

Figure 2. Polymerase error rates and the contributions of each fidelity process to mutation rate. The image illustrates the wide ranges over which polymerase nucleotide selectivity, exonucleolytic proofreading, and mismatch repair contribute to spontaneous mutation rates of organisms. Also depicted are the average rates at which purified eukaryotic DNA polymerases generate single-base substitution and single-base deletion errors when performing gap-filling DNA synthesis in vitro. See text for further descriptions. For details on the source and composition of the polymerases used and on their error specificity, see McCulloch and Kunkel (2008 and references therein).