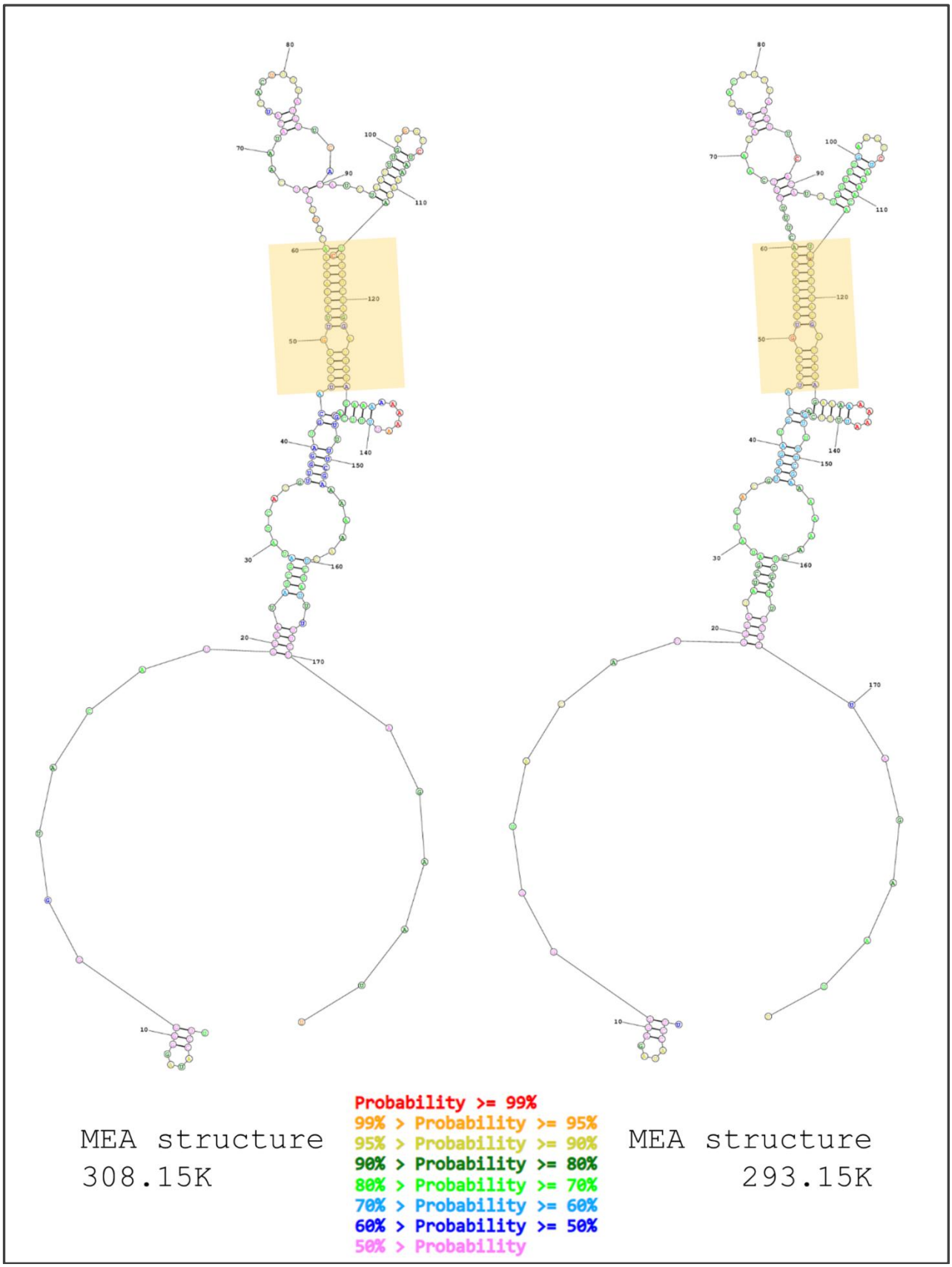

Figure S3. The maximum expected accuracy (MEA) structure predicted for CriTER-A at 308,15 K (35°C) and 293,15 K (20°C). Calculations were performed with RNAStructure 6.3 using default parameters. The region involving high base pairing probabilities is highlighted (shadowed).

CriTER-B. Secondary Structure Prediction

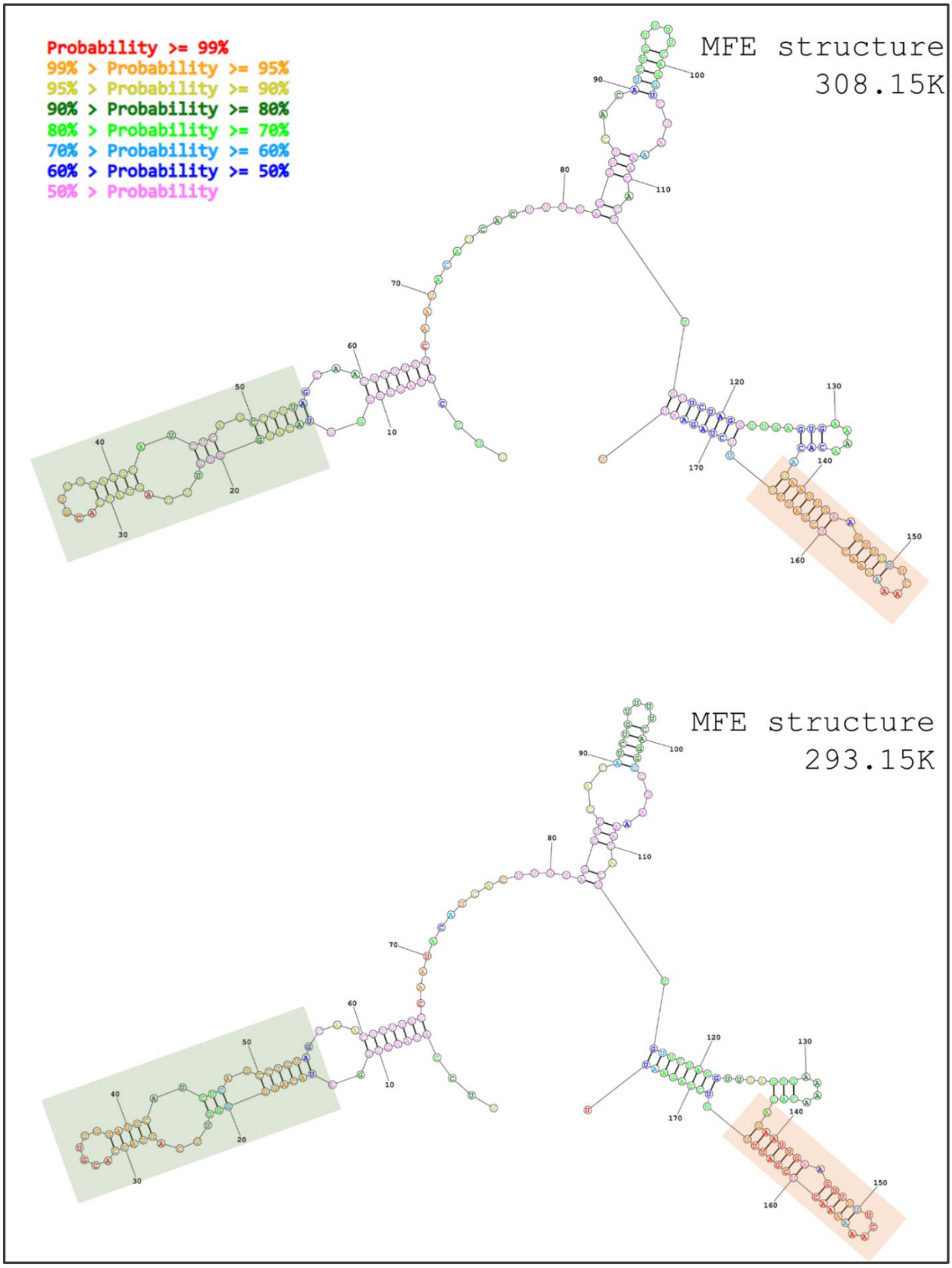

Figure S4. The minimun free energy (MFE) structure predicted for CriTER-B at 308,15 K (35°C) and 293,15 K (20°C). Calculations were performed with RNAStructure 6.3 using default parameters. The two stem-loops involving high base pairing probabilities are highlighted (shadowed).

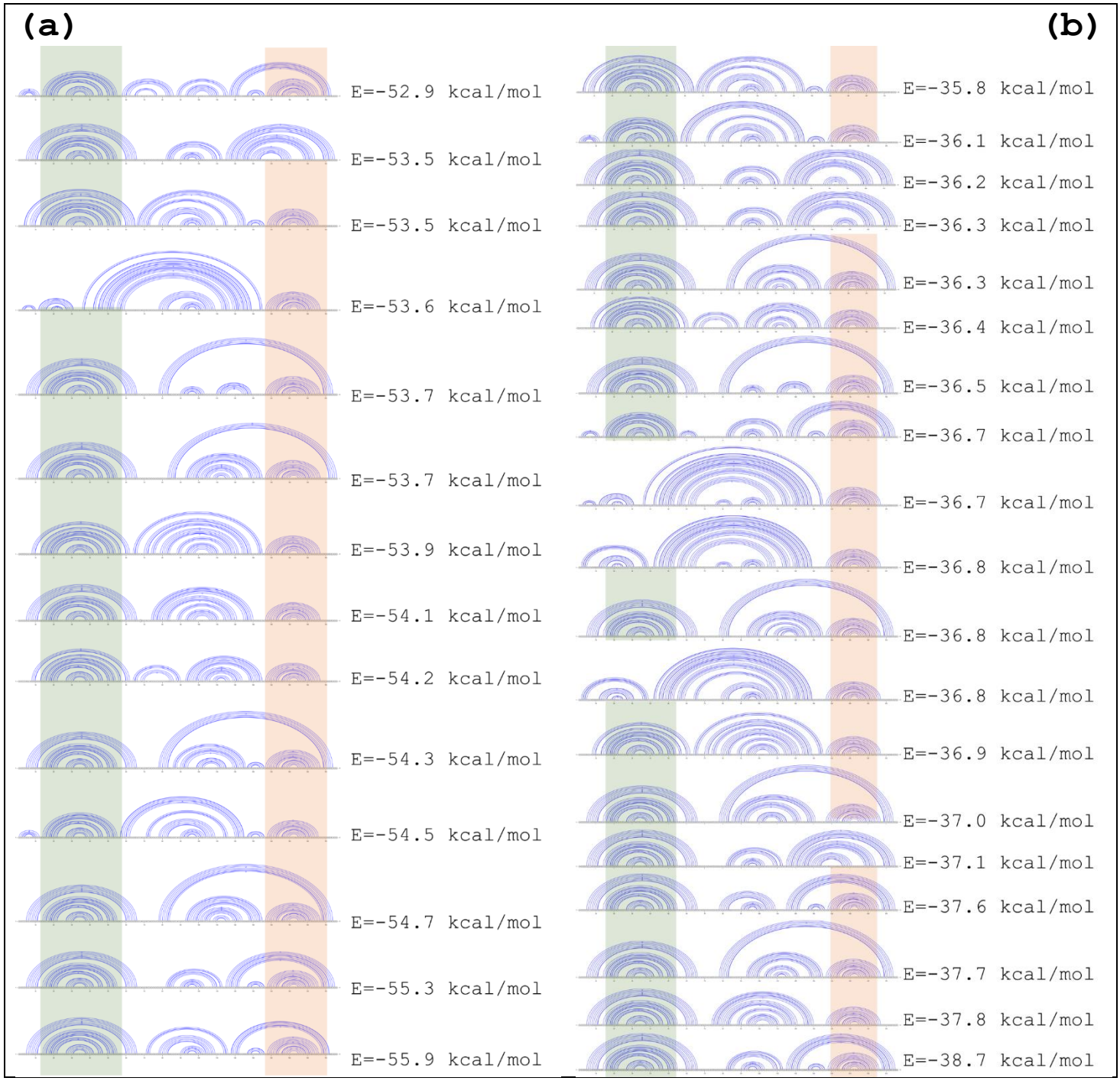

Figure S5. Arc diagram of predicted MFE and suboptimal structures in an energy range of 3 kcal/mol for CriTER-B. Calculations were performed with RNAStructure 6.3 using default parameters at (a) 293,15 K (20°C) and (b) 305,15 K (35°C). The two stem-loops involving high base pairing probabilities are highlighted (shadowed).

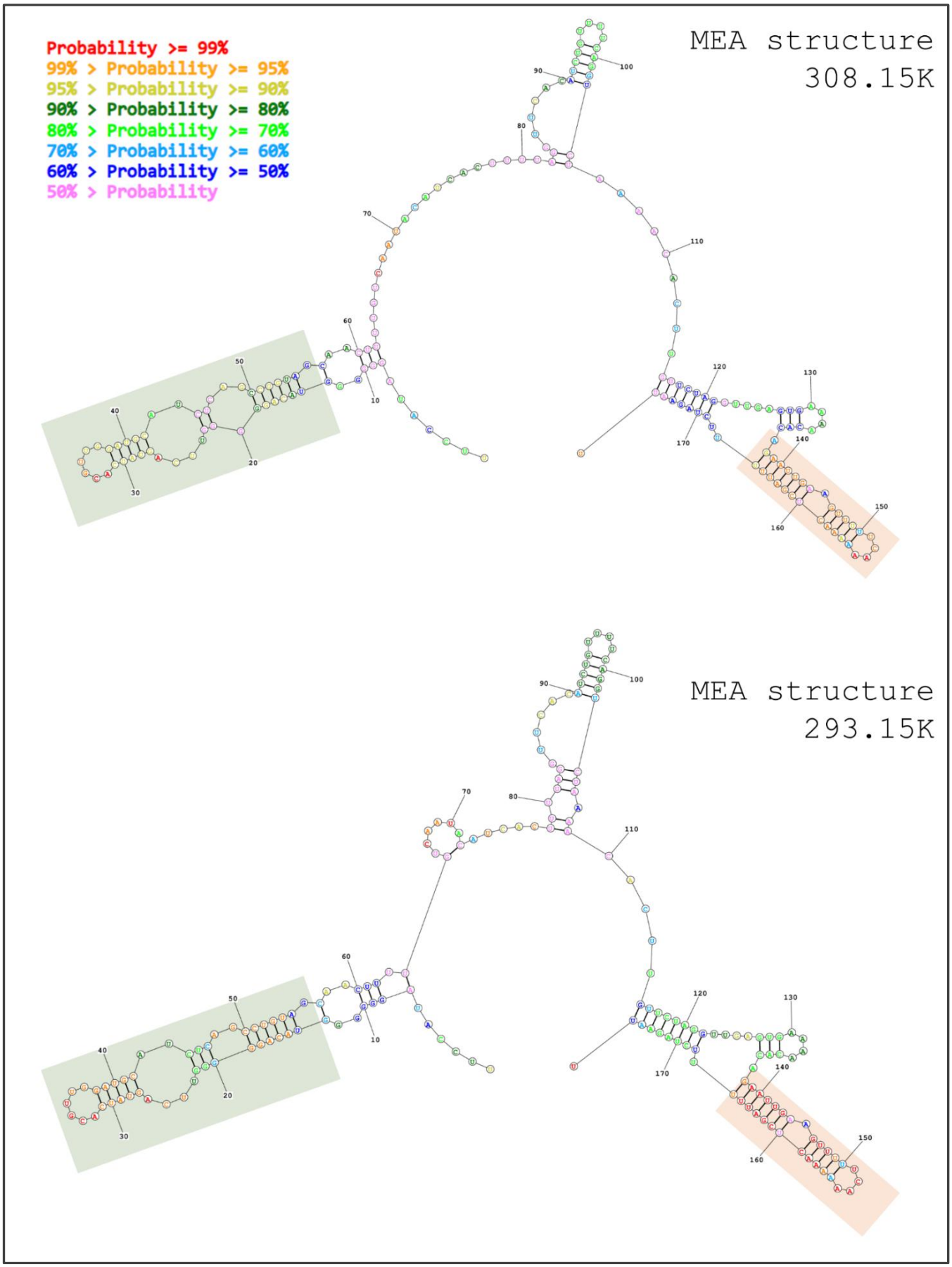

Figure S6. The maximum expected accuracy (MEA) structure predicted for CriTER-B at 308,15 K (35°C) and 293,15 K (20°C). Calculations were performed with RNAStructure 6.3 using default parameters. The two stem-loops involving high base pairing probabilities are highlighted (shadowed).

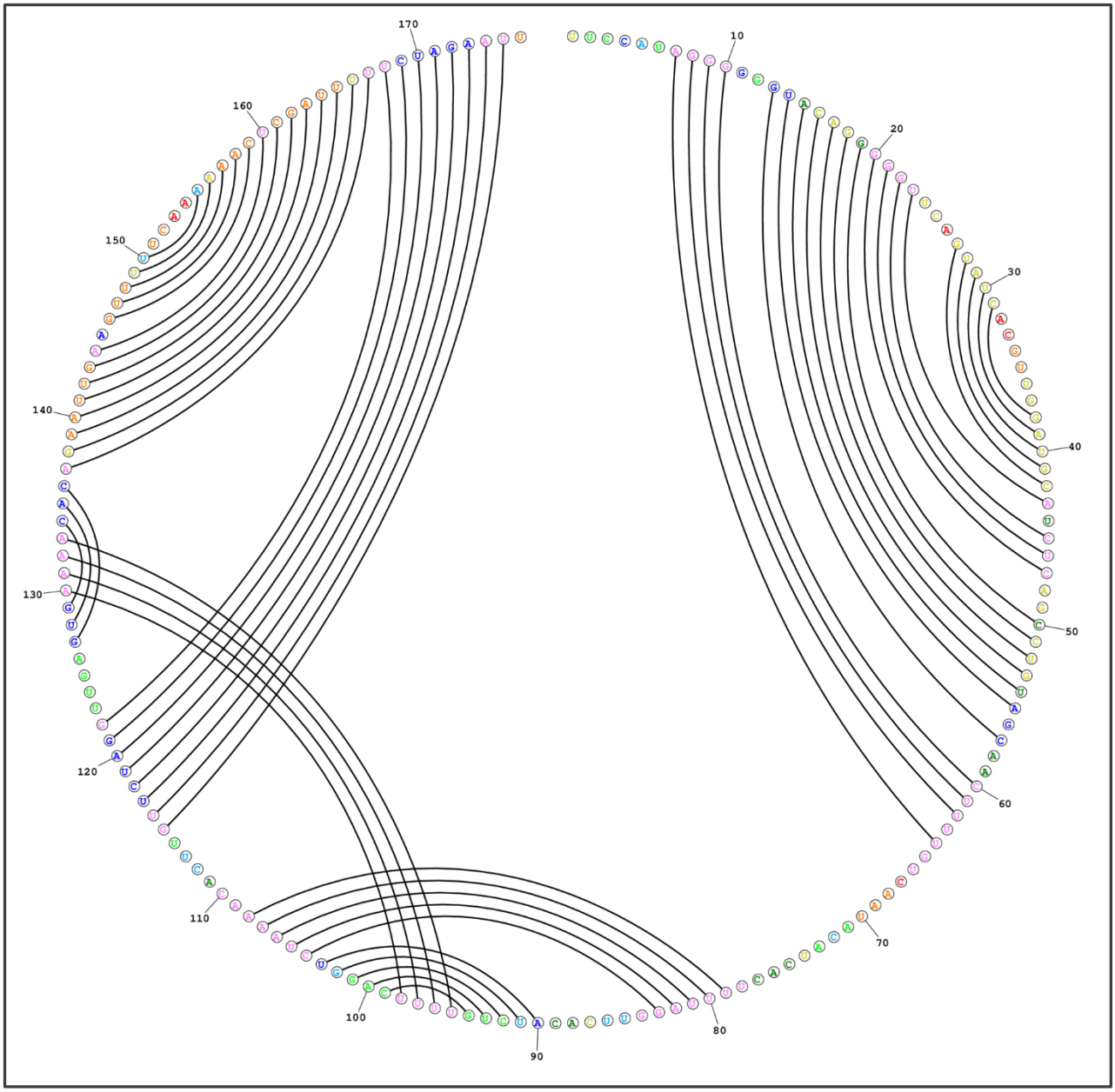

Figure S7. Secondary structure circular representation of probable base pairs of CriTER-B, including putative pseudoknots. Calculations were performed with RNAStructure 6.3 using default parameters.