

Table I
Structurally Conservative Mutations of the Valine and Isoleucine Residues Shown in Figure 1^b

GPDHase (lobster)	Lobster ^{19,20}	Pig ^{19,20}	Yeast ^{19,20}	<i>B. stearo- thermo- philus</i> ²²
116	Val	Val	Val	Val
92	Ile	Val	a	Ile
144	Val	Val	Val	Ile
117	Val	Ile	Val	Ile
93	Val	Val	Ile	Val
5	Ile	Val	Ile	Ile
30	Val	Ile	a	Val

^a Mutations structurally nonconservative. ^b The sequences are aligned according to the method of Rossmann et al.²³

GPDHases exhibit an additional doublet of the type Ile...Val corresponding to the amino acid residues in positions 91 and 3, respectively, of Figure 1.

On the other hand, again in agreement with our working hypothesis, only one of such doublets (Val³⁰⁵...Val²⁴⁴) occurs in the antiparallel-strand β sheet of lobster GPDHase;¹⁸ interestingly, this doublet is absent in pig²⁰ and *Bacillus stearothermophilus*²² GPDHases due to structurally non-conservative mutations of the valine residue in position 244.

References and Notes

- (1) This work is part 49 of the series; for part 48 see G. M. Bonora and C. Toniolo, *Makromol. Chem.*, in press.
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CORRECTION

"Helical Structures of Poly(D-L-peptides). A conformational Energy Analysis", by F. Colonna-Cesari, S. Premilat, F. Heitz, G. Spach, and B. Lotz, Volume 10, Number 6, November-December 1977, page 1284.

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