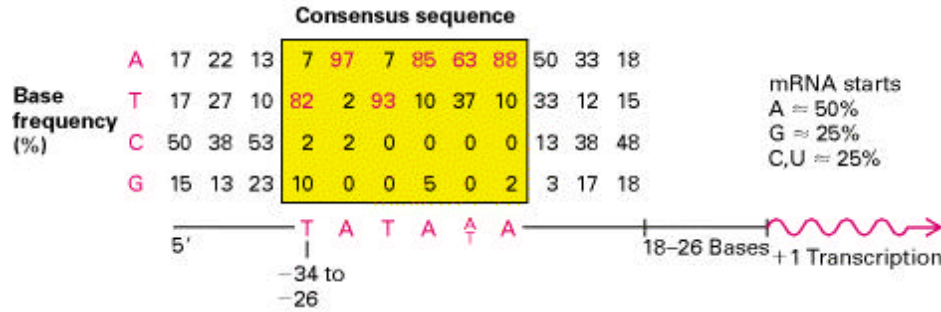


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**Figure 10-30. Comparison of nucleotide sequences upstream of the start site in 60 different vertebrate protein-coding genes.** Each sequence was aligned to maximize homology in the region from -35 to -20. The tabulated numbers are the percentage frequency of each base at each position. Maximum homology occurs over a six-base region, referred to as the TATA box, whose consensus sequence is shown at the bottom. The initial base in mRNAs encoded by genes containing a TATA box most frequently is an A. [See R. Breathnach and P. Chambon, 1981, *Ann. Rev. Biochem.* **50**:349; P. Bucher, 1990, *J. Mol. Biol.* **212**:563.]

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