

**Table 2.** Distribution of Canonical and Non-Canonical Base Pair Conformations on the Covariation-Based Structure Models of rRNAs in the *T. thermophilus* 30 S and *H. marismortui* 50 S Crystal Structures<sup>†</sup>

Location	Association	Canonical	Non-canonical	Total
Paired*		1241 (96.4%)	46 (3.6%)	1287
	Internal region	717 (98.9%)	8 (1.1%)	725
	Helix ends <sup>a</sup>	384 (93.7%)	26 (6.3%)	410
	Dipair helix <sup>b</sup>	110 (97.4%)	3 (2.6%)	113
	Lonepair helix <sup>c</sup>	30 (76.9%)	9 (23.1%)	39
Unpaired*		80 (17.5%)	378 (82.5%)	458
	Motifs <sup>d</sup>	13 (7.0%)	172 (93.0%)	185
	Unknown	67 (24.5%)	206 (75.5%)	273
Total		1321 (75.7%)	424 (24.3%)	1745

<sup>†</sup> While canonical conformations are defined as WC and Wb conformations of any base pair, the remaining 12 conformations are considered to be non-canonical.

\* Paired and unpaired in the covariation-based structure models.

<sup>a</sup> Helix ends are defined here as the terminal base pairs occurring at the ends of a regular secondary helix.

<sup>b,c</sup> Dipair and lonepair helices are covariation-based helices with two and one base pairs, respectively and, due to the absence of internal base pairs, they are distinguished from the regular secondary helices containing internal base pairs.

<sup>d</sup> Identified motifs are GNRA and UNCG tetraloops, AA.AG@helix.ends, E loops, and tandem GA base pairs, lonepair triloops, K-turns, H-turns, and sticky motifs (see text).