## Table referenced as "lonising groups of ribonuclease. (Tanford)"

#### **Contributors**

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o.03 solid The sis of owest least shown in Table I. The numbers of the various types of groups are in agreement with amino acid analysis. The intrinsic pK's are within the range expected for groups lying at the surface, in contact with solvent, except in so far as the carboxyl groups are concerned, about half of these having an

# SUMMARY OF NUMERICAL RESULTS

	Number of groups Predicted			
	Found by titration	by amino acid content	Intrinsi Obsd.	Normal valued
α-Carboxyl	$(1)^{a}$	1	$(3.75)^a$	3.75
$\beta, \gamma$ -Carboxyl	$10.2^{b}$	$10.2^{b}$	See text	4.6
Imidazole	4	4	6.5	6.5 - 7.0
α-Amino	$(1)^a$	1	7.8	7.8
ε-Amino	10	10	10.2	10.1-10.6
$Phenolic^c$	$3^c$	C	∫ 9.95°	9.6
	3° 5	6	Inaccessible	
Guanidyl	4	4	≥12	>12

rather than 10.2 free carboxyl groups. The 0.2 in the predicted value is due to the presence of more than one component in the ribonuclease used. <sup>c</sup> Cf. ref. 14. <sup>d</sup> The normal values have been discussed in several of our preceding papers.

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The curves drawn through the data of Fig. 1 are curves computed with the constants of Table I, and the "phenolic" values of w, i.e., 0.112, 0.093 and 0.061, respectively, at  $\mu = 0.01$ , 0.03 and 0.15. There is a slight discrepancy between calculation