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3 Computational modeling of an RNA-peptide world
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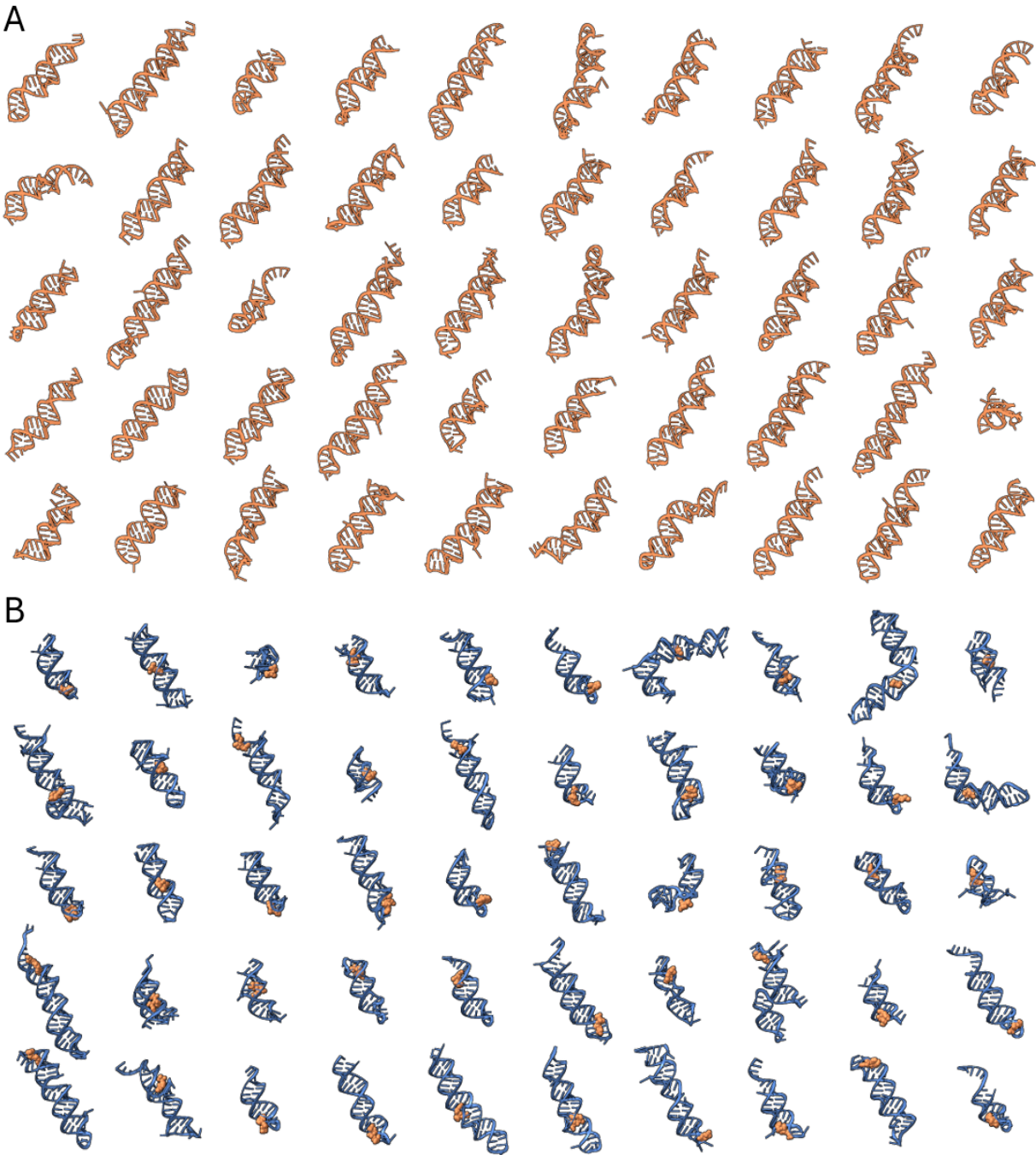


Figure S1. RNA structures evolved in simulations. **A)** RNA-only, **B)** RNA-peptide.

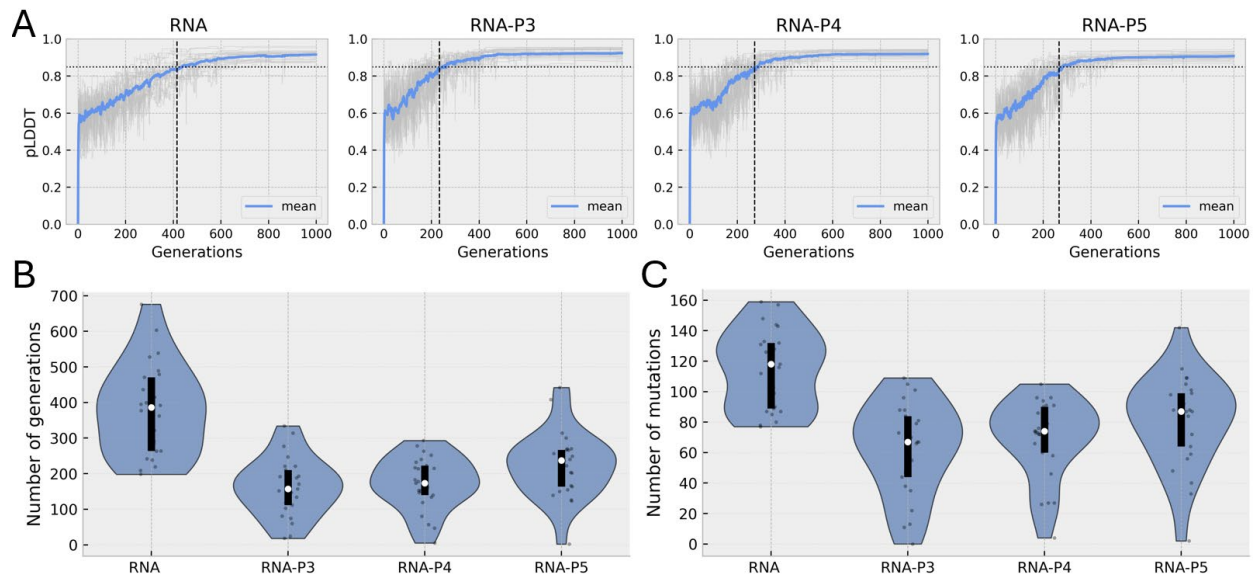


Figure S2. Mean pLDDT of RNA evolving in isolation and peptides. **A)** Mean pLDDT averaged across simulations and individual simulations is shown as gray lines in the background. The horizontal dashed line shows a pLDDT cutoff of 0.85. The vertical dashed lines show when the mean pLDDT reached the cutoff. **B)** Distributions showing the number of generations necessary for the individual simulations to reach the cutoff. **C)** The same for the number of mutations. N=25.

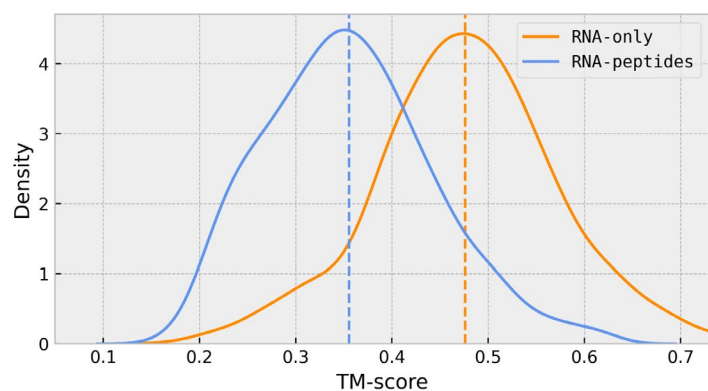


Figure S3. Pairwise TM-score distribution for RNA-only and RNA-peptide structures illustrated in Figures 1A and S1.

Table S1. Frequencies of different mutation types.

Mutation types	Probability
Adenine	0.127
Uracil	0.127
Guanine	0.127
Cytosine	0.127
Single residue insertion	0.127
Single residue deletion	0.127
Partial insertion	0.051
Partial deletion	0.115
Circular permutation	0.013
Partial duplication	0.051
Full duplication	0.006
Randomization	1*

*applied to peptides independently

Movie S1. Example of RNA-peptide evolution. RNA with a maximum length constraint of 80 nt and peptides with 3, 4, or 5 amino acids sampled randomly (RNA-peptide, run049).