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[†]

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[a]	384 (93.7%)	26 (6.3%)	410
	Dipair helix[b]	110 (97.4%)	3 (2.6%)	113
	Lonepair helix[c]	30 (76.9%)	9 (23.1%)	39
Unpaired[*]		80 (17.5%)	378 (82.5%)	458
	Motifs[d]	13 (7.0%)	172 (93.0%)	185
	Unknown	67 (24.5%)	206 (75.5%)	273
Total		1321 (75.7%)	424 (24.3%)	1745

[†] 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.

[a] Helix ends are defined here as the terminal base pairs occurring at the ends of a regular secondary helix.

[b,c] 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.

[d] 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).