# Diagram referenced as "Genetic map of the C region of the temperate bacteriophage $\lambda$ [lambda]"

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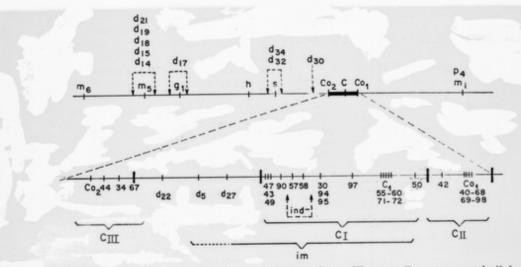
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Genetic map of the C region of the temperate bacteriophage  $\lambda$ . The upper line represents the linkage-group of  $\lambda$ . Symbols refer to various plaque size, plaque type, and host range markers. Symbols d refer to various defective mutations. The C region represented by a thicker line is enlarged in the lower diagram. Figures correspond to various C mutations.  $C_1$  corresponds to the regulator gene; ind $^-$  corresponds to the "non-inducible" mutation. The segment controlling immunity is designed im.

present in the curtures.

This table summarizes the results of several experiments. The three activities are given in per cent of those obtained with fully induced, haploid wild type. i: regulator gene ( $i^+$ : inducible;  $i^-$ : constitutive;  $i^s$ : superrepressed). z and y: structural genes for  $\beta$ -galactosidase and galactoside-permease respectively. F: sex factor of E. coli K12.

	No	Non-induced			Induced		
Genotypes	β-galactosi- dase	actoside- rmease	ctoside- ansace- lase	ulactosi- ase	actoside- ermease	actoside- ransace- ylase	
1 Atatut	< 0.1						

latter were the case, one would expect mutations of the gene which controls the synthesis of the positive agent (the internal inducer) to occur. These mutations would be expressed as a loss of the capacity to synthesize the proteins. They would be recessive to wild type, and mutations of the regulator gene to the constitutive state would not restore the capacity to synthesize the enzymes. Mutations characterized by these properties have not been found in any system.

In contrast, both in an inducible enzyme system and in a lysogenic system, certain mutations within the large been observed to result in a loss of ize the proteins controlled by