Copy of a printed diagram referenced as "Genetic map of the r II region showing the base pairs in the standard type"

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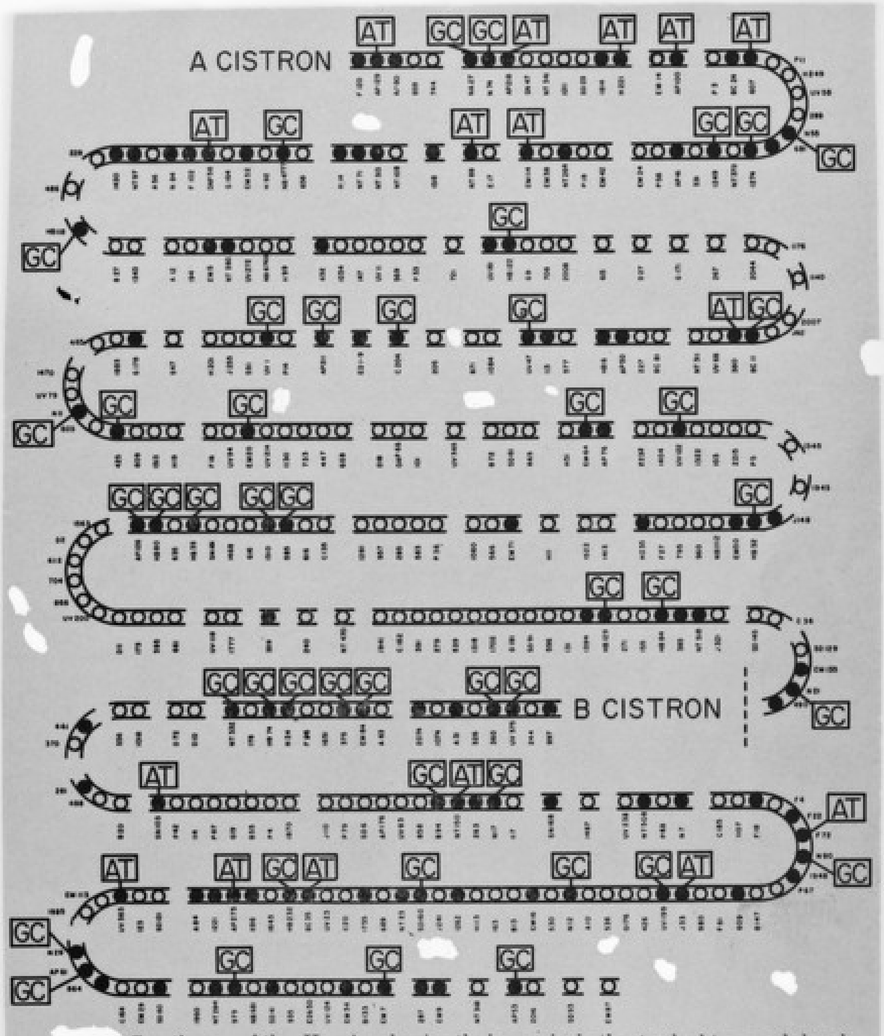

[illegible]-Genetic map of the rII region showing the base pairs in the standard type as deduced from the data of Table 1. Each circle represents a distinct mutational site. Breaks in the map indicate segments as defined by the ends of deletions. While the order of the segments is known, the arrangement of sites within any one segment has not been determined.

● Indicates mutants which are inducible to revert by one or more of the mutagens tested (2AP, BDU, or hydroxylamine). Where reversion was weak or false, no base pair is assigned.

○ Indicates mutants for which no induced reversion was detected with 2AP or BDU.